

The frequency of heterozygotes for the seven sequence variants ranged from 3-11% among the 36 individuals tested. Some of the sequence variances appear to occur more commonly in certain racial or ethnic groups. For example, heterozygotes for four sequence variances (at nucleotides 1059, 1428, 3324 and 3375) were detected solely or predominantly in North American Blacks, with heterozygote frequencies of 1/4 or 2/4. The nucleotide 2538 variance was detected solely in North American Whites (4/16) and results in an amino acid exchange (see below). The nucleotide 3397 sequence variance was detected solely in one Japanese individual (of four tested).

The nucleotide 2538 sequence variant results in an aspartic acid vs. glutamic acid substitution at amino acid 740 of the 1024 amino acid protein. This residue lies in the cytoplasmic loop of the α 1 subunit.

The α 1 subunit of Sodium Potassium ATPase maps to chromosome 1p13-p11

The gene for the α 1 subunit of sodium-potassium ATPase has been mapped to chromosome band 1p13-p11 by several techniques. Yang-Feng et al. (10) assigned the ATP1A1 gene to 1p21-cen by Southern analysis of DNA from panels of rodent/human somatic cell hybrid lines. This localization was confirmed and refined by Chehab et al., who showed that the gene for the ATP1A1 subunit is on 1p13-p11 using hybridization to flow-sorted chromosomes and *in situ* hybridization (9).

Chromosome band 1p13-p11 is a site of frequent loss of heterozygosity

The short arm of chromosome 1 is comparatively well investigated for allele loss, especially in breast and colon cancers, however most of these studies are principally concerned with the 1p36 region, and there is comparatively little data on 1p13-p11. The best studies of proximal 1p allele loss are in breast and testicular cancers. These studies show LOH occurs in approximately 15-35% of breast cancers (11,12) and 15-25% of testicular cancers (13). Data from more distal loci on 1p show >25% LOH in

glioma, colon cancer, stomach cancer, ovarian cancer, and liver cancer (14). The LOH observed in this region indicates that other essential genes mapping to the 1p chromosomal arm, and especially to the 1p11 region, which have LOH and for which sequence variances, and therefore heterozygotes for a sequence variance, exist in normal somatic cells of individuals in a population are potential target genes

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Example 12: Ribonucleotide Reductase, M1 subunit (RRM1) - Target Gene VARIA200

25 *Ribonucleotide Reductase is essential for cell growth*

Human ribonucleotide reductase (also called ribonucleoside diphosphate reductase) is essential in dividing cells for the production of deoxyribonucleotides prior to DNA synthesis in S phase. Ribonucleotide reductase catalyzes the reduction of all four

ribonucleoside diphosphates to the corresponding deoxyribonucleoside diphosphates by replacing the 2' hydroxyl moiety of ribose with a hydride ion to form deoxyribose; these reactions constitute the first committed steps in the creation of DNA precursors (deoxyribonucleotides), and are therefore tightly regulated by allosteric nucleotide binding sites on the M1 subunit (2,3). The enzyme is an 2 2 tetramer apparently conserved in all prokaryotes and eukaryotes (1). The two subunits, M1 and M2, are both required for enzyme activity. The RRM2 subunit contains the catalytic site, while the RRM1 subunit provides an indispensable allosteric function. (See pages 758-763 of Biochemistry by C.K. Mathews and K.E. van Holde, Benjamin/Cummings Publishing Biochemistry, Company, Redwood City, 1990 for a fuller account of ribonucleotide reductase function.)

Both ribonucleotide reductase subunits are expressed in all proliferating cells but are generally nondetectable in quiescent cells. Ribonucleotide reductase subunit M2 is the target of several antineoplastic compounds, including hydroxyurea. Hydroxyurea is used in the chemotherapy of a variety of myeloproliferative disorders (4). It acts by reversibly destroying a tyrosyl free radical in the catalytic site of the M2 subunit (3). Hydroxyurea and other ribonucleotide reductase poisons are specific for the S phase of the cell cycle, resulting in growth arrest at the G1-S boundary and apoptotic death in tumor cells (5). Exposure of cell cultures to hydroxyurea results in selection of cells expressing high levels ribonucleotide reductase, demonstrating that ribonucleotide reductase is required for these cells to grow (6).

The human ribonucleotide reductase gene has sequence variances

The cDNA sequence of the human ribonucleotide reductase M1 subunit has been published by two groups (7,8). We undertook a systematic search for DNA sequence variance in the cDNA of the M1 subunit by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed using

the sequence of Parker et al. (GENBANK accession X59543; see ref. 7). SSCP analysis revealed 4 sequence variances, and subsequent DNA sequence analysis confirmed that nucleotides 1037 (C vs. A), 2410 (A vs. G), 2419 (A vs. G) and 2717 (T vs. A) vary as shown in the Target Summary Table. (The sequence variance at nt 1037 was previously noted by Parker et al., ref. 7.) Also, DNA sequencing revealed an insertion/deletion sequence variance: the 9 consecutive T nucleotides between positions 2724 and 2732 (numbering from ref. 7) were augmented in some cDNAs by a tenth T. (This sequence variance is designated T9 vs. T10 in the Target Summary Table.)

Both alleles at nt 1037 were detected in North American Whites, Hispanics, Chinese, Japanese, Arabs and Indians. Similarly, both alleles of the sequence variance at nt 2410 were detected in virtually all tested populations: North American White, North American Black, Hispanic, Chinese, Arab and Indian. In contrast, the sequence variances at nt 2419 and 2717 were prevalent in North American Blacks, Hispanics, Chinese, and Japanese, but not North American Whites. The insertion/deletion sequence variance at nt 2724 was only studied in four individuals so no firm conclusions can be drawn regarding population distribution, however it appears to be in linkage disequilibrium with the 2419 and 2724 sequence variances.

The human ribonucleotide reductase gene maps to chromosome 11p15.5

The gene for human ribonucleotide reductase has been mapped to band 11p15.5 by several techniques. Initially the gene was localized by Southern hybridization analysis of human X rodent somatic cell hybrids and by chromosomal *in situ* hybridization (9). Subsequently RRM1 has been placed on a yeast artificial chromosome (YAC) physical map of chromosome 11p15 (10). The precise physical localization of the RRM1 gene facilitates interpretation of LOH results at adjacent polymorphic markers (see below).

Chromosome band 11p15.5 is a site of frequent loss of heterozygosity

The short arm of chromosome 11 is the site of several tumor suppressor genes, including the WT1 gene and the Beckwith-Weidemann syndrome gene. As a result there are many studies of LOH in 11p15.5, particularly focusing on breast, cervix, kidney, liver, lung, ovarian, stomach and testicular cancers. These studies show that the 11p15.5 band of chromosome 11 is frequently reduced to one copy (11-28). For example, LOH occurs in approximately 13-33% of breast cancers (11-13), 14-42% of cervical cancers (14), 0-50% of liver cancers (16), 0-80% of lung cancers (17-19), 18-54% of ovarian cancers (20,21), 0-71% of stomach cancers (22) and 0-50% of testicular cancers (23,24). Other studies show that 11p15.5 LOH may also be frequent in bladder cancer (25), esophageal cancer (26), some leukemias (27) and sarcomas (28). Many deletions in the 11p15.5 region span relatively short chromosomal segments (2 - 10 megabases; see ref. 17).

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Example 13: Thymidylate Synthase (TS) - Target Gene VARIA250*Thymidylate Synthase is essential for cell growth*

5 Human thymidylate synthase (TS) catalyzes the formation of thymidine monophosphate (dTMP) from deoxyuridine monophosphate (dUMP) by transfer of a methyl group from N5,N10-methylenetetrahydrofolate to carbon 5 of dUMP. This is the sole *de novo* pathway to dTMP, an essential precursor for DNA synthesis. TS also plays an important role in balancing the four nucleotide precursors for DNA polymer synthesis (1). Thus TS is an attractive target for antiproliferative drugs. (See Biochemistry by C.K. Mathews and K.E. van Holde, Benjamin/Cummings Publishing Company, Redwood City, 1990, pages 763-768, for a fuller account of thymidylate synthase function.)

15 Like some other growth associated genes involved in DNA synthesis, thymidylate synthase is expressed in proliferating cells at 20-40 fold higher levels than in quiescent cells. Increased expression occurs at the G1-S transition of the cell cycle when quiescent cells are stimulated with serum. Levels of thymidylate synthase are finely controlled by autoregulatory feedback loops wherein TS protein regulates the transcription, stability and translational efficiency of TS mRNA (2). Transcription increases by only 2-4 fold, so posttranscriptional events constitute the predominant regulatory mechanisms (3). One mechanism of 5-FU resistance is increased expression of TS Mrna.

25 Thymidylate synthase is the target of 5-fluorouracil (5-FU), a potent antineoplastic compound. Once inside cells 5-FU is ribosylated and phosphorylated to 5-fluoro-2'-deoxyuridine 5'-monophosphate (F-dUMP), which acts as an inhibitory transition state analog of TS when bound in the presence of the enzyme's second substrate, N5,N10-methylenetetrahydrofolate. (5-FU is also incorporated into both DNA and RNA,

augmenting its toxicity.) 5-FU induces partial responses in 10-30% of patients with a variety of cancers, including metastatic breast and gastrointestinal tract cancers (4). While 5-FU is a potent antiproliferative agent in tissue culture cells, as with most antineoplastic drugs, its clinical utility is limited by lack of discrimination between normal cells and tumor cells: common toxic effects include stomatitis, diarrhea, bone marrow suppression, hair loss and occasionally cardiac and neurologic symptoms.

The human thymidylate synthase gene has sequence variances

The sequence of a human thymidylate synthase cDNA was determined by Takeishi et al. (5), who later determined the genomic sequence as well (6). We undertook a systematic search for DNA sequence variance by analysing 36 unrelated individuals using the single strand conformation polymorphism. Primers were designed using the sequence of Takeishi et al. (5). SSCP analysis revealed 3 DNA fragments having sequence variances, and subsequent DNA sequence analysis showed that nucleotides 1066 (C vs. T), 1136 (A vs. G) and 1497 (A vs. T) vary among normal individuals as shown in the Target Summary Table. All three sequence variances are in the 3' untranslated region of the gene. The nucleotide 1066 and 1497 sequence variances are in complete linkage disequilibrium in the 36 individuals examined. Both alleles of all three sequence variances were detected in North American Whites, North American Blacks, Chinese, Japanese, Arabs and Indians.

Another TS sequence variance has been described by Berger and colleagues (7-9). They detected a T to C change at nucleotide 276 of the TS gene, resulting in the substitution of histidine for an evolutionarily conserved tyrosine at residue 33 of TS protein. So far the histidine allele has been detected in only one cell line, HCT116 (7). The rare his-33 form of the protein is 3-4 fold more resistant to FdUrd than the tyr-33 form, due to an 8 fold lower catalytic efficiency (kcat), suggesting that histidine at residue 33 perturbs the structure of the TS active site (9)

The human thymidylate synthase gene maps to chromosome 18p11.32

5 The gene for human thymidylate synthase was initially mapped to the long arm of chromosome 18 (18q21.31-qter) by somatic cell hybrid analysis (10), however two subsequent reports place the gene in band 18p11.32 using fluorescence *in situ* hybridization (11,12).

Chromosome band 18p11.32 is a site of loss of heterozygosity

10 The long arm of chromosome 18 contains the DCC (deleted in colon cancer) candidate tumor suppressor gene and has been well studied in a variety of tumors. The short arm (18p), where TS apparently resides, has not been studied as extensively. The available data suggests there is LOH in approximately 45% of colon cancers (13) and 25-30% of cervical (14), head and neck (15), lung (16) and ovarian (17) cancers and sarcomas.

15 LOH has also been described in breast, brain, esophagus, kidney and prostate cancers (0-15%). 18p has not been studied for allele loss in several other major cancers, including bladder, leukemia, lymphoma, liver, pancreas, stomach and testicular cancers.

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Example 14: Cytidine Triphosphate Synthetase (CTPS) - Target Gene VARIA260

Cytidine Triphosphate Synthetase is essential for cell growth

Human cytidine triphosphate synthetase catalyzes the glutamination of UTP to form CTP. The reaction is: $UTP + ATP + \text{glutamine} \rightarrow CTP + ADP + P_i + \text{glutamate}$. This is the rate limiting step in the synthesis of cytidine nucleotides from both the *de novo* and uridine salvage synthesis routes (see ref. 1 and references therein). CTPS also plays a vital regulatory function in balancing nucleotide pools for DNA polymer synthesis; it is allosterically regulated by CTP (negatively) and GTP (positively).

There is compelling evidence that CTPS is essential for cell survival:

CTPS is evolutionarily conserved in yeast and bacteria, with a high degree of amino acid identity in regions mediating allosteric regulation and catalysis (1-

3). (Another example: the human and hamster enzymes are identical in length and 98% amino acid identical over 591 amino acids.)

Mutant hamster cells lacking functional CTPS need exogenous cytidine to survive (3).

5 There is no known human deficiency disease of CTPS.

CTPS function is increased in proliferating cells (4).

10 Thus CTPS is an attractive target for antiproliferative drugs. Cyclopentyl cytosine (CPE-C) is a synthetic cytidine analog in which a cyclopentyl group replaces the furan ring of the ribose sugar. CPE-C has antineoplastic and antiviral effects in animal models (5). The drug is kinased intracellularly to the triphosphorylated nucleotide form (CPE-CTP). Exposure of cells to CPE-C leads to rapid depletion of CTP pools, as a result of inhibition of CTPS by CPE-CTP (6,7). Upregulation of CTP synthetase, or loss of negative allosteric modulation by CTP is associated with resistance to the cancer chemotherapy drugs arabinosyl cytosine (ara-C), 5-fluorouracil and other cytotoxic nucleoside analogs as well as alkylating agents (3).

The human cytidine triphosphate synthetase gene has sequence variances

20 The sequence of a human cytidine triphosphate synthetase cDNA was determined by Yamauchi et al. (1), who later determined the genomic sequence as well (2). We undertook a systematic search for DNA sequence variance by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed using the sequence of Yamauchi et al. (1). SSCP analysis revealed 3
25 DNA fragments having sequence variances, and subsequent DNA sequence analysis showed that nucleotides 576 (A vs. G), 2093 (C vs. T) and 2135 (G vs. A) vary among normal individuals as shown in the Target Summary Table. The nucleotide 576 sequence variance is a silent substitution in the coding region, while the latter two sequence variances are in the 3' untranslated region of the cDNA. All three sequence

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variances were detected at low frequency in the panel of 36 individuals (3-8%), however all but one of the heterozygotes is Asian, and it seems likely that a larger survey of Asian populations would show higher allele frequencies in Chinese and other groups. For example among the four Chinese in the panel two (50%) are heterozygous for the residue 2135 sequence variance, and one (25%) is heterozygous for the nt 576 sequence variance. Also, the one Cambodian in the panel is heterozygous for both the 2093 and 2135 sequence variances.

The human cytidine triphosphate synthetase gene maps to chromosome 1p34.1

The gene for human cytidine triphosphate synthetase has been mapped to 1p34.1 by somatic cell hybrid analysis (2).

Chromosome band 1p34.1 is a site of frequent loss of heterozygosity

The short arm of chromosome 1 is comparatively well investigated for allele loss, especially in breast and colon cancers. The 1p35-32 and 1p22-13 regions flank 1p34.1 and are the best available markers for LOH on 1p. Studies of these regions show 30-50% LOH frequency in breast cancer (8-12), 41-75% in glioma (a brain cancer subtype) (13), 20-40% in colon cancer (14,15), ~50% in stomach cancer (16), ~20% in lung cancer (17) and 20-30% in ovarian cancer (18). High frequency LOH has been detected in several uncommon cancers such as pheochromocytoma (50-86%) and neuroblastoma (~50%). Most other common cancers have not been adequately investigated to assess LOH frequency in this region.

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Example 15: Cysteinyl tRNA Synthetase (CARS) - Target Gene VARIA301

The human cysteinyl tRNA synthetase gene is essential for cell survival

Cysteinyl-tRNA synthetase (CARS) catalyzes ATP dependent covalent attachment of

cysteine to its cognate tRNA to form cysteinyl-tRNA. In the absence of cysteinyl-tRNA, protein synthesis is blocked. Since Cysteinyl-tRNA synthetase is a single copy gene in man, inhibition of its function is expected to be cell lethal. This has been shown for other tRNA synthetases (summarized above).

5

The human cysteinyl-tRNA synthetase gene and mRNA have sequence variances

10

A human cDNA encoding cysteinyl tRNA synthetase (CARS) was cloned based on the similarity of a human expressed sequence tag (EST) to *E. coli* cysteinyl tRNA synthetase (1). The published human CARS cDNA is 2048 nucleotides in length and includes a 30 nucleotide 5' untranslated region followed by an open reading frame of 1914 nucleotides and a 3' untranslated region of 134 nucleotides (1). An EMBL/GENBANK submission (accession # L06845) by the authors of ref. 1 includes a 3' untranslated region 423 nucleotides longer than the published sequence, but lacks 19 consecutive A nucleotides after position 2029 (making a net increase of: $423 - 19 = 404$ nucleotides, and a composite cDNA of: $2048 + 404 = 2452$ nucleotides in length. We have confirmed the existence of 2452 nt transcripts by PCR amplification of reverse transcribed mRNA.) We designed primers as shown on the annotated cDNA sequence and screened the composite 2452 nt cDNA for sequence variance in 36 unrelated individuals by the single strand conformation polymorphism (SSCP) technique. Two sequence variances were identified. One of the sequence variances, located in the 5' untranslated region, was below the desired level of 20% heterozygosity. The other sequence variance is a C vs. T transition near the 3' end of the coding sequence at nucleotide 1739 (see annotated sequence).

15

20

25

The human cysteinyl tRNA synthetase protein has sequence variances

The deduced amino acid sequence of the human CARS gene encodes a protein of 638 amino acids which probably functions as a monomer, by analogy to related synthetases. The deduced protein contains two sequence motifs, HIGH (residues 64-

67) and KMSKS (residues 406-410), which define Class I synthetases (see ref. 2 for background information on tRNA synthetases). These two conserved motifs form an ATP binding fold (the Rossman fold) in the amino terminal half of the protein. Cytosine at nucleotide 1739 encodes proline at residue 622 of the protein, while
5 thymine at nucleotide 1739 encodes leucine. The pro/leu amino acid sequence variance is a mere 16 residues from the C terminus of the protein. The C-terminal portion of CARS, by analogy to other class I synthetases, contains the tRNA binding site.

10 *Frequency of CARS heterozygotes*

The frequency of heterozygotes for the nucleotide 1739 sequence variance is ~45-50% in all major racial groups surveyed (see accompanying table), including North American Whites (8/15=53%), North American Blacks (2/4=50%), Chinese
15 (2/4=50%), Swedish (127/344=37%) and Japanese (1/4=25%). The wide population distribution of both alleles suggests that other population groups will also have a high frequency of heterozygotes.

20 *Gene Mapping of CARS to 11p15.5*

Human CARS cDNA has been mapped to chromosome 11p15.5 by screening human X Chinese hamster somatic cell hybrids informative for all human chromosomes, and by fluorescence *in situ* hybridization (3). Both mapping techniques were conclusive in showing only one locus for human CARS. Detailed physical maps of 11p15.5 have
25 subsequently allowed precise localization of the CARS gene relative to other DNA markers (4).

LOH at 11p15.5 is well documented in many cancer types

The short arm of chromosome 11, and particularly the 11p15.5 region, is deleted in a

variety of human cancers, including (but not limited to) ovarian (18 - 50% LOH), non-small cell lung (22 - 71%), breast (12 - 33%), bladder (40 - 50%), esophageal (18 - 40%) and testicular cancers (18 - 66%) (refs. 5-12). Many deletions in the 11p15.5 region span relatively short chromosomal segments (2 - 10 megabases; see ref. 8).
5 Using the specific variances identified in the CARS gene as markers for heterozygosity, we have determined that LOH occurs in 10/20 ovarian cancers (50%) and 10/52 non-small cell lung cancers (19%).

Assays for human CARS inhibitors

10 There is no published work on the protein encoded by the putative human CARS cDNA, nor on any other eukaryotic CARS protein, however the extensive characterization of other Class I synthetases from both prokaryotes and eukaryotes provides a template for modeling the structure of human CARS. (For an example of
15 how this can be done see ref. 14, in which the three dimensional structure of human alanyl-tRNA synthetase has been modeled up to amino 249 by neural net software and multiple alignments of partial and complete human AARS sequences with heterologous prokaryotic class II synthetases for which crystal structures exist.) With
20 respect to the C-terminal location of the variant amino acid residue in human CARS, it is worth noting that single amino acid substitutions in the C-terminal region of alanyl tRNA synthetase can have greater than 100 fold effects on catalytic activity (15).

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Example 16: Glutamyl-Prolyl tRNA Synthetase (EPRS): - Target Gene VARIA300

The human glutamyl-prolyl tRNA synthetase gene is essential for cell survival

Glutamyl-prolyl-tRNA synthetase (EPRS) catalyzes ATP dependent covalent attachment of glutamine and proline to their cognate tRNAs to form glutamyl-tRNA and prolyl-tRNA. In the absence of glutamyl-tRNA or prolyl-tRNA, protein synthesis is blocked. Since glutamyl-prolyl-tRNA synthetase is a single copy gene in man, inhibition of its function is expected to be cell lethal. This has been shown for other tRNA synthetases (summarized above).

The human glutamyl-prolyl tRNA synthetase gene, mRNA and protein have sequence variances

A human cDNA encoding glutamyl-prolyl tRNA synthetase (EPRS) was initially misidentified as glutaminyl-tRNA synthetase (1) based on misleading sequence alignments with bacterial and yeast glutaminyl-tRNA synthetase (2). Subsequently, biochemical studies of the protein encoded by a *D. melanogaster* gene ~70% identical to the human gene demonstrated glutamyl (not glutaminyl) tRNA synthetase activity, and also showed that a single gene encodes both glutamyl- and prolyl-tRNA synthetases in the fly (3). These observations eventually led to the realization that

human EPRS is also a single polypeptide containing two synthetases (2). The aminoacyl tRNA synthetases are divided into two classes (see *Background on tRNA Synthetases*, above). Glutamyl-tRNA synthetase belongs to Class I while Prolyl-tRNA synthetase belongs to class II. Thus the two halves of EPRS evolved independently and likely represent an evolutionarily recent fusion. The published human EPRS cDNA is 4,586 nt long and includes a 5' untranslated region of 58 nt followed by an open reading frame of 4320 nt and a 3' untranslated sequence of 208 nt (1). The gene encodes a polypeptide of 1440 amino acids. The glutamyl-tRNA synthetase activity is encoded by an imprecisely defined segment at 5' end of the gene probably spanning at least amino acids 105-426, while the prolyl-tRNA synthetase activity is encoded by a segment likely including residues 942-1369 at the 3' end of the gene (2). The two synthetase moieties are connected by a central domain of unknown function. It has been speculated that the central domain may attach the enzyme to the cytoskeleton or to other aminoacyl-tRNA synthetases in a multienzyme complex (2, 3).

The human glutamyl-prolyl-tRNA synthetase gene and mRNA have sequence variances

We designed primers and screened the 4586 nt cDNA for sequence variance in 36 unrelated individuals by the single strand conformation polymorphism technique. Seven sequence variances were identified, four located in the coding sequence and three located in the 3' untranslated region. As shown on the Annotated Glutamyl-Prolyl tRNA Synthetase cDNA Sequence and in the Target Summary Page, the sequence variance nucleotides are 2520 (C vs. A), 2944 (G vs. A), 2963 (C vs. T), 2969 (A vs. G), 3247 (A vs. G), 4459 (G vs. A) and 4506 (G vs. A). The sequences flanking the alternate allelic forms and their frequencies of occurrence are shown on the Target Summary Page. Less than 10% of individuals surveyed are heterozygous for sequence variances at 2520, 2944 and 2963. Heterozygotes for the other 4 sequence variances occur more frequently and appear to be widely distributed in the surveyed populations (see below).

The human glutamyl-prolyl tRNA synthetase protein has sequence variances Three nucleotide sequence variances, at 2520, 2963 and 2969, alter the amino acid coding sequence of EPRS at residues 821 (pro/his), 969 (his/tyr) and 971 (ile/val). The residue 821 his and 969 tyr alleles are relatively rare, with fewer than 10% heterozygotes in the surveyed populations. The more common residue 971 sequence variance lies in the PRS domain of the protein, near one of the widely conserved defining motifs for class II tRNA synthetases.

EPRS heterozygotes are frequent in non-Asian populations. While the overall frequency of residue 971 heterozygotes is 8/36 (24%), the frequency of heterozygotes varies among different populations. For example, there are no heterozygotes among 10 Asians surveyed (Chinese, Japanese, Filipino and Korean), while 8/26 (31%) of non-Asians, including North American Whites, Blacks and Hispanics, are heterozygotes.

15

The EPRS Gene Maps to 1q41-q42

Human EPRS cDNA has been mapped to chromosome 1q41-42 by screening human X Chinese hamster somatic cell hybrids informative for all human chromosomes, and by fluorescence *in situ* hybridization (3). Both mapping techniques were conclusive in showing only one locus for human EPRS.

20

Loss of heterozygosity at 1q41-42 is documented in several cancer types. 17-25% of breast cancers have allele loss in the 1q41-q42 region (4, 5), 29-46% of colon cancers (6, 7) and 17-26% of cervical cancers (8). One report describes 27% LOH in stomach cancer (9). One or two studies of brain, esophageal, kidney, liver and ovarian cancers also report LOH. No studies of LOH in the 1q41-q42 region have been reported in bladder, endocrine, head and neck, lung, or pancreas cancers or in leukemia or lymphoma.

25

Antisense considerations The sequence variances at 2963 and 2969 are close enough that a 20-mer antisense oligonucleotide could easily span them. Such an oligonucleotide should afford greater allele discrimination than is possible with a single nucleotide difference. However, the 2963 sequence variance is fairly rare (<10% heterozygotes) and not in linkage disequilibrium with the 2963 sequence variance, so there are more than two haplotypes in the populations tested.

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Example 17: Alanyl-tRNA Synthetase (AARS) - Target Gene VARIA304

The human glutamyl-prolyl tRNA synthetase gene is essential for cell survival

5 Alanyl-tRNA synthetase (AARS) catalyzes ATP dependent covalent attachment of alanine to its cognate tRNA to form alanyl-tRNA. In the absence of alanyl-tRNA, protein synthesis is blocked. Since alanyl-tRNA synthetase is a single copy gene in man (see below) inhibition of its function is expected to be cell lethal. This has been shown for other tRNA synthetases (summarized above).

The human alanyl-tRNA synthetase gene and mRNA have sequence variances

10

A human cDNA encoding alanyl tRNA synthetase (AARS) was cloned by Shiba et al. (1) using cross species PCR: AARS sequences from four evolutionarily distant species were compared and primers were designed to conserved regions specific to AARS. The cloned human cDNA is 3344 nt in length and includes a 110 nt 5' untranslated region, an open reading frame of 2904 nt encoding a 968 residue polypeptide, and a 3' untranslated region of 330 nt (ref. 1; Genbank accession D32050).

15

We designed primers. The 3344 nt cDNA was screened for sequence variance in 36 unrelated individuals by the single strand conformation polymorphism (SSCP) technique. One sequence variance was identified, a C vs. T transition at nucleotide 1013, within the coding sequence. The published nucleotide at position 1013 is T (1).

20

The frequency of AARS heterozygotes is 25-50% in all populations surveyed. The frequency of heterozygotes for the nucleotide 1013 sequence variance is 57% in the 36 individuals tested. Both alleles are present in all major racial groups surveyed (see Target Gene Summary Table), including North American Whites (9/15=60% heterozygotes), North American Blacks (3/4=75%), Chinese (2/4=50%), Japanese (1/4=25%) and Hispanic (1/2). The wide population distribution of both alleles suggests that other population groups will also have a high frequency of heterozygotes.

25

The AARS gene maps to 16q22

The human AARS cDNA has been mapped to chromosome 16q22 by us and by Nichols et al. (ref. 2). We designed primers to the 3' untranslated region of AARS and used PCR to analyze the National Institute of General Medical Sciences (NIGMS) Human/Rodent Somatic Cell Hybrid Mapping Panel #2 (see page 704 of the NIGMS 1994/1995 Catalog of Cell Lines, available from the Coriell Cell Repository, Camden, NJ). The panel consists of 24 hybrid cell lines, each monochromosomal for one human chromosome. The AARS PCR product mapped to the hybrid containing human chromosome 16. Subsequently we screened the Radiation Hybrid Mapping Panel created at Stanford University (rhserver@shgc.stanford.edu) and distributed by Research Genetics (RH01). The AARS PCR product mapped near D16S496 with a lod score >10. D16S496 is a polymorphic DNA marker at 16q22. The AARS PCR product mapped near D16S496 with a LOD score >10. DH16S496 is a polymorphic DNA marker at 16q22. (See, ref. 29 for a full explanation of modification hybrid mapping.) Similar results were obtained by Nichols et al., who mapped AARS by analysis of the same NIGMS hybrid mapping panel, by PCR mapping in a chromosome 16 regional mapping panel and by fluorescence *in situ* hybridization to metaphase chromosomes. All mapping techniques were conclusive in showing only one locus for human AARS.

LOH at 16q22 is well documented in many cancer types. Loss of heterozygosity studies of chromosome 16q have principally focused on breast and liver cancers. In six detailed studies of breast cancer in the 16q22 region LOH frequencies of 40-60% have been reported (refs 3-8). 16q22 LOH has been reported in 25-90% of liver cancers (9-13), with the average around 45%. Less extensive studies of other cancer types report 16q22 LOH in 19% of bladder cancers, 20% of colon cancers (14), 19-27% of esophageal cancers (15), 25% of small cell lung cancers (16), 16-37% of ovarian cancers (17-19) and 22% of uterine cancers (20), and 31-50% of prostate cancers (21-

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5

Example 18: Threonyl-tRNA Synthetase (TARS) - Target Gene VARIA302

The human threonyl-tRNA synthetase gene is essential for cell survival

10 Threonyl-tRNA synthetase (TARS) catalyzes ATP dependent covalent attachment of threonine to its cognate tRNA to form threonyl-tRNA. In the absence of threonyl-tRNA, protein synthesis is blocked. Threonyl-tRNA synthetase is a single copy gene in man (see below) and inhibition of TARS is cell lethal. This has been shown using the specific TARS inhibitor borrelidin, a threonine analog. Borrelidin resistant CHO
15 cell lines have been isolated; the most resistant lines contain ~60-100 fold more immunologically reactive protein and 10-20 fold higher TARS activity than non-selected CHO cells (1-3).

20 The human TARS enzyme is a homodimeric member of the class II tRNA synthetases. The human protein is 53% amino acid identical to *S. cerevisiae* cytoplasmic TARS, 40% amino acid identical to *E. coli* TARS and 39% amino acid identical to yeast mitochondrial TARS. The degree of evolutionary conservation is 52-64% when conservative substitutions are allowed.

25 *The human Threonyl-tRNA synthetase gene and mRNA have sequence variances.* A human cDNA encoding threonyl tRNA synthetase was cloned by Cruzen and Arfin (GENBANK accession M63180; ref. 2) using anti-TARS antibodies to screen a lgt11 expression library. The cDNA is 2644 nt in length and includes a 138 nt 5' untranslated region, an open reading frame of 2136 nt encoding a 712 residue polypeptide, and a 3'

untranslated region of 370 nt.

We designed primers for amplification. The 2644 nt cDNA was screened for sequence variance in 36 unrelated individuals by the single strand conformation polymorphism (SSCP) technique. Three sequence variances were identified: G vs. A transitions at nucleotides 1608 and 1755 within the coding sequence, and a C vs. T transition at nucleotide 2395 of the 3' untranslated region. None of the sequence variances alters the sense of the coding strand. The published sequence shows G, G and T at the three sequence variance sites

The frequency of TARS heterozygotes is 25-45% in all populations surveyed. The nucleotide 1608 sequence variance was genotyped only in North American Whites, 45% of whom were heterozygotes. The nucleotide 1608 and 1755 sequence variances were both genotyped in 36 individuals, with overall heterozygosity rates of 31% and 25%, respectively. Both sequence variances were detected in North American Whites, North American Blacks, Hispanics and Chinese. Of 14 North American Whites genotyped at all 3 sequence variance nucleotides, 11 (79%) were heterozygous for a least one polymorphism (see threonyl tRNA synthetase summary table).

The TARS gene maps to 5p13-CEN. The human TARS cDNA has been mapped to chromosome 5p13-CEN by analysis of TARS isoelectric focusing patterns in human/Chinese hamster hybrids (). The mapping studies were consistent with one human TARS locus.

LOH at 5p13-CEN is documented in several cancer types. The best data on 5p LOH is in cervical cancer where 9 markers have been tested in 3 different studies. The frequency of LOH ranges from 12-57%, averaging ~45%. Other cancers that have been studied are breast (10-24% LOH), head and neck (20% LOH), adenocarcinoma of the lung (40% LOH, but only 5 cancers were studied), melanoma (40%) and ovary (15-

21%).

Assays for human TARS inhibitors. Human TARS protein is a homodimeric class II synthetase. Antibodies to rat TARS were used to clone the human protein. The high degree of amino acid conservation throughout the protein suggests that it may be possible to create yeast and/or bacterial strains with human CARS.

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15 **Example 19: Glutaminyl-tRNA Synthetase (QARS) - Target Gene VARIA305**

The human glutaminyl-tRNA synthetase gene is essential for cell survival

20 Glutaminyl-tRNA synthetase (QARS) catalyzes ATP dependent covalent attachment of glutamine to its cognate tRNA to form glutaminyl-tRNA. In the absence of glutaminyl-tRNA, protein synthesis is blocked in eucaryotic cells. Glutaminyl-tRNA synthetase is a single copy gene in man. Inhibition of its function is expected to be cell lethal, as shown for other tRNA synthetases (summarized above).

25 *The human Glutaminyl-tRNA synthetase gene and mRNA have sequence variances.*

A human cDNA encoding glutaminyl tRNA synthetase (QARS) was cloned by Lamour et al. (1) who expressed the cDNA in *E. coli* and demonstrated glutaminyl tRNA synthetase activity in bacterial extracts. The cloned human cDNA

(Genbank/EMBL accession number X76013) is 2437 nt in length and includes a 5' untranslated region of 5 nucleotides, an open reading frame of 2325 nucleotides encoding a 775 amino acid polypeptide, and a 3' untranslated region of 107 nt including 8 terminal nt of poly A.

5

We designed primers for amplification. The QARS cDNA was screened for sequence variance in 36 unrelated individuals using the single strand conformation polymorphism (SSCP) technique. One sequence variance was identified, a C vs. T transition at nucleotide 404, within the coding sequence. The published nucleotide at position 404 is C. The sequence variance does not affect the protein encoded.

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The frequency of heterozygotes for the nucleotide 404 sequence variance is 11% in the 36 individuals tested (4/36). However three of 16 North American Whites are heterozygotes (19%), and one of four Japanese (25%) (see Target Gene Summary Table).

15

The QARS gene maps to 3p

The human QARS cDNA has been mapped to chromosome 3 by hybridization of a QARS probe to a panel of 25 human/rodent somatic cell hybrids (1). One somatic cell hybrid, not known to contain human chromosome 3, was positive for both the QARS probe and an ACY1 probe. ACY1 maps to human 3p21, suggesting QARS may also map in this area. We independently mapped QARS to chromosome 3 using primers from the 3' untranslated region to analyze the National Institute of General Medical Sciences (NIGMS) Human/Rodent Somatic Cell Hybrid Mapping Panel #2 by PCR (see page 704 of the NIGMS 1994/1995 Catalog of Cell Lines, available from the Coriell Cell Repository, Camden, NJ). The panel consists of 24 hybrid cell lines, each monochromosomal for one human chromosome. The QARS PCR product mapped to the hybrid containing human chromosome 3. All mapping techniques were conclusive

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in showing only one locus for human QARS.

Chromosome band 3p21 is a site of frequent loss of heterozygosity. The short arm of chromosome 3 has been well studied in breast, cervical, esophageal, kidney, and lung cancers. These studies report frequent allele loss at 3p21, varying up to 100% in some studies of small cell lung cancer. Among other cancers LOH occurs in approximately 20-30% of breast cancers (2,3), 30-60% of cervical cancers (4,5), 10-40% of esophageal cancers (6,7), 45-80% of kidney cancers (8-10), 50-100% of nasopharyngeal cancers (11), 0-75% of squamous cell head and neck cancers (12), 30-60% of melanomas (13), 30-100% of non-small cell lung cancers (14-16) and 80-100% in small cell lung cancer (17-19). Other for which there are reports of LOH in at least 20% of cases include leukemia, pancreas cancer, sarcoma, testis cancer and ovarian cancer. Other cancer types, including bladder and lymphoma, have not been studied for LOH at 3p21.

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Example 20: Lysyl-tRNA Synthetase (KARS) - Target Gene VARIA303

Human Lysyl t-RNA synthase gene is essential

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Lysyl-tRNA synthetase (KARS) catalyzes ATP dependent covalent attachment of lysine to its cognate tRNA to form lysyl-tRNA. In the absence of lysyl-tRNA, protein synthesis is blocked. Since lysyl-tRNA synthetase is a single copy gene in man, inhibition of its function is expected to be cell lethal. This has been shown for other tRNA synthetases (summarized above).

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The human Lysyl-tRNA synthetase gene and mRNA have sequence variances

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A human cDNA encoding a sequence similar to bacterial lysyl tRNA synthetases was cloned by Nomura et al. (GenBank/DDBJ submission D31890; see ref. 1) while sequencing random cDNAs. No biochemical studies of the protein encoded by this sequence have been reported. The 5' end of the sequence apparently begins in the coding region and the open reading frame continues for 1805 nucleotides, encoding 601 residues of a polypeptide (the full length of which has not been established), followed by a 3' untranslated region of 165 nucleotides.

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232/116

We designed primers for amplification. The reported partial cDNA was screened for sequence variance in 36 unrelated individuals using the single strand conformation polymorphism (SSCP) technique as described in the methods section. Two sequence variances were identified, an A vs. G transition at nucleotide 89 and a G vs. C transversion at nucleotide 1798, both within the coding sequence. The published nucleotides are A and G, respectively. The nucleotide 1798 sequence variance alters the sense of the 599th codon (the third codon from the end of the coding sequence) to serine vs. threonine.

The frequency of KARS heterozygotes varies among the populations surveyed. The frequency of heterozygotes for the nucleotide 89 sequence variance is 19% in the 36 individuals tested. However all heterozygous individuals were either North American Whites (4/16; 25% heterozygotes), North American Blacks (1/4; 25%), or Hispanics (1/3; 33% heterozygotes). The frequency of heterozygotes for the nucleotide 1798 sequence variance is 6% in the 36 individuals tested. However all heterozygous individuals were North American Blacks (2/4; 50%) (see Target Gene Summary Table). Further study of these and other population groups will better establish the frequency of heterozygotes for these two sequence variances.

The KARS gene maps to 16q23-q24

The human KARS cDNA has been mapped to chromosome 16q22 by Nichols et al. (ref. 2) and by us. We designed primers to the 3' untranslated region of KARS and used PCR to analyze the National Institute of General Medical Sciences (NIGMS) Human/Rodent Somatic Cell Hybrid Mapping Panel #2 (see page 704 of the NIGMS 1994/1995 Catalog of Cell Lines, available from the Coriell Cell Repository, Camden, NJ). The panel consists of 24 hybrid cell lines, each monochromosomal for one human chromosome. The KARS PCR product mapped to the hybrid containing human chromosome 16. Similar results were obtained by Nichols et al., who mapped KARS

by analysis of the same NIGMS hybrid mapping panel, by PCR mapping in a chromosome 16 regional mapping panel and by fluorescence *in situ* hybridization to metaphase chromosomes. The *in situ* hybridization showed KARS maps to 16q23-q24. All mapping techniques were conclusive in showing only one locus for human KARS.

Loss of heterozygosity occurs frequently at 16q23-q24 in many cancer types. Loss of heterozygosity studies of chromosome 16q have principally focused on breast and liver cancers. In six detailed studies of breast cancer in the 16q23-q24 region LOH frequencies of 30-60% have been reported (refs 3-8). 16q22 LOH has been reported in 35-65% of liver cancers (9-13), with the average around 45%. Studies of other cancer types report 16q22 LOH in 19% of colon cancers (14), 17-27% of esophageal cancers (15,16), 37% of ovarian cancers (new ref) (17-19), 18% of prostate cancers (20) and 23% of uterine cancers (21). Cancer types not yet investigated for LOH include kidney, leukemia and lymphoma, lung, melanoma, neuroblastoma, stomach and testis.

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15 **Example 21: Ribosomal Protein S14 (RPS14) - Target Gene VARIA326**

Ribosomal protein S14 is essential for cell growth

20 Human ribosomal protein S14 (RPS14) is one of ~80 unique protein constituents of the mammalian ribosome. Many of the protein subunits of ribosomes, the protein making machines of all cells, are highly conserved throughout prokaryotic and eukaryotic evolution (1). For example, human RPS14 protein is 100% amino acid identical to hamster S14 protein, 72% identical to yeast rp59 protein and 43% identical to *E. Coli* ribosomal protein S11 (2,3). Mammalian S14 and yeast rp59 are components of the 40S ribosomal subunit while *E. coli* S11 is part of the corresponding bacterial S30 subunit. Thus human RPS14 is a ribosomal component fixed early in evolution.

25

There are many antibiotics and eukaryotic cell poisons that act by inhibiting ribosome function (reviewed in ref. 4). One such drug is emetine, which inhibits protein translation by interacting with the eukaryotic RPS14 subunit to prevent elongation

factor dependent translocation of peptidyl-tRNAs bound to eukaryotic ribosomes in vitro (4).

Chinese hamster ovary (CHO) cell lines resistant to emetine have been shown to contain mutant RPS14 loci (also referred to as the EMTB locus) (5). Such lines have been used to investigate the effects of mutant RPS14 on ribosome function (5-8). Human-CHO cell hybrids are emetine-sensitive, indicating that the EMTB/RPS14 mutation is recessive in CHO cells. This is apparently because arrest of protein synthesis in half of ribosomes blocks translation of all polysomic mRNAs by blocking any functional ribosomes upstream of frozen mutant ribosomes. RPS14 appears to contribute to the structural integrity of the 40S subunit: 40S subunits containing mutant S14 protein are more easily dissociable in high ionic strength wash buffers (9). Ribosomal subunit genes are coordinately expressed in all cells and ribosomal proteins constitute a large fraction of the cell mass in all cell types.

The human RPS14 gene has sequence variances

Rhoads et al. reported the sequence of the human RPS14 gene and cDNA (3). The cDNA contains a 33 nucleotide 5' untranslated region, a 453 nt coding region and a 60 nt 3' untranslated region (including 12 nt of polyA). We undertook a systematic search for DNA sequence variance in the cDNA of RPS14 by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed using the sequence of Rhoads et al. (GENBANK accession M13934, M13641; see ref. 3). SSCP analysis revealed 1 sequence variance, and subsequent DNA sequence analysis confirmed an A vs. G transition at nucleotide 183 of the coding sequence. (This change was noted as a difference between the cDNA and genomic sequences in ref. 3.)

As shown in the Target Summary Table, both alleles were detected in all major

populations surveyed, including North American Whites, North American Blacks, Hispanics, Chinese and Japanese.

The human RPS14 gene maps to chromosome 5q23-q33

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Dana and Wasmuth (11) used Chinese hamster/human somatic cell hybrids to map the RPS14 gene (designated EMTB) to 5q23-5q35. Later Nakamichi et al. (12) placed the RPS14 gene on the segment 5q23-q33 using similar techniques.

10

Chromosome band 5q23-q33 is a site of frequent loss of heterozygosity. There have been many studies of LOH on 5q, particularly the 5q21-q22 region where the Adenomatous Polyposis Coli (APC) tumor suppressor gene lies. The most extensively studied cancers are those of the gastrointestinal tract, lung and ovary. The available data on the 5q23-q33 region just distal to APC (where RPS14 lies), suggests that LOH occurs in this region at a frequency of ~30% in cervical cancer (13), 20-40% in colon cancer (14,15), 30-50% in ovarian cancer (16,17), 38% in stomach cancer (18) and 23% in testicular cancer (19). There is also evidence for LOH in head and neck, lung, and liver cancers.

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Example 22: Eukaryotic Initiation Factor 5A (eIF-5A) - Target Gene VARIA351

Initiation Factor 5A is essential for cell growth

Human Initiation Factor 5A (eIF-5A), formerly named Initiation Factor 4D, is an 18-kD protein which promotes formation of the first peptide bond in *in vitro* translation systems - hence the name 'initiation factor' (1,2); however, the full physiological role of eIF-5A is not understood. Inhibition of eIF 5A formation blocks proliferation in all tested cell types (3); the presence of functional eIF 5A has been shown to correlate with the onset of DNA replication (4) - perhaps due to eIF 5A dependent translation of mRNAs encoding proteins necessary for DNA replication (3), and eIF-5A is an essential co-factor for HIV-1 Rev protein (5).

eIF 5A is an unusual protein: one of its lysine residues (amino acid 50) is modified by transfer and hydroxylation of the butylamino-group from the polyamine spermidine to form hypusine, a post translational modification unique to eIF 5A. All of the biological activities of eIF 5A are abrogated in the absence of the hypusine modification, as demonstrated by pharmacological inhibition of hypusine formation in human cell lines (3) and by site directed mutagenesis of the modified lysine residue in the yeast enzyme (6). There are two enzymes responsible for hypusine formation, one of which, deoxyhypusyl hydroxylase, can be inhibited with the drug mimosine (3), providing a convenient pharmacological inhibitor of eIF 5A formation.

The genome of the yeast *Saccharomyces cerevisiae* encodes two eIF 5A genes. Disruption of one (form A) slows growth, disruption of the other (form B) arrests growth and strains with both forms disrupted are non-viable (6). The yeast A form substitutes for human eIF 5A in the mammalian methionyl-puromycin synthesis assay (6), while the human gene complements eIF 5A disrupted yeast (7). eIF 5A is a highly conserved protein, with counterparts in archaee, bacteria and eukaryotes. The yeast proteins are ~63% identical to the human protein (6).

The human eIF 5A gene and mRNA have sequence variances

Smit-McBride, et al. reported the sequence of a human cDNA encoding eIF-5A (8) and Koettnitz et al. (8) later reported the sequence of the active eIF 5A gene, which contains three introns (GenBank accession U17969). A composite sequence made from the cDNA and genomic versions is 1309 nucleotides long and contains a 5' untranslated region of 145 nucleotides, a 462 nt coding region and a 702 nt 3' untranslated region (see annotated sequence). We undertook a systematic search for DNA sequence variance in the cDNA of eIF 5A by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed for amplification. SSCP analysis revealed 2 sequence variances, and subsequent DNA sequence analysis confirmed an A vs. G transition at nucleotide 623 and a T vs. C transition at nucleotide 1012, both in the 3' untranslated sequence.

Neither sequence variance affects the protein coding sequence, however nucleotide 623 is one nucleotide away from a splice acceptor site at position 622, and could therefore be targeted by an oligonucleotide intended to abrogate splicing in an allele specific manner. The second exonic nucleotide (+2 position) of a splice acceptor site is not highly conserved, nonetheless the A vs. G transition at nucleotide 623 may affect the mechanics of splicing.

As shown in the Target Summary Table, both alleles were detected in all major populations surveyed, including North American Whites, North American Blacks, Hispanics, Arabs, Indians and Japanese, except only the nucleotide 1012 variance was detected in the four Chinese surveyed. The overall frequency of heterozygotes was 37% for the nucleotide 623 sequence variance and 52% for the nucleotide 1012 sequence variance.

The human eIF 5A gene maps to chromosome 17p13-p12

Steinkasserer et al. (1995) mapped the eIF 5A gene to 17p13-p12 by fluorescence *in situ* hybridization (9). Three eIF 5A pseudogenes were mapped to 10q23, 17q25 and 19q13.

Chromosome band 17p13-p12 is a site of frequent loss of heterozygosity. There have been many studies of LOH on 17p, particularly the 17p13 region where the p53 tumor suppressor gene maps. Virtually all cancer types have been surveyed for LOH in this area, with particularly extensive studies of breast, colon, ovarian, and stomach cancers. These studies report LOH in approximately 40-60% of breast cancers (10-18), 50-70% of colon cancers (19-25), 25-75% of ovarian cancers (26-30), 20-60% of stomach cancers (31-34), 20-50% of brain cancers (35,36), 45-70% of esophageal cancers (37), 35-65% of non-small cell lung cancers (38,39) and 100% of small cell lung cancers, 15-50% of cervical cancers, 30-80% of head and neck cancers, 20-60% of liver cancers, over 50% of sarcomas and 10-30% of a variety of other cancer types.

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15 **Example 23: Replication Protein A, 32 kDa Subunit (RPA32) - Target Gene VARIA402**

The human RPA32 gene encodes a protein essential for cell survival

20 Replication Protein A (RPA; also known as Replication Factor A, Activator 1, Single Strand Binding Protein or SSB) is a heterotrimeric protein which participates in DNA replication, homologous recombination and nucleotide excision repair (1-3). The evidence that RPA is an essential protein comes from *in vitro* and *in vivo* data.

25 DNA replication is essential for cell proliferation, as discussed above for RPA70.

The best studied function of RPA32 is in DNA replication. Because of the complexity of DNA replication in higher eukaryotic genomes, the small genome of the papovavirus SV40 has been used as a model system to study DNA replication in human cell extracts. In the 1980s several research groups

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developed cell free systems to study DNA replication using SV40 chromosomes as templates (4-8). An effort to identify the minimal set of factors required for DNA replication led to the discovery of RPA. Subsequent work proved that each of the three subunits of RPA is essential for DNA replication (9,10). This was proved in several ways, including by using antibodies to various constituents of the replication complex. Anti-RPA32 antibodies inhibit DNA replication, providing clear *in vitro* evidence for the essential function of this subunit of RPA in human DNA replication (10).

The yeast *S. cerevisiae* has a trimeric replication protein A which is structurally and functionally homologous to the human protein. It consists of three subunits similar in size to the human subunits. All three yeast subunits have been disrupted and each disruption produces non-viable yeast (9).

The human RPA32 gene and mRNA are polymorphic.

The published cDNA for the 32 kD subunit of Replication Protein A is 1512 nucleotides long and includes a 5' untranslated segment of 77 nucleotides, followed by a protein coding region of 810 nucleotides and a 3' untranslated region of 625 nucleotides (10). We undertook a systematic search for DNA polymorphism by analysing the RPA32 cDNA from 36 unrelated individuals using the single strand conformation polymorphism technique (described in the methods section). Primers were designed using the sequence of Erdile et al. (GenBank accession J05249; see ref. 10). SSCP analysis revealed 2 variances, one of which was sequenced. Sequencing revealed a G vs. A transition at nucleotide 40 of the 5' untranslated region. Four of 36 individuals were heterozygotes, all of them Caucasians. Thus the allele frequency is 25% (4/16) in North American Whites, while no heterozygosity was detected in other populations (see Target Summary sheet).

The RPA32 gene maps to chromosome 1p35

The gene for RPA32 was mapped to chromosome band 1p35 by *in situ* hybridization, somatic cell hybrid analysis and yeast artificial chromosome mapping (11,12). Only one locus was detected by all methods.

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Chromosome band 1p35 is a site of frequent loss of heterozygosity. The short arm of chromosome 1 is comparatively well investigated for allele loss, especially in breast and colon cancers. Studies of the 1p35 region show LOH in 15-40% of breast cancers (13,14), ~50% of gliomas (a brain cancer subtype) (15), 20-70% of colon cancers (16,17), ~50% of stomach cancers (18), ~20% of lung cancers (19) and 10-30% of ovarian cancers. High frequency LOH has been detected in several uncommon cancers such as pheochromocytoma (50-80%) and neuroblastoma (~50%).

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Example 24: Replication Protein A, 70 kD subunit (RPA70) - Target Gene VARIA401

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The human RPA70 gene encodes a protein essential for cell survival

Replication Protein A (also known as Replication Factor A, Activator or Single Strand Binding protein [SSB]) is a heterotrimeric protein which participates in DNA replication, homologous recombination and nucleotide excision repair (1-3). The evidence that RPA is an essential protein comes from *in vitro*, *in vivo* and evolutionary data.

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DNA replication is essential for cell proliferation, and a variety of antiproliferative drugs act, at least in part, by inhibiting DNA replication. Such drugs include nucleotide analogs that block DNA polymerases, such as 2',3' dideoxy NTPs and 3' deoxy ATP (cordycepin); inhibitors that bind to or modify DNA such as intercalating agents, DNA crosslinking drugs or alkylating agents, and inhibitors that bind to polymerases and replication proteins such as topoisomerase inhibitors like the epipodophyllotoxins, which prevent DNA unwinding necessary for replication (and transcription) and antibiotics which bind to polymerases such as arylhydrazino-pyrimidines.

The best studied function of RPA70 is in DNA replication. Because of the complexity of DNA replication in higher eukaryotic genomes, the small genome of the papovavirus SV40 has been used as a model system to study DNA replication in human cell extracts. In the 1980s several research groups

developed cell free systems to study DNA replication using SV40 chromosomes as templates (4-8). These studies, in seeking to identify the minimal set of factors required for DNA replication, led to the discovery of replication protein A. Subsequent work proved that each of the three subunits of RPA is essential for DNA replications. This was proved in several ways, including by using antibodies to various constituents of the replication complex. These antibodies are effectively inhibitors of RPA70. Anti-RPA70 antibody mediated abrogation of DNA replication provides clear *in vitro* evidence for the essential function of RPA70 in human DNA replication (10). The yeast *S. cerevisiae* has a trimeric replication protein A which is structurally and functionally homologous to the human protein. It consists of three subunits similar in size to the human subunits. The yeast 70 kDa subunit is 31% identical and 75% similar (including conserved amino acids) to its human counterpart (1). All three yeast subunits have been disrupted and each disruption produces non-viable yeast. The yeast 70 kD protein is also a single stranded DNA binding protein.

Single stranded DNA binding proteins (SSBs) are required for DNA replication in a wide variety of organisms, including bacteriophage, bacteria and some DNA viruses of higher eukaryotes. Recently the crystal structure of the DNA binding domain of human RPA was solved and found to be remarkably similar in three dimensional shape to the bacteriophage single stranded DNA binding proteins Pf3 and gene V from f1 phage.

The human RPA70 gene, mRNA and protein have sequence variances

The published cDNA for the 70 kD subunit of Replication Protein A is 2393 nucleotides long and includes a 5' untranslated segment of 69 nucleotides, followed by a protein coding region of 1848 nucleotides and a 3' untranslated region of 476 nucleotides (1). We undertook a systematic search for DNA polymorphism by

analyzing the RPA70 cDNA from 36 unrelated individuals using the single strand conformation polymorphism technique (described in the methods section). Primers were designed using the sequence of Erdile et al. (GenBank accession M63488; see ref. 1). SSCP analysis revealed 5 variances, and subsequent DNA sequence analysis of those variances led to identification of four additional variances. SSCP revealed the variances at nucleotides 81 (G vs. A), 1120 (A vs. G), 1674 (T vs. C), 2050 (T vs. C) and 2297, where an insertion/deletion variance of one C nucleotide was observed (8 vs. 9 C's in a row). In the course of sequencing around the nucleotide 2297 polymorphism an additional variance was detected at nucleotide 2341 (A vs. G). Also, while sequencing additional Swedish individuals around nucleotide 1120 two new variances were observed at nucleotides 1124 and 125 (both C vs. T). Finally, in three individuals sequenced for the 2050 variance we noted a difference from the published sequence at nucleotide 2046: we detect 3 T's while the published clone shows just two. This difference may represent another insertion/deletion polymorphism. Five of the nine detected variances are in the coding sequence while four are in the 3' untranslated region.

The frequency of heterozygotes for the five SSCP positive variances ranged from 25-42% among the 36 individuals tested. The small number of individuals genotyped for the other four variances precludes definitive assessment of heterozygosity rates. Some of the polymorphisms appear to occur more commonly in certain racial or ethnic groups (see Target Summary sheet for details). For example, only one of the variances (nt 1674) was detected in Japanese individuals. In general, higher levels of polymorphism were detected in North American Whites than in other groups. The nucleotide 1120 polymorphism, for instance, was heterozygous in 9/36 individuals overall (25%), but in 8/16 North American Whites (50%).

The RPA70 cDNA encodes a 616 amino acid protein. The nucleotide 1120 and 1124 variances result in amino acid substitutions at residues 351 and 352, the former an alanine-threonine exchange (approximately 50% of caucasians are heterozygotes) and

the latter a serine-phenylalanine exchange (rare in the populations tested). In the recently published crystal structure of the DNA binding segment of RPA70 (amino acids 181-422) it is possible to place residue 351 in the second of two tandemly arrayed DNA binding domains (domain B; see ref. 10). Domain B extends from residue I305 to N402, thus the variant residue 351 is in the middle. The published structure is a co-crystal of RPA70 amino acids 181-422 complexed to octadeoxycytosine. Several RPA70 residues contact the oligonucleotide (Figure 4 of ref. 11), including amino acids K343 and T359, which lie 8 residues away from the polymorphism in either direction. Modeling the two variant forms of the protein using the atomic coordinates deposited in the Protein Data Bank (1JMC) should clarify the structural consequences of the alanine-threonine variance. Residue 351 lies in the center of a 50 amino acid segment of the protein that is relatively poorly conserved between yeast and man: 11 of the 50 residues are identical and 25 more are conservative substitutions. Towards the C terminus there is strong conservation: starting 25 residues C-terminal of the polymorphism, 27 of the next 37 residues are identical between yeast and man. Towards the N terminus there is ~30% conservation. Both yeast and human 70 kD RPA subunits contain putative C4-type zinc finger motifs at positions ~480-500.

The RPA70 gene maps to chromosome 17p13.3

The gene for RPA70 has been mapped to chromosome band 17p13.3 by *in situ* hybridization (12). Only one locus was detected.

Chromosome band 17p13.3 is a site of frequent loss of heterozygosity. RPA70 lies just telomeric to the TP53 tumor suppressor gene which is located in cytogenetic band 17p13.1. This region of chromosome 17 is extremely well investigated for allele loss. In general, studies report LOH in approximately 40-60% of breast cancers (13-21), 50-70% of colon cancers (22-28), 25-75% of ovarian cancers (29-33), 20-60% of stomach cancers (34-37), 20-50% of brain cancers (38,39), 45-70% of esophageal cancers (40),

35-65% of non-small cell lung cancers (41,42) and 100% of small cell lung cancers, 15-50% of cervical cancers, 30-80% of head and neck cancers, 20-60% of liver cancers, over 50% of sarcomas and 10-30% of a variety of other cancer types.

5 *Assays developed for RPA: Protein and DNA contacts*

Human cDNAs encoding all 3 subunits (70, 34 and 11 kD) of RPA have been cloned and expressed in *E. coli* and in insect cells via baculovirus vectors. The bacterially expressed 70 kDa protein is indistinguishable from its purified human counterpart immunologically and in several functional assays (see Table below). There is good evidence that the 70 kD subunit of RPA interacts with a number of different molecules. A partial list would include the 34 and 11 kD subunits of RPA, DNA, the xeroderma pigmentosum damage recognition and endonuclease proteins XPA and XPG, and DNA polymerase α -primase. These experimentally proven contacts (and almost certainly others) may constrain the topology of the protein in ways that have implications for inhibitor design. In summary a broad array of assays exists to screen for small molecule inhibitors of RPA (possibly including modified nucleotides), that act via competitive, allosteric or protein-protein blocking mechanisms.

Table 4

20 **Assays and reagents available for RPA inhibitor screening**

| ASSAY | RPA 70 kD, Assay Systems | |
|---------------------------------|--------------------------|---|
| | Purified Human Protein | Purified Bacterial or Baculovirus Protein |
| Immunoreactivity | X | X |
| Single stranded DNA binding | X | X |
| DNA Polymerase α primase | X | X |

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|----------------------------|---|---|
| DNA strand exchange | X | X |
| Nucleotide excision repair | X | X |
| Support SV40 Replication | X | X |

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25 **Example 25: RNA Polymerase II, 220-kD subunit (RPOL2A) - Target Gene VARIA500**

The human RPOL2A gene encodes a protein essential for cell survival

DNA-dependent RNA polymerase II (also known as RPB1 or POLR2A), a complex

multisubunit enzyme, is responsible for the transcription of mRNA from all protein coding genes.

5 RNA polymerases are found in all cellular organisms. The subunit structure of RNA polymerases is highly conserved in eukaryotes. RNA polymerase acts in concert with as many as 50 other proteins in gene transcription (reviewed in ref. 1). See refs. 2 and 3 for a review of basal transcription by RNA polymerase II and recent progress in identifying and purifying transcription factors and cloning the genes that encode them.

10 Several subunits of *S. cerevisiae* RPOL2A have been disrupted, always resulting in non-viable yeast.

15 A variety of inhibitors of RNA polymerase are cytotoxic drugs, such as actinomycin D, which intercalates into double stranded DNA and blocks the movement of RNA polymerase; rifampicin binds the β subunit of *E. coli* RNA polymerase and blocks initiation of transcription. The best studied specific inhibitor of eukaryotic RPOL2A, however, is the potent mushroom toxin - amanitin, a cyclic octapeptide which binds with high affinity ($K_d \sim 10^{-9}$ M) to RPOL2A. Several mutations conferring resistance to α -amanitin have been characterized and they all map to the RPOL2A protein coding sequence. 20 Recently α -amanitin binding has been shown to trigger specific degradation of RPOL2A (4).

25 Damage to actively transcribed DNA is preferentially repaired by the transcription-coupled repair (TCR) system. TCR requires RNA pol II, but the mechanism by which repair enzymes preferentially recognize and repair DNA lesions on PolB II-transcribed genes is incompletely understood.

The human RPOL2A gene and mRNA have sequence variances

Wintzerith et al. and later Mita et al. cloned and sequenced the complete human gene

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for RPOL2A (5, 6); the deduced amino acid sequences are identical. The RPOL2A gene contains 29 exons and spans about 32 kb of DNA. The cDNA sequence we evaluated is 6732 nucleotides long (see Annotated RPOL2A Sequence) and contains a 5' untranslated region of 386 nucleotides, a 5910 nucleotide coding region specifying 1970 amino acids, and a 436 nucleotide 3' untranslated region (see annotated sequence). We undertook a systematic search for DNA sequence variance in the cDNA of RPOL2A by analyzing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed for amplification. SSCP analysis revealed 10 sequence variances, and subsequent DNA sequence analysis confirmed a G vs. A transition at nucleotide 857, a C vs. T transition at nucleotide 1260, a C vs. T transition at nucleotide 1346, a C vs. T transition at nucleotide 1544, a C vs. T transition at nucleotide 1847, a C vs. T transition at nucleotide 2678, a C vs. T transition at nucleotide 3059, a C vs. T transition at nucleotide 3827, a T vs. C transition at nucleotide 6466 and a T vs. C transition at nucleotide 6557. The former seven sequence variances are in coding sequence and the latter two are in the 3' untranslated sequence. Only one of the ten sequence variances alters the protein coding sequence: the nucleotide 1260 alleles encode arginine (common) or cysteine (rare) at amino acid 292. Only 2/36 individuals surveyed are heterozygotes (6%), however both are North American Whites (2/16 = 12.5%) so further investigation of this population is required. The prevalence of heterozygotes for the other sequence variances varies from 3% to 50%, with 6 sequence variances above 22% (see RPOL2A Target Summary Sheet). The 6 common sequence variances are widely prevalent among all or nearly all the tested populations.

The human RPOL2A gene maps to chromosome 17p13.105

The human RPOL2A gene was initially assigned to the distal portion of the short arm of chromosome 17 (17pter-p12) by *in situ* hybridization and Southern analysis of DNA from human/rodent somatic cell hybrids (7, 8). Subsequent somatic cell hybrid studies narrowed the assignment to 17p13.105-p12 [vanTuinen and Ledbetter (1987)], which

was later confirmed by *in situ* hybridization to 17p13 (9).

Chromosome band 17p13.1 is a site of frequent loss of heterozygosity There have been many studies of LOH on 17p, particularly the 17p13.1 region where the p53 tumor suppressor gene maps. Virtually all cancer types have been surveyed for LOH in this area, with particularly extensive studies of breast, colon, ovarian, and stomach cancers. These studies report LOH in approximately 40-60% of breast cancers (10-18), 50-70% of colon cancers (19-25), 25-75% of ovarian cancers (26-30), 20-60% of stomach cancers (31-34), 20-50% of brain cancers (35,36), 45-70% of esophageal cancers (37), 35-65% of non-small cell lung cancers (38,39) and 100% of small cell lung cancers, 15-50% of cervical cancers, 30-80% of head and neck cancers, 20-60% of liver cancers, over 50% of sarcomas and 10-30% of a variety of other cancer types.

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Example 26: TATA Associated Factor 30 kD subunit (TAF2H) - Target Gene VARIA 520

The human TAF2H gene encodes a component of the transcriptional apparatus

Transcription initiation by RNA polymerase II requires the assembly of a complex of

basic transcription factors which include TFIIA, TFIIB, TFIID, TFIIIE, TFIIF, TFIIG/TFIIJ and TFIIH/BTF2 into a preinitiation complex (1,2). TFIID is the first factor to contact the promotor, and subsequent assembly of the transcription complex is dependent on TFIID binding. TFIID is a 700-750 kD multiprotein complex which includes TATA binding protein (TBP) and between eight and 13 TBP-associated factors (TAFs) ranging from 250 to 17 kDa. The TAFs have been shown necessary to reconstitute activation of transcription *in vitro*, leading to the hypothesis that some TAFs link transcription activation domains to the basal transcription complex. The TFIID complex also supports transcription from TATA-less promoters, while TBP fails to do so. Therefore TAFs may also contribute to formation of stable initiation complexes by interacting directly with DNA (2). Conditional temperature sensitive Chinese hamster mutants of another TAF, TAFII250, were detected because, at the non-permissive temperature, DNA synthesis was inhibited leading to arrest of cell division at the G1 phase (3,4). Transfection of a human TAFII250 gene relieved the block at the non-permissive temperature. Thus an essential role has been proven for TAFs in mammalian cells.

A gene (TAF2H) encoding the 30 kDa human TAF protein (TAFII30) was cloned and its functional properties examined by Jacq, et al. (5). The protein was shown to be present in a subset of TFIID complexes and to mediate transcriptional activation by a specific region of the estrogen receptor. Estrogen mediated transcriptional activation could be abrogated by adding an antibody against TAFII30. TAFII30 was not required for basal transcription or for transcription activation by VP-16. It is likely that TAFII30 is required for transcriptional activation by a variety of other transactivating proteins, and is therefore essential for cell proliferation or cell survival.

The human TAF2H gene and mRNA have sequence variants

A human TAF2H cDNA has been cloned and sequenced (5). It encodes a cDNA of 756 nucleotides including a 5' untranslated region of 17 nucleotides, a 657 nucleotide

coding region specifying 218 amino acids, and an 82 nucleotide 3' untranslated region (GenBank accession U13991; see annotated TAF2H cDNA sequence). (Note that the numbering of the sequence in ref. 5 differs slightly from that in the GenBank accession.) We undertook a systematic search for DNA variance in the cDNA of TAF2H by analysing 36 unrelated individuals using the single strand conformation polymorphism technique. Primers were designed for amplification. SSCP analysis revealed 1 polymorphism, and subsequent DNA sequence analysis confirmed a G vs. A transition at nucleotide 554 (nt 556 of the sequence in ref. 3) of the coding sequence. This variance does not alter the protein coding sequence. Eight of 36 individuals surveyed are heterozygotes (22%). The variance occurs in North American Whites (3/16 = 19%), North American Blacks (2/4) and Hispanics (3/3).

The human TAF2H gene maps to chromosome 11p15.5-p15.2 The human TAF2H cDNA has been mapped to 11p15.5-p15.2 by fluorescent *in situ* hybridization (6). There appears to be a single TAF2H locus. *Chromosome band 11p15-p14 is a site of frequent loss of heterozygosity*

There have been many studies of LOH on 11p, particularly the 11p15 and 11p13 segments where the Beckwith-Weidemann syndrome and WT1 genes reside. As a result there are many studies of LOH in 11p15.5, particularly focusing on breast, cervix, kidney, liver, lung, ovarian, stomach and testicular cancers. These studies show that the 11p15.5 band of chromosome 11 is frequently reduced to one copy (7-24). For example, LOH occurs in approximately 13-33% of breast cancers (7-9), 14-42% of cervical cancers (10), 0-50% of liver cancers (11,12), 0-80% of lung cancers (13-15), 18-54% of ovarian cancers (14,15), 0-71% of stomach cancers (18) and 0-50% of testicular cancers (19,20). Other studies show that 11p15.5 LOH may also be frequent in bladder cancer (21), esophageal cancer (22), some leukemias (23) and sarcomas (24). Many deletions in the 11p15.5 region span relatively short chromosomal segments (2 - 10 megabases; see ref. 13).

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Example 27 - cDNA synthesis

In order to analyze an essential gene for sequence variances, it is generally useful to have a cDNA(s) containing the coding sequence for further sequencing or amplification purposes. cDNAs for some genes are available, however, in some cases it is useful to synthesize the cDNA *de novo*. Methods for obtaining cDNA are known to those skilled in the art, as are methods for sequencing or amplifying the cDNA or portions thereof. An example of a useful cDNA production protocol is provided below, however, as recognized by those skilled in the art, other specific protocols can also be used.

cDNA Production

** Make sure that all tubes and pipette tips are RNase-free. (Bake them overnight at 100oC in the vacuum oven to make them RNase-free.)

1 Add the following to a RNase-free 0.2 ml micro-amp tube and mix gently:

24 ul water (DEPC treated)

12 ul RNA (1ug/ul)

12 ul random hexamers(50 ng/ul)

2 Heat the mixture to 70oC for ten minutes.

3 Incubate on ice for 1 minute.

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4 Add the following:

16 ul 5 X Synthesis Buffer

8 ul 0.1 M DTT

5 4 ul 10 mM dNTP mix (10 mM each dNTP)

4 ul SuperScript RT II enzyme

Pipette gently to mix.

5 Incubate at 42°C for 50 minutes.

6 Heat to 70°C for ten minutes to kill the enzyme, then place it on ice.

10 7 Add 160 ul of water to the reaction so that the final volume is 240 ul.

8 Use PCR to check the quality of the cDNA. Use primer pairs that will give a
~800 base pair long piece. See "PCR Optimization" for the PCR protocol.

15 The following chart shows the reagent amounts for a 20 ul reaction, a 80 ul
reaction, and a batch of 39 (which makes enough mix for 36) reactions:

| | 20 ul X 1 tube | 80 ul X 1 tube | 80ul X 39 tubes | |
|---------------------|----------------|----------------|-----------------|------------------|
| | | | | |
| 20 water | 6 ul | 24 ul | 936 | water |
| RNA | 3 ul | 12 ul | | RNA |
| random hexamers | 3 ul | 12 ul | 468 | random hexamers |
| | | | | |
| 25 synthesis buffer | 4 ul | 16 ul | 624 | synthesis buffer |
| 0.1 M DTT | 2 ul | 8 ul | 312 | 0.1 M DTT |
| 10mM dNTP | 1 ul | 4 ul | 156 | 10mM dNTP |
| SSRT | 1 ul | 4 ul | 156 | SSRT |

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Example 28 - Variance detection by SSCP

This example describes the SSCP technique as used for the identification of sequence variances of the exemplary genes, which were then sequenced to confirm the specific base variances. One common technique currently employed in the identification of such single nucleotide differences is the single strand conformation polymorphism (SSCP) method. (originally described in Orita, *et al.*, "Rapid and Sensitive Detection of Point Mutations and DNA Polymorphisms Using the Polymerase Chain Reaction, *Genomics*, 5:874-879 (1989)) Also employed are restriction fragment length polymorphism (RFLP), heteroduplex analysis, ligase chain reaction (LCR), denaturing gradient gel electrophoresis (DGGE) (Myers, Maniatis, and Lerman, *Methods Enzymol.*, 155:501-527 (1987)) or direct nucleotide sequencing. A review of polymorphism detection techniques, including SSCP, is provided in Grompe, 1993, *Nature Genetics* 5:111-117, which includes a comparison of the commonly used methods.

The SSCP method reveals the presence of sequence variation between individuals as shifts in electrophoretic mobility, but does not show the sequence itself. Direct sequencing of DNAs with altered mobility in the SSCP assay identifies the precise nucleic acid sequence differences among the various alleles. From the nucleic acid sequence data, the amino acid sequence can be determined. One example of the use of this technique is in Pelletier *et al.*, *Cell*, 67:437-447 (1991). The single strand conformation polymorphism methodology is effective for scanning essential genes for sequence variants. It remains the standard technique in human genetics for variance detection, with numerous studies of its efficacy (>90%) and schemes for improved throughput. The SSCP method has been shown to be quite sensitive in the detection of single base changes, for example as shown in Ravnik-Glava *et al.*, 1994, *Human Mol. Genet.* 3:801-807 (human cystic fibrosis gene) and Glava & Dean, 1993, *Human Mutation* 2:404-414 (mouse α -globin gene).

A flow chart of the SSCP method as used to identify essential gene sequence variants is shown in Fig. 2 (SSCP OVERVIEW). The method involves the steps of 1) PCR

amplifying a portion of an essential gene cDNA of known sequence (labeled products),
2) selecting restriction enzymes which will produce fragments approximately 100-400
bases in length for 3 independent digestions of the PCR products, 3) heat denaturing
the digestion products, 4) running single strand digestion products on non-denaturing
5 gels, 5) identifying bands having different mobilities when compared between
individuals, thereby identifying potential sequence variants, 6) sequence at least the
region around the potential sequence variance, that region being identified by
comparison of the expected fragment sizes resulting from the digestions, 7) record the
specific location and base identity of the confirmed sequence variant, 8) calculate the
10 percent occurrence of each sequence variance for the gene as found for the sample of
the population. The method is further described in Example 2.

Single strand conformation polymorphism screening is a widely used technique for
identifying an discriminating DNA fragments which differ from each other by as little
15 as a single nucleotide. As originally developed by Orita (supra), the technique was
used on genomic DNA, however the same group showed that the technique works very
well on PCR amplified DNA as well. In the last 8 years the technique has been used
in hundreds of published papers, and the modifications of the technique have been
described in dozens of papers. The enduring popularity of the technique is due to (1)
20 a high degree of sensitivity to single base differences (>90%) (2) a high degree of
selectivity, measured as a low frequency of false positives, and (3) technical ease.
SSCP is almost always used together with DNA sequencing because SSCP does not
directly provide the sequence basis of differential fragment mobility. The basic steps
of the SSCP procedure are described below and summarized in Fig. 2 in flow chart
25 form.

Because the intent of our SSCP screening was to identify as many target gene
variances as practically possible, we developed a protocol designed to look at a
relatively large number of individuals (36) with a high degree of redundancy, so as to
minimize both the false negative and false positive rates.

The 36 individuals examined are reasonably representative of most of the worlds major populations. The racial or geographic origin of the 36 cell lines is detailed in the Target Summary Tables (Figure 5). All cell lines are EBV immortalized lymphoblastoid cells obtained from the Coriell Cell Repository (Camden, NJ), which includes the racial/ethnic/geographic background of cell line donors in its catalog. The cell lines were also selected for their rapid growth rates. In several cases a panel of cDNAs isolated from French Canadians was used instead, or in addition to, the Coriell panel.

SSCP was used to analyze cDNAs (rather than genomic DNAs) because in many cases the full genomic sequence of the target gene is not available, however, the technique is also applicable to genomic sequences. To produce cDNA requires RNA. Therefore each of the 36 cell lines was grown to mass culture and RNA was isolated using the acid/phenol protocol, sold in kit form as TRIAZOL™ by Life Technologies (Gaithersburg, MD). The unfractionated RNA was used to produce cDNA by the action of a modified Maloney Murine Leukemia Virus Reverse Transcriptase, purchased in kit form from Life Technologies (SUPERScript II™ kit). The reverse transcriptase was primed with random hexamer primers to initiate cDNA synthesis along the whole length of the RNAs. This proved useful later in obtaining good PCR products from the 5' ends of some genes.

Material for SSCP analysis was prepared by PCR amplification of the cDNA in the presence of one ³²P labeled dNTP (usually ³²P dCTP). Usually the concentration of nonradioactive dCTP was dropped from 200 uM (the standard concentration for all four dNTPs) to about 100 uM, and ³²P dCTP was added to a concentration of about 0.1-0.3 uM. This involved adding a 0.3- 1 ul (3-10 uCi) of ³²P cCTP to a 10 ul PCR reaction. All radioactivity was purchased from DuPont/New England Nuclear.

The customary practice is to amplify about 200 base pair PCR products for SSCP, however, we found that it was preferable to amplify about 0.8-1.4 kb fragments and

then use several cocktails of restriction endonucleases to digest those into smaller fragments of about 0.1-0.4kb, aiming to have as many fragments as possible between .15 and .3 kb. The digestion strategy had the advantage that less PCR was required, reducing both time and costs. Also, we routinely performed three different digests on each sample (for all 36 cDNAs), and then ran each of the digests separately on SSCP gels. This had the effect of increasing the redundancy of our method, lessening both the false negative and false positive rates. For example: a site of variance might lie within 2 bases of the end of a fragment in one digest, and as a result not affect the conformation of that strand; the same variance, in a second or third digest, would likely lie in a location more prone to affect strand folding, and therefore be detected by SSCP.

After digestion, the radiolabeled PCR products were diluted 1:5 by adding formamide load buffer (80% formamide, 1X SSCP gel buffer) and then denatured by heating to 90°C for 10 minutes, and then allowed to renature by quickly chilling on ice. This procedure (both the dilution and the quick chilling) promotes intra- (rather than inter-) strand association and secondary structure formation. The secondary structure of the single strands influences their mobility on nondenaturing gels, presumably by influencing the number of collisions between the molecule and the gel matrix (i.e., gel sieving). Even single base differences consistently produce changes in intrastrand folding sufficient to register as mobility differences on SSCP.

The single strands were then resolved on two gels, one a 5.5% acrylamide, 0.5X TBE gel, the other an 8% acrylamide, 10% glycerol, 1X TTE gel. The use of two gels provides a greater opportunity to recognize mobility differences. Both glycerol and acrylamide concentration have been shown to influence SSCP performance. The gel apparatus we use (from Owl Scientific, MA) allows 108 samples to be loaded per gel. Since all 36 samples are routinely digested with three different endonuclease mixes there are 108 samples to be analyzed for each PCR product. By routinely analyzing three different digests under two gel conditions (effectively 6 conditions), and by

looking at both strands under all 6 conditions, we achieve a 12-fold sampling of each base pair of cDNA.

5 All of the sequence variances described in this disclosure were determined by DNA cycle sequencing of ^{32}P labeled PCR products using the femtomole DNA cycle sequencing kit from Promega (WI) and the instructions provided with the kit. Fragments were selected for DNA sequencing based on their behavior in the SSCP assay.

10 **Example 29 - Variance detection by using T4 endonuclease VII mismatch cleavage method**

15 The enzyme T4 endonuclease VII is derived from the bacteriophage T4. T4 endonuclease VII is used by the bacteriophage to cleave branched DNA intermediates which form during replication so the DNA can be processed and packaged. T4 endonuclease can also recognize and cleave heteroduplex DNA containing single base mismatches as well as deletions and insertions. This activity of the T4 endonuclease VII enzyme can be exploited to detect sequence variances present in the general population.

20 The following are the major steps involved in identifying sequence variations in a candidate gene by T4 endonuclease VII mismatch cleavage:

- 25
1. Amplification by the polymerase chain reaction (PCR) of 400-600 bp regions of the candidate gene from a panel of DNA samples. The DNA samples can either be cDNA or genomic DNA and will represent some cross section of the world population.
 2. Mixing of a fluorescently labeled probe DNA with the sample DNA. Heating

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and cooling the mixtures causing heteroduplex formation between the probe DNA and the sample DNA.

3. Addition of T4 endonuclease VII to the heteroduplex DNA samples. T4 endonuclease will recognize and cleave at sequence variance mismatches formed in the heteroduplex DNA.
4. Electrophoresis of the cleaved fragments on an ABI sequencer to determine the site of cleavage.
5. Sequencing of a subset of PCR fragments identified by T4 endonuclease VI to contain variances to establish the specific base variation at that location.

A more detailed description of the procedure is as follows:

A candidate gene sequence is downloaded from an appropriate database. Primers for PCR amplification are designed which will result in the target sequence being divided into amplification products of between 400 and 600 bp. There will be a minimum of a 50 bp of overlap not including the primer sequences between the 5' and 3' ends of adjacent fragments to ensure the detection of variances which are located close to one of the primers.

Optimal PCR conditions for each of the primer pairs is determined experimentally. Parameters including but not limited to annealing temperature, pH, $MgCl_2$ concentration, and KCl concentration will be varied until conditions for optimal PCR amplification are established. The PCR conditions derived for each primer pair is then used to amplify a panel of DNA samples (cDNA or genomic DNA) which is chosen to best represent the various ethnic backgrounds of the world population or some designated subset of that population.

One of the DNA samples is chosen to be used as a probe. The same PCR conditions used to amplify the panel are used to amplify the probe DNA. However, a

fluorescently labeled nucleotide is included in the deoxy-nucleotide mix so that a percentage of the incorporated nucleotides will be fluorescently labeled.

5 The labeled probe is mixed with the corresponding PCR products from each of the DNA samples and then heated and cooled rapidly. This allows the formation of heteroduplexes between the probe and the PCR fragments from each of the DNA samples. T4 endonuclease VII is added directly to these reactions and allowed to incubate for 30 min. at 37 C. 10 ul of the Formamide loading buffer is added directly to each of the samples and then denatured by heating and cooling. A portion of each
10 of these samples is electrophoresed on an ABI 377 sequencer. If there is a sequence variance between the probe DNA and the sample DNA a mismatch will be present in the heteroduplex fragment formed. The enzyme T4 endonuclease VII will recognize the mismatch and cleave at the site of the mismatch. This will result in the appearance of two peaks corresponding to the two cleavage products when run on the ABI 377
15 sequencer.

Fragments identified as containing sequencing variances are subsequently sequenced using conventional methods to establish the exact location and sequence variance.

20 **Example 30 - Identification of Sequence Variances by Informatics-based analysis of gene-sequence databases**

In addition to and/or in conjunction with the molecular biology based approaches for identifying sequence variances in genes, particularly in essential genes, such sequence
25 variances can be identified by analysis of public and/or private genetic sequence databases. Such information can be either genomic or cDNA sequence information.

The data base analysis process includes the following major steps:

1.

1. capture of homologous sequences of a particular gene from data bases. It is preferable to obtain a large number of independent sequences of a particular gene

5

2. analysis of collected sequences of a particular gene to identify authentic sequence variances. This step involves the discrimination of authentic sequence variances, which are sequence variances which actually exist in the population, from sequencing errors and artifacts. It is expected that about 0.1-0.3% of the bases will occur as true variances, while the frequency of sequencing artifacts is expected to be 1-3%. This discrimination utilizes the expected frequencies of occurrence of specific types of nucleotide sequence changes. Such information includes the characteristic frequency of specific transitions and transversions and of the characteristic frequency of deletions and insertions in authentic variations. It uses the frequency of occurrence of known types of sequencing artifacts such as single base insertions or deletions adjacent to repeated C or G nucleotides. Additional information for such discrimination is provided if particular putative authentic variations are observed in multiple independently derived sequences of the gene.

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An implementation of this sequence variance identification process utilizes a reference sequence of an essential gene. Preferably, the reference sequence is a high quality sequence, meaning that there is a low frequency of occurrence of sequencing errors or artifacts. The second step is the retrieval of allelic sequences of that essential gene from available databases such as the BLAST server, the UNIGENE database, or other such sequence database. Such allelic sequences need not be complete, but are preferably long enough to ensure that they are in fact allelic sequences. The third step involves alignment analysis to identify and tabulate sequence differences between the different available sequences. An algorithm for such analysis is the Smith-Waterman local alignment algorithm. Use of an algorithm of this type involves a series of pair-

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wise alignments of each retrieved sequence with the reference sequence. The fourth step involves analysis of the observed sequence differences and assignment of a probability that each sequence difference represents an authentic variance. This analysis utilizes program filters which are combined in a weighted fashion to determine a final probability. Such program filters include comparison of the observed difference with common mutational changes and sequencing errors, a weighting of the reliability of a particular retrieved sequence based on the total number of differences observed, a weighting based on the location within a retrieved sequence where a change was observed and a significant weighting based on the observance of a particular difference in multiple independently derived retrieved sequences.

Using such an implementation, a database analysis with respect to a particular reference sequence produces a list of putative authentic sequence variances and a probability for each of those variances that the sequence difference is an authentic variance. As described above, the probability is obtained through the use of a series of weighted program filters and thus these filters are modified to produce optimal authentic variance discrimination.

Example 31 - Antiproliferative effects of variance specific inhibition of RPA70

This example describes experiments showing the practicality and utility of variance-specific inhibition of essential genes for cancer therapy. Specifically, this example describes *in vitro* experiments showing the design and production of variance-specific oligonucleotides for antisense inhibition of variant alleles of the essential Replication Protein A, 70 kDa subunit (RPA70) for inhibition of RPA70 mRNA, and the use of these oligonucleotides to inhibit cell proliferation and to reduce the number of cells in a variance-specific manner.

Variance-specific inhibition and cell killing with antisense oligonucleotides against

RPA70

These experiments with RPA70 illustrate the feasibility of each of the steps for development of a variance specific inhibitor:

5 Select candidate target gene essential for cell survival or proliferation. As described above, RPA is essential for replication in prokaryotic and eukaryotic cells, mitochondria, phage, viruses and in *in vitro* (SV40) replication systems. The protein is a heterotrimer required for loading DNA polymerase onto the DNA template during cell replication. The 70 kDa subunit, RPA70, is a single strand binding protein that
10 mediates the interaction of RPA with DNA. Without this protein, the replication complex does not associate with DNA and the replication of DNA does not occur.

Confirm chromosome location and LOH frequency. RPA70 is encoded by a single gene locus on chromosome 17p13.3, immediately adjacent to the p53 gene at 17p13.1.
15 LOH involving chromosome band 17p13.3 has been documented in 50-70% of colon, lung, breast, and ovarian cancers. LOH at this locus also occurs in other cancers. The inventor as confirmed LOH involving RPA 70 in breast, colon, lung and other cancers.

Identify common variances in the normal population. We have identified five common
20 variances in the RPA70 gene (Figure 8). The most common occurs in 42% of the normal population. One variance alters the amino acid sequence and is present in 25% of the normal population (44% of Caucasians). This variance occurs within the active DNA binding domain (discussed below). These variances are described in the description above and in Fig. 1.

25 Demonstrate antiproliferative effects due to inhibition of candidate gene. The inventor has shown that inhibition of RPA70 in T24 bladder carcinoma cells with an antisense oligonucleotide reduces cell number. This effect is comparable to treatment of these cells with antisense oligonucleotide against *ras*, previously shown to have antitumor

effects *in vitro* and *in vivo* (Figure 9).

Design variance-specific inhibitor. Variance specific antisense oligonucleotides were designed to differentially inhibit the two variant forms of RPA70. Experiments were performed using tumor cell lines that are homozygous for each form of the target gene. Figure 10 shows inhibition of mRNA levels in Mia Paca II cells by the 13085 oligonucleotide which matches the variance in these cells. In contrast, in T24 cells (and A549 cells, see below) the 12781 oligonucleotide matches the target gene and inhibits mRNA levels. In both cell lines neither the control oligonucleotide differing by one base (13085 in T24 cells and 12781 in Mia Paca II cells) nor a random-sequence oligonucleotide control (13706) inhibit mRNA levels to the same extent as the matched oligonucleotide.

Figure 10 demonstrates that the RPA 70 mRNA can be specifically down regulated in an allele-specific manner. However, the 13085 oligomer used also has a small effect on the level of the unmatched RNA. In order to increase the discrimination we altered the structure of the targeting oligomer, 13085. The results are shown in Figure 11. By shortening the oligomer we retain its ability to down-regulate its matched target RNA (Mia Paca II cells, right half of Figure 11). Strikingly, however, this alteration dramatically altered the ability of this oligomer to down-regulate the mismatched variant RNA T24 cells, left half of Figure 11. The reciprocal regulation by oligomer 12781 was augmented by altering transfection conditions. These data suggest that even simple changes to the rudimentary "first generation" chemistry and transfection techniques can have significant effects in enhancing the ability of the oligomers to recognize and down regulate specific mRNAs.

Achieve variance-specific antiproliferative effects in cancer cells. Cell proliferation in each cell line, determined by BrdU incorporation, was suppressed to a greater degree by the matched oligonucleotide than by the controls differing by one base (Figure 12).

Cell proliferation in A549 cells was inhibited by oligomer 12781 to a greater degree than by oligomer 13085. Cell proliferation in Mia Paca 11 cells was inhibited more by oligomer 13085.

5 Additional studies were performed to characterize the antiproliferative effect in A549 cells (12781 genotype). A dose response curve demonstrates inhibition of BrdU incorporation by the matched oligonucleotide (12781) at concentrations 8-fold lower than the oligonucleotide with one base mismatch (13085) (Figure 13).

10 Cell survival was measured by staining cells with Sulforhodamine B dye 72 hours after treatment with oligonucleotides. Dose dependent reductions in cell number were observed in cells treated with the matched oligonucleotide (12781) but not with an oligonucleotide containing the one base mismatch (13085) (Figure 14). In contrast, in
15 Mia Paca II cells, more cell killing was observed with the 13085 oligonucleotide than with the 12781 oligonucleotide (Figure 15). The oligonucleotides used in these studies have not been optimized for achieving allele-specific effects. Oligonucleotides using advanced chemistries can be utilized to optimize the potency and provide greater discrimination between variant targets at lower levels.

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Example 32 - variance specific inhibition of essential genes

This example describes experiments showing the practicality and utility of variance-specific inhibition of essential genes for cancer therapy including RNA Pol II, and ribonucleotide reductase. Specifically, this example describes *in vitro* experiments
25 showing the design and production of variance-specific oligonucleotides for antisense inhibition of variant alleles of the essential Ribonucleotide Reductase (RR), the design and production of variance-specific oligonucleotides against RR, and the use of these oligonucleotides to inhibit RR mRNA in a variance-specific manner.

Variance-specific inhibition of Ribonucleotide Reductase.

Ribonucleotide Reductase (RR) is an essential gene of nucleoside metabolism. Inhibitors of this function are known to be cell lethal. Two variances were discovered at position 2410 and 2419. Oligonucleotides were synthesized to a sequence spanning these two variations. In one case the oligomer targeted the GnnnnnnnnA variation (oligomer Varia 2410GA or RR2410GA) and in the other case the oligomer targeted the AnnnnnnnnG variant (oligomer Varia 2410AG or RR2410AG). In Mia Paca II cells which contain the GnnnnnnnnA variance, the RR2410GA antisense oligomer dramatically knocked down the level of RR mRNA. However, the oligomer targeting the other variance, oligomer Varia 2410AG, had little to no effect on the level of mRNA (Figure 16). The reciprocal regulation was demonstrated in MDA-MB 468 cells which express the other variance, AnnnnnnnnG (Figure 17). In these cells Varia 2410AG dramatically lowered the level of RR mRNA. In contrast, Varia 2410GA had no effect on the level of mRNA. These data taken together, are another example of allele-specific targeting of gene expression. We are also determining the effect of down regulating RR gene expression on cellular growth.

Example 33 - variance specific inhibition of essential genes using advanced oligonucleotide chemistries.

This example describes experiments showing the practicality and utility of variance-specific inhibition of essential genes for cancer therapy. Specifically, this example describes *in vitro* experiments showing the design and production of variance-specific oligonucleotides for antisense inhibition of variant alleles of the essential Glutamyl/prolyl tRNA Synthetase (EPRS), the design and production of variance-specific oligonucleotides against EPRS, and the use of these oligonucleotides to inhibit EPRS mRNA in a variance-specific manner.

Glutamyl-prolyl-tRNA synthetase (EPRS) is an essential gene, required for the synthesis of both glutamic acid tRNA and proline tRNA. Without EPRS protein synthesis is blocked. Two variances were discovered in this gene at positions 2963 and 2969 in the cDNA. We have demonstrated variance-specific inhibition of this gene with antisense oligonucleotides exploiting several different types of chemistry.

The experiments described above with RPA70 and RR utilized phosphorothioate chemistry. This chemistry was developed to achieve greater stability *in vivo*, and this compound has been used in several successful clinical trials. Phosphorothioates, however have low affinity for the RNA target, and, consequently, relatively lower specificity. We have achieved improved variance-specific inhibition using alternative chemistries. Specifically, we have synthesized hybrid oligonucleotides that contain both phosphorothioate and nucleotides with higher affinities. These hybrids contain "wings" consisting of six nucleotides with a 2' sugar modification (ethoxy-methoxy radical at the 2' position) and either a phosphorothioate or phosphodiester backbone. Between the "wings" is a 8 nucleotide sequence of phosphorothioates that overlaps the variance. (In these constructs the 5' position of cytosine has been methylated.) As shown in Figure 18, variance specific inhibition is observed with the conventional phosphorothioates. Greater inhibition of target mRNA is observed using the hybrid chemistries at lower doses. Inhibition by the matched hybrid oligomer, 14977, occurs at approximately 50-100 nM. The effect is extremely oligomer-specific. The mismatched oligomer, 14971, has no effect on mRNA levels at concentrations as high as 400 nM (Figure 19).

Example 34 - *in vivo* cancer therapy using oligonucleotides

This example describes reported *in vitro* and *in vivo* data on the treatment of cancer in animal models using antisense oligonucleotides against c-raf, showing the expected

correlation between *in vitro* suppression of mRNA and cell proliferation with oligonucleotides, and *in vivo* anticancer activity.

5 *In vitro* evidence for inhibition of mRNA by antisense oligonucleotides and inhibition of cell proliferation is commonly used to predict *in vivo* effects on tumors. This is exemplified by the publication by Monia et al (Nature Medicine, Volume 2 Number 6, June 1996) who demonstrated anticancer effects using oligonucleotides against C-raf kinase. *In vitro* treatment of human tumor cells with appropriate phosphorothioate antisense oligomers led to specific inhibition of C-raf kinase gene expression and
10 subsequent decrease in cellular proliferation, IC₅₀=50-100nM. Administration of C-raf antisense oligomers to nude mice having a tumor burden derived from these cells significantly inhibited tumor growth *in vivo*, IC₅₀= 0.06-0.6 mg/kg. Remarkably, the investigators were able to show that the anti-C-raf oligomers down-regulated the level of C-raf kinase mRNA *in vivo* by assaying mRNA levels in cells removed from the
15 tumor.

Example 35 - *in vivo* cancer therapy by oligonucleotide inhibition of ras

20 This example describes reported *in vivo* data showing an anticancer effect using an allele-specific inhibitor for suppression of mutant H-ras. Schwab *et al* (*Proc. Nat. Acad. Sci. USA* 91:10460-464, Oct 1994) demonstrated antitumor effects of an antisense oligonucleotide specific for the mutant ras in animal models. In these experiments HBL100 cells were transformed with the RAS oncogene. *In vitro* studies
25 demonstrated that the RAS mRNA could be specifically down-regulated by a nanoparticle conjugated phosphodiester antisense oligomer. Only the transforming RAS mRNA was targeted by the oligomer. The normal cellular RAS mRNA, differing by a single base, was not affected by the antisense oligomer. The decrease in RAS expression was associated with a decrease in the growth rate of the cells. The

transformed HBL100 cells were injected into nude mice to form tumors; following subcutaneous injection of nanoparticle-conjugated phosphodiester antisense oligomers, Schwab et al measured both a decrease in targeted tumor weight and volume. Specificity for tumor cell growth correlated well with the *in vitro* data having a 5-fold differential between antisense and control groups.

The authors of this paper are proceeding with clinical trial of these oligonucleotides for the treatment of cancer, demonstrating the potential clinical utility of these methods.

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Example 36. Variance detection by DGGE

This example describes denaturing gradient gel electrophoresis (DGGE), a technique used for the identification of DNA sequence variances in genomic DNA, cDNA or in PCR products amplified from genomic DNA or cDNA. The DGGE method was originally described by Fischer and Lerman (Two Dimensional Electrophoretic Separation of Restriction Enzyme Fragments of DNA. Methods in Enzymology, vol. 68: 183-191, 1979; DNA Fragments Differing by Single Base-Pair Substitutions are Separated in Denaturing Gradient Gels: Correspondence with Melting Theory. Proc. Natl. Acad. Sci. U.S.A. 80:1579, 1983) and has been improved since then by many investigators. See, for example: Myers, et al., Mutation Detection by PCR, GC-Clamps, and Denaturing Gradient Gel Electrophoresis, pp. 71-88 in Erlich, H.A., editor: PCR Technology: Principles and Applications for DNA Amplification, Stockton Press, New York, 1989; Myers, et al., Detecting Changes in DNA: Ribonuclease Cleavage and Denaturing Gradient Gel Electrophoresis, in Davies, K.E., editor: Genomic Analysis: A Practical Approach, IRL Press Ltd., Oxford, 1988, pp. 95-139; E.S. Abrams and V.P. Stanton Jr., Use of Denaturing Gradient Gel Electrophoresis, pp. 71-104 in Lilley, D.M.J. and Dahlberg, J.E., editors: DNA Structures. Part B: Chemical and Electrophoretic Analysis of DNA, Methods in

Enzymology, volume 212, Academic Press, 1992; .) Descriptions of current applications of the technique can be found in

5 The basic principal of DGGE involves the creation of a gradient of denaturant in a gel, which is then used to resolve double stranded DNA (or RNA) fragments on the basis of conformational differences associated with strand melting. The denaturant can be chemical (as in DGGE, where a gradient of formamide and urea is typically used) or thermal (as in a related technique called thermal gradient gel electrophoresis, or TGGE, where a gradient of heat is used). To obtain conditions where double stranded DNA
10 is close to melting, DGGE gels are immersed in a heated bath of electrophoresis buffer, while TGGE gels have a fixed concentration of chemical denaturant.

15 As a double stranded DNA molecule migrates through a DGGE gel from a low concentration of denaturant at the origin to higher concentrations of denaturant toward the end of the gel it eventually reaches a level of denaturant that will cause partial melting. (Some design of DNA molecules is often necessary to assure that the partial melting will occur as desired; see below.) The concentration of denaturant required to melt a given DNA segment is highly sensitive to sequence differences in the DNA, including changes as subtle as a single nucleotide substitution. Partially melted DNA
20 fragments move through gels at a much slower rates than their fully duplex counterparts. Thus two DNA fragments differing at a single nucleotide can be distinguished on the basis of their gel position after an appropriate period of electrophoresis: the fragment with the more stable structure (resulting from, for example, a G:C base pair in place of an A:T pair) will travel further in the gel than its
25 less stable counterpart, because it will encounter the concentration of gradient required to melt it (and consequently dramatically retard or nearly stop its movement) at a point further along in the gel.

The DGGE method reveals the presence of sequence variation between individuals as

shifts in electrophoretic mobility, but does not show the sequence itself. Direct sequencing of DNA fragments (from different individuals) with altered mobility in the DGGE assay will reveal the precise sequence differences among them (see example 37, Variance Detection by DNA Sequencing). From the nucleic acid sequence data, the amino acid sequence can be determined and any amino acid differences can be identified.

The DGGE method is suitable for analysis of restriction enzyme digested genomic DNAs, as initially described by Lerman and co-workers (*supra*) and later extended (Gray; M. Detection of DNA Sequence Polymorphisms in Human Genomic DNA by Denaturing Gradient Blots, American Journal of Human Genetics, 50: 331-346, 1992). DGGE is equally suitable for analysis of cloned DNA fragments or DNA fragments produced by PCR. The analysis of cloned fragments or PCR fragments has the advantage that non-natural sequences, rich in G and C nucleotides can easily be added to the 5' ends (either flanking the cloning site or at the 5' ends of PCR primers). Such DNA fragments have very stable double stranded segments, called GC clamps, at one or both ends. The GC clamps alter the melting properties of the fragments, and can be designed so as to insure melting of the inter-primer segment of the PCR product at a lower temperature than the clamps, thereby optimizing the detection of sequence differences (see Myers *et alia*, *supra* and Myers *et alia*, Nearly All Single Base Substitutions in DNA Fragments Joined to a GC Clamp Can be Detected by Denaturing Gradient Gel Electrophoresis. Nucleic Acids Research 13: 3131, 1985). GC clamps can be rationally designed for any specific DNA fragment of known sequence by use of a computer program (MELT87, written by L. Lerman) that accurately predicts melting behavior based on analysis of primary sequence. When GC clamps are used correctly, the DGGE method is highly efficient at detecting DNA sequence differences. Not only are nearly 100% of differences detected, but the false positive rate is essentially zero. (Abrams, E.S., *et alia*, Comprehensive Detection of Single Base Changes in Human Genomic DNA Using Denaturing Gradient Gel

Electrophoresis and a GC Clamp. Genomics 7: 463-475, 1990.) Recently methods for increasing the throughput of DGGE have been developed, based on multiplex PCR.

The steps in carrying out DGGE with GC clamps are:

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1. *Design DNA fragments with optimal melting behavior.* Select oligonucleotide primers, using GC clamps as necessary, to produce a single melting domain over the length of the sequence to be analyzed. (It may be necessary to divide the sequence into overlapping fragments to achieve this goal.) Design of primers and simulated analysis of fragments can be performed with the computer program described by Lerman. (Lerman, L.S. and Silverstein, K. Computational Simulation of DNA Melting and its Application to Denaturing Gradient Gel Electrophoresis. Methods in Enzymology 155: 482-501, 1987.) The output of the program is the melting map of the fragment, from which it will also be possible to determine the optimal range of denaturant in the gradient and the approximate electrophoresis time for fragments to reach the point of melting in the gradient.

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2. *Amplify the fragment by PCR.* Procedures for optimizing PCR are briefly described in other examples and are well known in the art. Template DNA samples can either be cDNA or genomic DNA and will typically be drawn from a panel of unrelated individuals.

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3. *Pour a denaturing gradient gel.* Briefly, make up two gel solutions containing the desired beginning and end concentrations of denaturant. The gel solutions are generally made up by mixing "0%" and "100%" denaturant stock solutions, where the 0% stock consists of 7% acrylamide in Tris-acetate EDTA (TAE) electrophoresis buffer, and the 100% stock is also 7% acrylamide in TAE, plus 40% formamide by volume and 7 molar urea. Equal volumes of the two solutions (e.g. twelve milliliters of each solution) are poured into the two chambers of a gradient maker (usually between 20 and 40% denaturant in the upstream chamber and 60 to 80% in the lower

25

one) immediately after addition of ammonium persulfate and TEMED for acrylamide polymerization. Open the stopcock of the gradient maker and pour the gradient gel. Usually gels are .75 to 1 mm in thickness, and gel combs that form 10-30 wells are used. With commercially available apparatus multiple gradient gels can be poured simultaneously. Suitable apparatus is sold by several vendors, including the BioRad (Hercules, CA) Dcode system and the C.B.S. Scientific DGGE system.

4. *Place the gel in a heated bath of electrophoresis buffer.* Gels are electrophoresed at elevated temperature which, together with the denaturant, brings the DNA fragments to their melting point. Gels are often run at 60°C in 1X TAE buffer, with constant recirculation of buffer to the upper buffer chamber. Once the gel has been placed in the heated tank and allowed to equilibrate it can be loaded. Multiple gels can be run simultaneously in the same tank with the apparatus listed above.

5. *Load and run gel.* Usually enough PCR product from each sample is loaded on the gel so that samples can be detected by a simple DNA staining procedure; use of radioactivity, dyes or hybridization procedures can thereby be avoided. At least 100 mg of each sample should be loaded, but preferably over 200 ng. Gel running conditions can be estimated from the output of the MELT87 program, however empirical adjustment will often be necessary. Usually a voltage of ~80 to 200V is applied for periods of 5-20 hours, depending on the characteristics of the fragments being analyzed.

6. *Stain and analyze gel.* After electrophoresis gels are stained with ethidium bromide, SYBR Green, silver or some other procedure. The location of PCR products produced with the same primer pairs should be compared. Altered location, and usually the appearance of two or more bands instead of one, signify the presence of DNA sequence differences. (The reason for more than two bands from a diploid sample is that during the terminal cycle of heating and cooling of the PCR

step heteroduplexes are formed between the maternally and paternally inherited alleles. If those alleles differ in sequence, the heteroduplexes will have mispaired nucleotides at the sites of difference. As a result the heteroduplexes will be less stable than either of the homoduplex species, and will consequently melt and be retarded in the gel at a lower concentration of denaturant. Altogether one may see four bands in such samples: two reciprocal heteroduplexes and two homoduplexes.) The specific pattern of fragments in each lane constitutes a signature for a specific nucleotide change.

7. *Sequence DNA fragments with altered mobility.* Examples of all different signatures should next be analyzed by DNA sequencing to identify the base difference(s) accounting for altered mobility in the gradient gel. See example 37 for a description of this procedure and the subsequent steps of recording the sequence variances and analyzing their frequency and structural and functional consequences.

Example 37: Variance detection by sequencing.

Sequencing by the Sanger dideoxy method or the Maxim Gilbert chemical cleavage method is widely used to determine the nucleotide sequence of genes. Presently, a worldwide effort is being put forward to sequence the entire human genome. The Human Genome Project as it is called has already resulted in the identification and sequencing of many new human genes. Sequencing can not only be used to identify new genes, but can also be used to identify variations between individuals in the sequence of those genes.

The following are the major steps involved in identifying sequence variations in a candidate gene by sequencing:

1. Amplification by the polymerase chain reaction (PCR) of 400-700 bp regions of the candidate gene from a panel of DNA samples. The DNA samples can either be cDNA or genomic DNA and will represent some cross section of the world population.
- 5 2. Sequencing of the resulting PCR fragments using the Sanger dideoxy method. Sequencing reactions are performed using fluorescently labeled dideoxy terminators and electrophoresed on an ABI 377 sequencer or its equivalent.
3. Analysis of the resulting data from the ABI 377 sequencer using software programs designed to identify sequence variations between the different
10 samples analyzed.

A more detailed description of the procedure is as follows:

15 A candidate gene sequence is downloaded from an appropriate database. Primers for PCR amplification are designed which will result in the target sequence being divided into amplification products of between 400 and 700 bp. There will be a minimum of a 50 bp of overlap not including the primer sequences between the 5' and 3' ends of adjacent fragments to ensure the detection of variances which are located close to one of the primers.

20 Optimal PCR conditions for each of the primer pairs is determined experimentally. Parameters including but not limited to annealing temperature, pH, $MgCl_2$ concentration, and KCl concentration will be varied until conditions for optimal PCR amplification are established. The PCR conditions derived for each primer pair is
25 then used to amplify a panel of DNA samples (cDNA or genomic DNA) which is chosen to best represent the various ethnic backgrounds of the world population or some designated subset of that population.

PCR reactions are purified using the QIAquick 8 PCR purification kit (Qiagen cat#

28142) to remove nucleotides, proteins and buffers. The PCR reactions are mixed with 5 volumes of Buffer PB and applied to the wells of the QIAquick strips. The liquid is pulled through the strips by applying a vacuum. The wells are then washed two times with 1 ml of buffer PE and allowed to dry for 5 minutes under vacuum.

5 The PCR products are eluted from the strips using 60 ul of elution buffer.

The purified PCR fragments are sequenced in both directions using the Perkin Elmer ABI Prism™ Big Dye™ terminator Cycle Sequencing Ready Reaction Kit (Cat# 4303150). The following sequencing reaction is set up: 8.0 ul Terminator Ready

10 Reaction Mix, 6.0 ul of purified PCR fragment, 20 picomoles of primer, deionized water to 20 ul. The reactions are run through the following cycles 25 times: 96°C for 10 second, annealing temperature for that particular PCR product for 5 seconds, 60°C for 4 minutes.

15 The above sequencing reactions are ethanol precipitated directly in the PCR plate, washed with 70% ethanol, and brought up in a volume of 6 ul of formamide dye. The reactions are heated to 90°C for 2 minutes and then quickly cooled to 4°C. 1 ul of each sequencing reaction is then loaded and run on an ABI 377 sequencer.

20 The output for the ABI sequencer appears as a series of peaks where each of the different nucleotides, A, C, G, and T appear as a different color. The nucleotide at each position in the sequence is determined by the most prominent peak at each location. Comparison of each of the sequencing outputs for each sample can be examined using software programs to determine the presence of a variance in the

25 sequence. One example of heterozygote detection using sequencing with dye labeled terminators is described in Pui-Yan Kwok *et. al.* (Pui-Yan Kwok, Christopher Carlson, Thomas D. Yager, Wendy Ankener, and Deborah A. Nickerson, *Genomics* 23, 138-144 (1994)). The software compares each of the normalized peaks between all the samples base by base and looks for a 40% decrease in peak height and the concomitant

appearance of a new peak underneath. Possible variances flagged by the software are further analyzed visually to confirm their validity

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Example 38. Loss of heterozygosity.

Loss of chromosomes or segments of chromosomes in disease cells results in loss of alleles in the disease cells compared to normal diploid cells. Such allele losses are a common occurrence in cancer, where they have been documented in over 1,500 publications in the past 14 years. More recent work has documented the occurrence of allele loss in other proliferative diseases. Several cytogenetic and molecular techniques have been developed to measure chromosome losses. The molecular techniques are preferable for identification of allele loss because they also show which allele is lost, and are therefore best suited to provide the information needed to implement the present invention.

In order to measure chromosome loss using molecular techniques it is necessary to be able to distinguish the paternally and maternally inherited copies of a given chromosome. DNA variances allow the two copies of a given chromosome to be distinguished because different alleles can be resolved electrophoretically. The standard method for analyzing allele loss in cancer is to compare tumor cell DNA with normal cell DNA, either in a Southern blot or using PCR based techniques. A patient's tumor DNA is said to be "informative" for allele loss only at loci where the patient's normal cells are heterozygous. When such heterozygous loci are examined in tumor cells often only one allele is detected. Such tumor cells have lost the heterozygous state which characterizes all normal somatic cells of the patient, hence the term loss of heterozygosity (LOH).

Several effective molecular procedures have been developed to measure LOH. These procedures have been applied most extensively to cancer tissues, however the same methods are effective in the study of nonmalignant diseases such as atherosclerotic plaques and endometriosis. The main steps are:

5

1. *Identify DNA variances at or near the locus to be investigated for LOH.*

10

LOH usually affects large segments of DNA, ranging from several megabases to an entire chromosome. As a result, accurate estimation of LOH at a specific locus can be obtained by measuring the frequency of LOH at neighboring polymorphic markers on the same chromosome, or more preferably on the same chromosome arm, or most preferably within several 10-20 megabases of the locus. However, to precisely measure LOH at a specific locus requires a variance at the locus. Different types of variances have been used to study LOH, including single nucleotide polymorphisms (SNPs), specifically SNPs that alter restriction endonuclease cleavage sites, called RFLPs. (For details of this approach see Vogelstein, B., et al., Allelotype of colorectal carcinomas. *Science* 244: 207-211, 1989). Also short tandem repeat polymorphisms (STRPs), including di-, tri- and tetranucleotide repeat polymorphisms have been used to measure LOH. (For details of this procedure see Jones and Nakamura, Deletion Mapping of Chromosome 3p in Female Genital Tract Malignancies Using Microsatellite Polymorphisms. *Oncogene* 7: 1631-1634, 1992.) Procedures for identifying variances are described in Examples 28, 29, 30 and 36.

15

20

25

2. *Prepare DNA from paired normal and disease tissue samples from patients being studied.*

Before preparing genomic DNA from tumor tissue it is important to assess tumor cell purity and viability, using microscopic examination of frozen sections if necessary. If embedded pathological specimens are being analyzed tumor cell purity can be

assessed by examining histologic sections before selecting areas for cell isolation and DNA purification. (See Johnson, et al., Direct Molecular Analysis of Archival Tumor Tissue for Loss of Heterozygosity, BioTechniques 19:190-191, 1995, and references therein for description of techniques for purifying tumor cell DNA from archival pathology samples.) Areas of necrosis and extensive admixture of normal and tumor tissue should be avoided. For Southern blotting ~5-10 ug of genomic DNA is required for each sample being analyzed. For PCR based methods as little as 5 to 10 ng of genomic DNA is sufficient; much less will suffice if two successive rounds of PCR amplification are used.

3. *Determine genotype in the normal and disease tissues using a quantitative or semi-quantitative procedure that allows the amount of each allele to be measured. Compare the ratio of alleles in the normal tissue to the ratio in the tumor tissue*

In order to show LOH at a given locus it is necessary to establish that the patient is constitutionally heterozygous at the locus. Thus DNA from normal tissue must be tested, either before or in parallel with tumor tissue DNA. A variety of methods can be used for quantitation of signal from the two alleles. If the alleles are compared on a Southern blot then signal in the bands corresponding to the two alleles can be counted by radioactive or nonradioactive techniques (see Ausubel, et al., Current Protocols in Molecular Biology, John Wiley & Sons). One method employs phosphor technology using a Molecular Dynamics PhosphorImager with ImageQuant software to measure signals. If the alleles are compared after PCR amplification then DNA sequencing can provide accurate quantitation of allele ratios. See, for example, Goldsborough and Kornberg, Allele-Specific Quantification of Drosophila Engrailed and Inverted Transcripts, Proc. Natl. Acad. Sci. U.S.A. 91:12696-12700, 1994.

Using highly variable markers distributed across the genome a comprehensive map of LOH can be assembled for a specific cancer type. Such data sets have been termed allelotypes. Separate studies are necessary for different cancer (or other disease) types

as the patterns of LOH differ significantly in different diseases.

Other techniques that have been used to detect allele loss in cancer include Comparative Genomic Hybridization (CGH) and Representation Difference Analysis (RDA) however these methods are more complex than the Southern blot or PCR based techniques. Chromosome loss can also be detected cytogenetically. Mitelman (Catalog of Chromosome Aberrations in Cancer. Wiley-Liss, New York, 1995.) has compiled a catalog of over 10,000 published karyotypes of cancer cells which documents chromosome deletions as well as other changes.

Example 39. Small molecule inhibitors of variant sequences:

Methylguanine Methyltransferase (MGMT)

Gene VARIA 1534

The methylguanine methyltransferase gene is essential for cell growth or survival in the presence of alkylating agents

Methylguanine methyltransferase (MGMT) is a nuclear protein that repairs alkylating agent damage, specifically alkylation of the O6 position of guanine bases in genomic DNA. MGMT acts as a suicide protein in removing methyl or alkyl groups from guanine and covalently binding them to cysteine 145 of MGMT. The protein is subsequently degraded; it does not act as an enzyme. O6-benzylguanine is an inhibitor of MGMT that mimics the natural substrate, alkylated DNA; transfer of the benzyl group to cysteine 145 of MGMT inactivates the protein. Concurrent administration of O6-benzylguanine and an alkylating agent such as carmustine (BCNU) or lomustine (CCNU) renders tumor cells more sensitive to the toxic effects of the nitrosoureas by inactivating MGMT and thereby inhibiting the tumor cells ability to repair alkylated

DNA. MGMT is thus a conditionally essential gene in the presence of nitrosoureas and other alkylating agents. The conditional essentiality of MGMT has been demonstrated in mice. Animals homozygous for disrupted MGMT genes are more than ten times as sensitive to alkylating agents as normal mice. The relative sensitivity has been measured as the LD50, the dose required to kill 50% of treated animals. (Tsuzuki, T., et al. Targeted disruption of the DNA repair methyltransferase gene renders mice hypersensitive to alkylating agent. *Carcinogenesis* 17: 1215-1220, 1996.) O6-benzylguanine is being developed as a chemosensitizing agent (with alkylating agents) for treatment of human cancer. This treatment regimen is not specific for cancer cells.

In a cancer patient with two alternative functional MGMT alleles in normal tissues and LOH at 10q23 resulting in only one copy of MGMT in cancer cells, an allele specific inhibitor of MGMT could be used to specifically sensitize cancer cells to the action of alkylating agents. Treatment would consist of the administration of the appropriate allele specific inhibitor (directed to the one allele remaining in cancer cells) plus an alkylating agent. The tumor cells would be unable to effectively repair the alkylating agent induced DNA damage, while the uninhibited allele in normal cells would be able to function. Thus normal cells, including sensitive normal cell populations such as bone marrow stem cells, would be able to tolerate higher doses of alkylating agents than cancer cells.

The MGMT gene and encoded protein are polymorphic

Four variances in human MGMT have been discovered by the inventors or reported in the literature, including three variances that affect the protein sequence. There is a C/T variance at nucleotide 255 (11% heterozygotes among 36 individuals surveyed) which does not affect the encoded protein. There is a second C/T variance at nt. 346 which results in a L84F amino acid variance (5% heterozygotes among 36 individuals surveyed). There is an A/G variance at nt. 523 which results in a I143V amino acid

variance (24% heterozygotes among 36 individuals surveyed). This variance occurs only two residues from the active site cysteine at 145. A fourth variance, G/A has been reported in the Japanese population at codon 160, GGA vs. AGA, resulting in a glycine vs. arginine amino acid variance. Fifteen percent of 40 Japanese individuals studied were heterozygotes for this variance. (Imai, Y., et al. A polymorphism at codon 160 of human O6-methylguanine-DNA methyltransferase gene in young patients with adult type cancers and functional assay. *Carcinogenesis* [London] 16:2441-24445, 1995.)

Allele specific inhibitors of MGMT

Two of the amino acid variances in MGMT, at residues 143 and 160, are near the active site of the protein. Substantial work has already been done to characterize the functional consequences of the residue 160 glycine/arginine variance. Studies of MGMT kinetics and activity have shown that the 160arginine allele is at least 20 fold more resistant to O6 benzylguanine inactivation, measured as an increase in the ED50 and or as a reduction in the production of guanine from O6-benzyl[8-3H] guanine. The 160gly and 160arg forms of MGMT were nearly equal in alkyltransferase activity in an assay that measured repair of O6-methylguanine in methylated DNA. These results demonstrate variance-specific effects of a small molecule, O6-benzylguanine, on normal (non-mutant) alleles of the conditionally essential MGMT gene. (Edara, S., et al. Resistance of the human O6-alkylguanine-DNA alkyltransferase containing arginine at codon 160 to inactivation by O6-benzylguanine. *Cancer Research* 56: 5571-5575, 1996)

Administration of O6-benzylguanine to patients who are heterozygous for the variance in their normal cells, and contain only the alternative form of the gene with a glycine residue at position 160 in their cancer cells, together with methylating or chloroethylating agents, will specifically sensitize cancer cells to the cytotoxic effects of the alkylating agents without increasing toxicity to normal cells which, since they

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contain the O6-benzylguanine resistant 160arginine form of the protein, will continue to repair alkylated DNA.

5 There is no published data concerning the residue 143 variance, however the proximity of this variance to the active site - both in the primary sequence and upon inspection of the three dimensional structure of the bacterial AGT protein, a functional and structural homolog of human MGMT - suggests that allele specific drugs could be discovered for this variance.

10 The structural difference between 143isoleucine and 143valine is a hydrophobic methyl group. It is well known that most small molecule protein inhibitors interact via hydrophobic interactions. Favorable Van der Waals distances between hydrophobic groups of a substrate and a ligand are vital for high affinity interaction. One possible mechanism of allele specific inhibition would be to exploit the greater
15 bulk of the isoleucine by finding a small molecule that fits into the active site pocket of the valine allele but has a very unfavorable Van der Waals interaction the methyl group of the isoleucine. Other schemes based on the different size and geometry of isoleucine and valine could also be effective.

20 One approach to identification of such inhibitors would be to make small molecule libraries in which various positions of guanine are substituted with moities of appropriate size and structure. Such libraries could then be tested in various screens of MGMT activity. The two alleles (143isoleucine and 143valine, or any of the other allele pairs of MGMT described above) would be assayed in parallel.

25 Identification of molecules with allele specific inhibitory activity could be the basis for synthesis of additional libraries in which the moities that are best correlated with differential activity are further varied. Methods for the iterative design of high affinity or highly discriminating small molecule inhibitors are known in the art.

Libraries of restricted size can be screened for allele specific inhibitors using a combinatorial strategy based on known inhibitors of MGMT such as O6-benzyl-guanine. A library or libraries can be constructed in which substitutions are introduced at positions C6 and N9 which have previously been found to affect inactivation of MGMT, or at positions C2 and N8 which can be easily substituted. For example a series of 4(6)-(benzyloxy)-2,6(4)-diamino-5-(nitro or nitroso)pyrimidine derivatives and analogs in which 4(6)-benzyloxy groups were replaced with (2-, 3-, or 4 fluorobenzyl)oxy or (2-, 3-, or 4-pyridylmethyl)oxy groups have been synthesized and tested for MGMT inhibition. (Terashima I., and K. Kohda. Inhibition of human O6-alkylguanine-DNA alkyltransferase and potentiation of the cytotoxicity of chloroethylnitrosourea by 4(6)-(Benzyloxy)-2,6(4)-diamino-5-(nitro or nitroso)pyrimidine derivatives and analogues. *J Med Chem* 41: 503-508, 1998.) Substitutions at N7 have been found to be detrimental in general (Moschel, R.C. et al & Pegg, A. E., *J. Med. Chem.* 35: 4486-4491, 1992).

Combinatorial libraries can be constructed according to a published procedure (Norman, T. C. et al., A Structure-Based Library Approach to Kinase Inhibitors. *J. Am. Chem.Soc.* 118: 7430-7431, 1996) where guanine based libraries were made by anchoring a chemically modified guanine (at C6, C2, or C8) to solid supports at C2 via a glycinamide linkage or at N9 via a hydroxyethyl linkage. Chemical reactions can be carried out to introduce a library of hydrophobic substituents of different size at positions C6, C2, or C8. Hydrophobic substituents of various bulkiness and orientation can be introduced through derivatives of O6-benzyl and O6-phenyl groups, O6-alkyl groups, N9-alkyl groups, and C2-amino-alkyl groups.

Libraries constructed as above can be screened for MGMT activity in several types of assays. Methods for bacterial expression and purification of human MGMT protein have been described (see Edara, et al., cited above). Both allelic forms of MGMT could be screened for repair of alkylated or methylated DNA by measuring transfer of tritium from a tritium labelled (methylated) DNA substrate in the

presence of various concentrations of library compounds for various times.

Alternatively, library compounds could be tritiated and MGMT proteins could be screened for the rate at which they interact with (either via association or cleavage of a moiety from the compound). Other assays for MGMT activity are known in the art.

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Example 41. Clinical use of variance specific inhibitors for treating cancer

10 Inhibitors that are the object of the present invention are designed to be administered to patients who are heterozygous for the target gene, meaning that their cells normally contain two alternative copies of the gene, one that is sensitive to inhibition by said inhibitors, and one that is not sensitive to said inhibitors. It is apparent that several such inhibitors may be developed according to this invention

15 targeted to alternative alleles of a single target gene or to several different target genes. The inventors propose that a series of such inhibitors will be developed according to this invention.

The clinical use of this invention involves the steps of:

- 20 (a) testing normal cells from a patient to identify target genes that are heterozygous, present in two alternative forms.
- (b) testing biopsy tissue from a tumor or proliferative lesion to determine whether one of the two alternative forms is eliminated due to LOH.
- (c) selecting a drug for inhibition based on the presence of the sensitive allele in the
- 25 tumor and the presence of an insensitive allele in normal cells
- (d) administering said drug to the patient in an appropriate dose to inhibit the essential function in the cancer cell.

Testing of normal cells to identify heterozygosity of the target gene is performed

using conventional diagnostic methods that are known in the art. Normal cells are commonly derived from a blood sample, hair sample, or buccal smear.

Alternatively normal cells may be obtained by cultivating primary cells such as lymphoblasts or fibroblasts in vitro. The presence of two alternative alleles may be determined by methods including allele-specific hybridization with oligonucleotides containing the variant sequences and a number of non-variant nucleotides to allow differential binding to the alternative forms of the gene or other methods known in the art using purified DNA or RNA or amplified DNA or cDNA sequences.

Testing of biopsy tissue is performed by separating tumor cells or cells of the proliferative lesion to isolate a sample of cells characteristic of the proliferative lesion for analysis. This is performed by a variety of methods known in the art including manual dissection or laser assisted methods for eliminating normal cells or selecting abnormal cells. Samples of abnormal tissue, and samples of normal tissue as a control, are analyzed to identify the presence or absence of alternative forms of the target gene. The presence of two alternative alleles may be determined by methods including allele-specific hybridization with oligonucleotides containing the variant sequences and a number of non-variant nucleotides to allow differential binding to the alternative forms of the gene or other methods known in the art using purified DNA or RNA or amplified DNA or cDNA sequences.

Selection of a drug for administration will be based on clinical trial data indicating that the drug is effective in eliminating abnormally proliferating cells and causing an improvement in the patient's clinical condition for patients who have the sensitive allele of the target gene in their pathological lesion. In one aspect of this invention, the product label will describe that the drug is indicated in patients who have only a specific allele of the target gene in their lesion and an alternative allele in their normal cells. Any such drug will be indicated only for a fraction of patients having two alternative alleles of the target gene in their normal cells and LOH. The fraction of patients who may be treated with any one drug may be determined by

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5 multiplying the number of patients with a given cancer times the fraction of tumors exhibiting LOH of the target gene locus times the fraction of patients who will be heterozygous. For a target gene exhibiting 50% heterozygosity in the population and a 70% fraction of LOH in a specific cancer (several such examples are shown), a single inhibitor will treat ~17% of such cancers. A second compound directed against the alternative allele would treat another 17% of said cancer. In the preferred use of this invention, a panel of such drugs will be available enabling therapy with at least one such drug in most patients.

10 Administration of the drug to the patient ration to the patient will involve conventional means such as parenteral, oral, or intratumoral administration. The route of administration will be determined separately for each inhibitor and will be based on the bioavailability of the compound to the lesion. The compound may be administered in one or more doses as a single agent or in combination with other
15 allele specific agents or conventional antiproliferative drugs or agents commonly used for the treatment of cancer or support of cancer patients.

20 **Example 42. Cell Division Cycle 25C (CDC25C) - Gene VARIA10**

Cdc25C is essential for cell growth

25 A vital regulator of cell proliferation is the protein kinase Cdc2, whose activation at the end of G2 of the cell cycle initiates mitosis. Gene disruption experiments in yeast confirm the importance of this protein, as cells lacking Cdc2 fail to progress through the cell cycle. As would be expected for such an important protein, Cdc2 activity is tightly regulated. Its activity depends on complex formation with Cyclin B, a protein that accumulates through the cell cycle and is then abruptly degraded during mitosis. Phosphorylation of Cdc2 on Tyr-15 and Thr-14 by the Wee1/Mik1

kinases maintains the Cdc2/Cyclin B complex in an inactive state until the end of G2. The dual-specificity phosphatase Cdc25C is then stimulated to dephosphorylate Cdc2 on both residues, resulting in activation of the complex. Just as Cdc2 is essential for cell growth, the regulation of its activity is essential. The best evidence for this is that the individual disruption of *cdc2*, cyclin B, *wee 1* and *cdc25* in the yeast *S. pombe* are lethal events. When *cdc25* is deleted from these cells they display a phenotype consistent with their function; they grow without dividing, becoming dramatically elongated.

The human CDC25C gene and protein have variances

The CDC25C cDNA was cloned by Sadhu *et al.* (1) (Genbank accession number M34065, GI number 181075). To determine whether CDC25 is polymorphic, VARIAGENICS scanned cDNA from 32 unrelated individuals using the T4 Endonuclease VII method, which involves the cleavage of DNA heteroduplexes followed by DNA sequencing of polymorphic regions (see description of method in examples). A transversion at nucleotide 1099 (G or C) was identified (nucleotide numbering is from reference 1). This results in an amino acid difference at residue 297, with G encoding glycine and C encoding arginine. Overall, 9.4% of individuals analyzed are heterozygous. The rate of heterozygosity increases to 33.3% in Caucasians.

The human CDC25C gene maps to chromosome 5q31, a site of frequent loss of heterozygosity

Sartor *et al.* (2) mapped the human CDC25 gene to 5q31 by fluorescence in situ hybridization using the cDNA cloned by Sadhu *et al.* This mapping location was confirmed by Taviaux and Demaille (3), also using fluorescence in situ hybridization. There have been many studies of LOH on 5q, particularly the 5q21-

q22 region where the Adenomatous Polyposis Coli (APC) tumor suppressor gene lies. The most extensively studied cancers are those of the gastrointestinal tract, lung and ovary. There have been fewer studies of the 5q23-q33 region just distal to APC (where CDC25C lies), however the available data suggests that LOH occurs in this region at a frequency of ~30% in cervical cancer (4), 20-40% in colon cancer (5,6), 30-50% in ovarian cancer (7,8), up to 38% in stomach cancer (9), and 23% in testicular cancer (10). There is also evidence for LOH in head and neck, lung and liver cancers. In most of these studies only one or two markers were used. Definitive assessment of LOH frequency at the CDC25C locus will require direct analysis of the polymorphisms identified in various tumor types.

References

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Example 43. Dihydropyrimidine Dehydrogenase (DPD)

DPD is conditionally essential

Dihydropyrimidine Dehydrogenase is essential for cell survival in the presence of pyrimidine nucleotide analogs such as 5-FU and fluorodeoxyuridine. 5-fluorouracil (5-FU) and related compounds are antineoplastic drugs used in the treatment of breast, gastrointestinal, head and neck and other cancers. These drugs have widely varying clinical effects in cancer patients, ranging from induction of complete response (tumor disappearance) in some patients to severe toxicity in others. There is currently no reliable basis for predicting individual patient responses, and therefore patients receiving 5-FU must be monitored carefully for toxic reactions.

There are a variety of anabolic and catabolic pathways that affect the action of 5-FU (reviewed in Goodman and Gilman, *The Pharmacological Basis of Therapeutics*, 8th edition). For example, in order to exert its antiproliferative effects the pyrimidine analog 5-FU must be converted enzymatically to the nucleotide level (fluorodeoxyuridine) by phosphorylation and ribosylation; fluorodeoxyuridine is sometimes given directly because it bypasses most of these steps, and simply requires phosphorylation by thymidine kinase. The 5-fluoronucleotide is an irreversible inhibitor of thymidylate synthase, the enzyme which converts dUMP to dTMP and is required for de novo synthesis of thymidine, and hence for DNA

synthesis.

There is a three step pathway for catabolism of pyrimidines (thymine and uracil) to beta alanine. Pyrimidine analogs such as 5-FU are catabolized by the same pathway. The first and rate limiting step in this pathway is catalyzed by dihydropyrimidine dehydrogenase (DPD). DPD accounts for catabolism of as much as 90% of a 5-FU dose in normal individuals, and the half life of 5-FU in normals is ~8-20 minutes. Patients homozygous for mutant DPD alleles have been identified, a condition variously called DPD Deficiency, Hereditary Thymine-Uraciluria or Familial Pyrimidinemia. In such patients ~90% of 5-FU is excreted unchanged in the urine, and the drug has a half life longer than 2.5 hours. As a result of the drastically reduced catabolism of 5-FU the toxic effects of the drug are magnified and patients are subject to severe toxic reactions. There are reports of deaths in patients with DPD deficiency after treatment with 5-FU. Thus cell (and organism) survival in the presence of 5-FU depends on presence of functional DPD protein to transform 5-FU to the inactive dihydroxy metabolite.

This principal has also been demonstrated in cancer cells both in vitro and in vivo: cancer cells with lower DPD levels are more susceptible to the toxic effects of 5-FU. It has been suggested that measuring DPD levels would be useful for calibration of 5-FU dosage.

The DPD gene exhibits variances

We have identified four common sites of variance in DPD mRNA by screening cDNA from 36 unrelated individuals. The variant nucleotides are 166, 577, 3925 and 3937 (see DPD Variance Table; numbering is from Yokota, et al. cDNA Cloning and Chromosome Mapping of Human Dihydropyrimidine Dehydrogenase, an Enzyme Associated with 5-fluorouracil Toxicity and Congenital Thymine

Uraciluria. Journal of Biological Chemistry. 269: 23192-23196, 1994). Two of the
variances in nucleotide sequence alter the amino acid coding sequence: amino acid
29 is usually cysteine but arginine alleles were also detected; cys/arg heterozygotes
were found at a frequency of 11%. Residue 166 of DPD is reported to be
5 methionine but valine is present at 166 in some alleles; 9% of the population
surveyed are met/val heterozygotes. One double heterozygote was identified out of
36 patients. Both these amino acid polymorphisms are located in the N-terminal
NAD/FAD binding domain of DPD. Residue 166 is located in a highly conserved
domain of DPD. Two other polymorphisms are located in the 3' untranslated region
10 of DPD, only 11 nucleotides apart.

*The DPD gene maps to chromosome 1p22, a region frequently subject to LOH in
different cancers*

The DPD gene has been mapped to chromosome 1p22 by fluorescence in situ
15 hybridization. LOH at 1p22 has been reported in colon, breast, and other cancers.

*Allele specific inhibition of DPD to potentiate 5-FU action in cancer cells with
LOH at the DPD locus*

20 The DPD gene is polymorphic and conditionally essential in the presence of 5-FU.
These properties can be exploited in a therapeutic strategy for cancer patients with
LOH at the DPD locus. Specifically, in a patient with two alternative alleles for
DPD in normal cells and one allele in cancer cells due to LOH, an allele specific
drug can be used to sensitize cancer cells to the action of 5-FU by inhibiting its
25 catabolism. Cancer cells (but not normal cells) would be poisoned by high levels of
5-FU due to low clearance. Normal cells, containing an uninhibited allele, would be
able to catabolize DPD at close to normal levels.

Alternatively, patients heterozygous for functional and defective copies of DPD,

and in whom LOH resulted in loss of the functional allele, could be treated by 5-FU without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at DPD and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to 5-FU even though they might have cancers not traditionally treated with pyrimidine analogs.

Example 44. Fanconi Anemia genes A, B, C, D, E, F, G and H (FAA, FAB, FAC, FAD, FAE, FAF, FAG, FAH)

The Fanconi Anemia genes are conditionally essential.

The Fanconi Anemia genes are essential for cell growth or survival in the presence of DNA cross linking agents. In order for cells to survive or proliferate in an abnormal environment characterized by the presence of DNA cross linking molecules such as Mitomycin C and diepoxybutane it is necessary that the cells are capable of efficiently repairing damage caused by these agents. Cells contain proteins necessary for such repair. One way such repair proteins can be identified is by absence of function in specific patients who, as a consequence, are particularly susceptible to the toxic effects of cross linking agents.

Fanconi Anemia (FA) is a hereditary disease, autosomal recessive in transmission, characterized by progressive bone marrow failure, birth defects and predisposition to malignancies. FA patients are hypersensitive to the toxicity of DNA cross linking agents. This hypersensitivity can be measured in cultured FA cells, which is one method used to establish the diagnosis of FA.

Patients heterozygous for defective FA genes are generally not hypersensitive to

DNA crosslinking agents in contrast to those that are homozygous. This suggests that treating heterozygous cancer patients with an inhibitor specific for one allele of the FA gene (and thereby reducing levels of FA protein function by up to 50% in normal cells) would be well tolerated. Inhibition of the FA allele present in cancer cells but not the alternative form present only in normal cells would make cancer cells selectively sensitive to crosslinking agents, leading to a cytotoxic antiproliferative effect. Normal cells would be able to repair damage caused by such agents, by analogy to the clinical data from patients heterozygous for defective FA genes.

The FA genes and gene products are polymorphic

Seven FA genes have been identified by complementation studies. The genes for FAA and FAC have been cloned. DNA variances have been reported in both genes. For example, Savino et al. report three variances in FAA, all of which alter the protein coding sequence. (Savino, M., et al. Mutations in the Fanconi Anemia Group A Gene (FAA) in Italian Patients. American Journal of Human Genetics 61:1246-1253, 1997.) The location of these variances is shown in the Table below, reproduced from the paper by Savino.

Variances in the FAA Gene

| Polymorphic nucleotide | Alternate bases | Affected amino acid residue | Alternate amino acids | Frequency of rare allele |
|------------------------|-----------------|-----------------------------|-----------------------|--------------------------|
| 796 | A, G | 266 | Thr, Ala | .29 |
| 1501 | G, A | 501 | Gly, Ser | .40 |
| 2426 | G, A | 809 | Gly, Asp | .30 |

FA genes map to chromosomes that are frequently subject to LOH in different cancers

The FAC gene maps to chromosome 9q22.3, (as do three other FA complementation

groups according to Stratthdee, C.A., et al. Evidence for at least four Fanconi anaemia genes including FACC on chromosome 9. *Nature Genetics* 1: 196-198, 1992). The FAA gene maps to chromosome 16q24.3. FAD maps to 3p26-p22. All FA genes mapped so far lie in regions subject to frequent LOH. LOH affecting chromosome 9 is well documented in many cancers. For example, loss of the 9q arm is well documented in cancers such as bladder, esophagus, ovary, testis and uterus. LOH frequencies in these cancers range from 20% to 62%. LOH affecting chromosome arm 16q, particularly the 16q24 region is well documented, particularly in breast, prostate and liver cancers. For example, in six detailed studies of breast cancer in the 16q22-q24 region LOH frequencies of 40-60% have been reported. Further, 16q22 LOH has been reported in 25-90% of liver cancers, with the average around 45%. Less extensive studies of other cancer types report 16q22 LOH in 19% of bladder cancers, 20% of colon cancers, 19-27% of esophageal cancers, 25% of small cell lung cancers, 16-37% of ovarian cancers 22% of uterine cancers, and 31-50% of prostate cancers. Loss of chromosome 3p26-21 is common in lung cancer, kidney cancer, head and neck cancer and breast cancer among other cancers. Reports of >50% LOH are common in these cancer types.

Other genes conditionally essential for response to DNA cross linking agents

In a related aspect, other genes which, when defective, sensitize cells to toxic effects of DNA crosslinking agents would be amenable to the therapeutic strategy outlined above for the FA genes. Specifically, in a patient with two alternative alleles for such a gene and LOH at the relevant locus, an allele specific drug could be used to sensitize cancer cells to the action of cross linking agents. Such drugs could then be used to treat cancer patients constitutionally heterozygous for two normal alleles at the relevant locus, in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist in the administration of the appropriate allele specific inhibitor plus a cross linking agent or treatment to induce damage in all cells. Cancer

cells (but not normal cells) would be rendered unable to respond by inhibition of expression of the relevant repair gene. Examples of such genes are the excision repair cross complementing (ERCC) genes, twelve of which have been identified (see Target Gene Table). Defects in these genes are associated with Xeroderma Pigmentosum and Cockayne Syndrome. (Scriver, C. R. et al., The Metabolic and Molecular Bases of Inherited Disease, 7th edition, McGraw Hill, New York, 1995.)

Alternatively, patients heterozygous for functional and defective copies of such genes, and in whom LOH resulted in loss of the functional allele, could be treated by a cross-link inducing procedure without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at the target locus and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to cross linking agents or procedures even though they might have cancers not traditionally treated with such agents.

Example 45. Asparagine Synthetase (AS).

Variagenics Target Gene _____

Asparagine Synthase is conditionally essential

Cells require a continuous supply of amino acids for protein biosynthesis. Cells can import amino acids from serum via amino acid transporters (the only source besides protein catabolism for the ten essential amino acids), or amino acids cells can be synthesized *de novo* by cells (only an option for the ten nonessential amino acids). The essential amino acids are isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, valine and histidine. Alterations in the nutritional environment of growing cells that result in a decreased extracellular concentration of essential amino

acids cause arrested cell growth and may result in cell death.

Even a nonessential amino acid can become essential in a cell where (i) at least one enzyme required for its biosynthesis is not expressed (perhaps due to downregulation in response to an abundant extracellular supply of the amino acid), or (ii) the biosynthetic pathway is blocked by an inhibitor.

Asparagine is a nonessential amino acid which is, however, essential for survival of rapidly dividing cells that are not expressing asparagine synthetase, the terminal enzyme in asparagine biosynthesis. Asparagine synthetase, considered to be a housekeeping gene, catalyzes the ATP dependent conversion of aspartic acid to asparagine in mammalian cells. A number of different cancer types do not usually express asparagine synthetase, including childhood acute leukemias. One common therapeutic used in the treatment of childhood acute lymphocytic leukemia is the enzyme L-asparaginase (purified from *E. coli* or *Erwinia carotovora*) which, upon injection, rapidly depletes serum asparagine (by hydrolysis to aspartate), thereby lowering blood levels of asparagine to undetectable levels within hours of injection. (Ohnuma, T. et al. Biochemical and Pharmacological Studies with L-Asparaginase in Man. Cancer Research 30: 2297-2305, 1970.) Leukemic cells have high rates of protein synthesis but do not express asparagine synthetase and are therefore highly vulnerable to the rapid loss of asparagine and consequent shutdown of protein synthesis. Cell death after L-asparaginase induced asparagine starvation has been shown to be apoptotic. (Bussolati, O. Characterization of Apoptotic Phenomena Induced by Treatment with L-Asparaginase in NIH3T3 Cells. Experimental Cell Research 220: 283-291, 1995.) After one or more doses leukemic cells often become resistant to L-asparaginase due to induction of asparagine synthetase activity and consequent autonomy for asparagine.

In a patient with two alternative alleles for asparagine synthetase and LOH at 7q, an

allele specific drug could be used to sensitize cancer cells to the action of L-asparaginase. Such drugs could then be used to treat cancer patients constitutionally heterozygous for two normal alleles at the asparagine synthetase locus, in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist in the administration of the appropriate allele specific inhibitor plus L-asparaginase to deplete the concentration of this amino acid in serum while rendering cancer cells (but not normal cells) unable to respond by upregulating asparagine synthetase.

The Asparagine Synthetase gene maps to chromosome 7q21.3, a region frequently subject to LOH in different cancers

The asparagine synthetase gene has been mapped to chromosome 7q21.3 by fluorescence in situ hybridization, following localization to 7q by analysis of somatic cell hybrids. The q21 region of chromosome 7 is subject to frequent LOH, particularly in colon, breast and prostate cancers. 7q21.3 LOH is detected in up to 50% of colon cancers, up to 37% of prostate cancers (83% of prostate cancers have LOH in the adjacent chromosome band, 7q31) and in 10-55% of breast cancers, where again, there is even more frequent LOH in 7q31. LOH at 7q21 has also been reported in uterine cancer and head and neck cancer. Several other cancer types have not yet been well studied for LOH affecting this region.

Example 46. Methionine Synthase (MS).

Variagenics Target Gene _____

Methionine Synthase is conditionally essential in dividing cells

Cells require a continuous supply of amino acids for protein biosynthesis. L-

methionine is one of ten essential amino acids. Consequently dividing cells must obtain their methionine from serum via amino acid transporter (the only source besides protein catabolism for the ten essential amino acids). Alterations in the nutritional environment of growing cells that result in a decreased extracellular concentration of essential amino acids such as methionine cause arrested cell growth and may result in cell death. Cancer cells are particularly sensitive to methionine deprivation. (Tan, Y., et al., Anticancer Efficacy of Methioninase in vivo. *Anticancer Research* 16: 3931-3936.)

The cellular requirement for methionine can be bypassed: if L-homocysteine is provided to cells it can be methylated to form methionine by the enzyme methionine synthase (MS). In this reaction the methyl group is provided by 5-methyltetrahydrofolate and MS-bound methylcobalamin serves as an intermediate methyl carrier. A second enzyme may be required for reductive activation of methionine synthase, based on complementation studies.

It occurred to the inventors that the apparent antineoplastic effects of methionine deprivation could be enhanced and made tumor cell specific by preventing cells from converting endogenous homocysteine to methionine by allele specific inhibition of methionine synthase (or other enzymes required for the conversion of homocysteine to methionine; see: Scriver, C., et al., editors, The Metabolic and Molecular Basis of Inherited Disease. McGraw Hill, New York, pp. 3111-3128 and 3129-3149). This strategy would be useful in cancer patients that are heterozygous for methionine synthase (or another enzyme required for conversion of homocysteine to methionine) and who have LOH at the methionine synthase (or other) gene locus. In such patients an allele specific inhibitor of MS directed to the sole allele present in cancer cells, coupled with methionine starvation or methioninase treatment, would selectively prevent tumor cells from responding to methionine deprivation. The provision of supplemental homocysteine, which could only be converted to methionine by the

normal cells, would provide a way to amplify the differential toxicity to cancer cells. Also, the methionine analog ethionine has been shown to potentiate the effects of methionine starvation. (Poirson-Bichat, F., et al., Growth of methionine-dependent human prostate cancer (PC-3) is inhibited by ethionine combined with methionine starvation. Br. J. Cancer 75: 1605-1612.) Ethionine or similar agents could be used in conjunction with an allele specific inhibitor of methionine synthesis.

An alternative approach to allele specific therapy of cancer cells with LOH would be to target the amino acid transport system for methionine in patients heterozygous for this protein and in whom only one allele is present in cancer tissue as a result of LOH. This would result in selective methionine starvation for cancer cells. Allele specific transport inhibition could be combined with methionine starvation or methioninase treatment to enhance the cytotoxic effect.

The Methionine Synthase gene maps to chromosome 1q43, a region subject to LOH in several cancers

The MS gene has been mapped to chromosome 1q43 by fluorescence in situ hybridization. The q43 region of chromosome 1 is subject to frequent LOH particularly in colon, head and neck, ovarian and liver cancers, where LOH frequencies vary from 11 to 39%. LOH at 1q43 has also been reported in cervix, pancreas, stomach and testis cancers. Several other cancer types have not yet been well studied for LOH in this region.

Other amino acid biosynthetic enzymes are candidates for allele specific inhibition

It will be evident to one skilled in the art that strategies similar to those described above for asparagine (an essential amino acid) and methionine (a non-essential amino acid) could be undertaken for other amino acid biosynthetic enzymes. For example,

L-glutaminase has also been shown to have antiproliferative effects on mammalian cell growth. Allele specific blockade of glutamine synthesis in heterozygous patients with LOH for genes essential for glutamine synthesis could be the basis of a cancer specific therapy.

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Example 47. Methylthioadenosine phosphorylase (MTAP).

Variagenics Target Gene _____

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Methylthioadenosine phosphorylase can convert methylthioadenosine to methionine, an essential amino acid

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Cells require a continuous supply of amino acids for protein biosynthesis. L-methionine is one of ten essential amino acids. Consequently dividing cells must obtain methionine from serum via amino acid transporter (the only source besides protein catabolism or conversion of L-homocysteine). Alterations in the nutritional environment of growing cells that result in a decreased extracellular concentration of essential amino acids such as methionine cause arrested cell growth and may result in cell death. Cancer cells are particularly sensitive to methionine deprivation. (Tan, Y., et al., Anticancer Efficacy of Methioninase in vivo. *Anticancer Research* 16: 3931-3936.)

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The cellular requirement for methionine can be bypassed by conversion of L-homocysteine to methionine as discussed above. An alternative pathway for methionine synthesis is conversion of 5'-methylthioadenosine (5'-MTA) via the action of 5'-MTA phosphorylase (MTAP). (Tisdale, M.J., Methionine Synthesis from 5'-methylthioadenosine by Tumor Cells. *Biochemical Pharmacology* 32: 2915-2920.) In tissue culture experiments low concentrations of 5'-MTA can substitute for

methionine in some cell lines. Thus 5'-MTA can rescue cells from methionine deprivation.

5 It occurred to the inventors that allele specific inhibition of MTAP in cancer patients heterozygous for MTAP and whose cancer cells have only one allele of MTAP as a consequence of LOH, in combination with methionine deprivation (methionine starvation or L-methioninase treatment) and dietary supplementation with 5'-methylthioadenosine would provide a source of convertible methionine substrate selectively useful to normal cells. Tumor cells would have no source of methionine,
10 being unable to convert the 5'-methylthioadenosine, and hence would be selectively poisoned. This therapeutic strategy would not necessarily require an allele specific inhibitor as *all copies* of MTAP are deleted in some cancers. Such cancers should be differentially poisoned vis a vis normal cells by methionine deprivation in the presence of 5'-methylthioadenosine.

15 *The MTAP gene maps to 9p21, a region frequently subject to LOH in many cancers*

The MTAP gene has been mapped to chromosome 9p21 by physical techniques (pulsed field gel electrophoresis and yeast artificial chromosome mapping). The gene
20 lies near the cyclin dependent kinase inhibitors p16 and p15 which are frequently reduced to one or zero copies in cancer cells. (Nobori, et al., Genomic cloning of methylthioadenosine phosphorylase: a purine metabolic enzyme deficient in multiple different cancers. *Proc. Natl. Acad. Sci. U.S.A.* 93: 6203-6208.) The p21 region of chromosome 9 is subject to frequent LOH particularly in cancers of the bladder, breast,
25 esophagus, head and neck, kidney, lung, melanoma and ovary. The frequency of LOH in these cancers ranges from 20% to nearly 100%.

Example 48. DNA dependent protein kinase (DNA-PK) and associated factors.
Variagenics Target Genes _____

DNA dependent protein kinase is conditionally essential

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Cells exposed to ionizing radiation, such as gamma radiation, are damaged by base modifications and DNA strand breaks. Double strand DNA breaks are among the most lethal form of radiation damage; one such break, if unrepaired, can be cell lethal. Four complementation groups of mammalian cell mutants that are defective in repair of double strand (ds) breaks have been identified. All four complementation groups are hypersensitive to ionizing radiation. The loci for three of these groups have been shown to encode components of DNA-dependent protein kinase (DNA-PK). The fourth group is deficient in the gene encoding XRCC4, a factor that associates with and stimulates DNA Ligase IV. Ligation of ds breaks by DNA ligase IV in a cell free system is increased 7-8 fold by co-expression of XRCC4.

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DNA-PK is a multiprotein complex with a DNA binding regulatory subunit, the Ku heterodimer [Ku70 (XRCC6) and Ku80, also referred to as Ku86 (XRCC5)], and a catalytic subunit, DNA-PKcs (probably XRCC7), that is activated by the regulatory subunit upon binding to DNA ds ends, with consequent expression of serine/threonine kinase activity resulting in phosphorylation of a variety of DNA binding proteins. A fourth protein called KARP-1 is expressed from the Ku80/86 locus and is also implicated in DNA-PK function.

20

25

Cells lacking any of the components of DNA-PK are exquisitely sensitive to gamma irradiation. This has been demonstrated directly in mice with targeted disruption of the Ku80/86 and DNA-PKcs genes. The Ku80/86 deficient mice were also sensitive to methyl methane sulfonate, a DNA alkylating agent that induces single strand breaks and to etoposide, a topoisomerase II inhibitor. Thus the components of DNA-PK can

also be important for repair of a variety of chemically induced DNA lesions as well as ionizing radiation.

5 In a cancer patient with two alternative alleles for a component of DNA-PK and LOH at the heterozygous locus, an allele specific inhibitory drug could be used to sensitize cancer cells to the action of ds break inducing treatments. Such a drug could be used to treat cancer patients constitutionally heterozygous for two normal alleles at any of the DNA-PK loci in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist in the administration of the appropriate allele
10 specific inhibitor plus a ds break inducing agent or procedure. The tumor cells would be unable to effectively repair ds breaks, while the uninhibited allele in normal cells would be able to function. Alternatively, patients heterozygous for functional and defective copies of genes required for repair of strand breaks, and in whom LOH resulted in loss of the functional allele, could be treated by a strand break inducing
15 procedure without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at the target locus and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to strand breaking agents or procedures (exposure to ionizing radiation) even though they might have cancers not
20 traditionally treated with such measures.

The genes encoding constituents of DNA-PK map to chromosomes frequently subject to LOH in different cancers

25 The DNA-PKcs gene has been mapped to 8q11, the Ku80/86 gene to 2q11-q13 and the Ku70 gene to 22q11-q13. All three regions are subject to LOH in different cancers. LOH on 2q has been reported in lung ovary and cervical cancers at frequencies ranging from 11% to 39%. LOH for 8q has been reported in cervix, head and neck, kidney, lung, ovary, prostate and testis cancers at frequencies ranging from 20% to 50% of

cancers. LOH on 22q has been reported in brain, breast colon, head and neck, lung, ovary, pediatric and stomach cancers at frequencies ranging from 10 to 76%. Several other cancer types have not yet been well studied for LOH affecting either region.

5 *Other proteins required for repair of DNA strand breaks are also candidates for allele specific therapy of cancer*

It will be evident to one skilled in the art that strategies similar to those described above for DNA-PK could be undertaken for other proteins required for repair of DNA strand breaks. For a recent review of such proteins see: Zdzienicka, M.Z., Mammalian mutants defective in the response to ionizing radiation-induced DNA damage. *Mutation Research* 336: 203-213, 1995; Thompson, L.H. and P.A. Jeggo, Nomenclature of human genes involved in ionizing radiation sensitivity. *Mutation Research* 337: 131-134, 1995; Thacker, J. and R.E. Wilkinson, The genetic basis of cellular recovery from radiation damage: response of the radiosensitive irs lines to low-dose rate irradiation. *Radiation Research* 144: 294-300, 1995. Two other syndromes with hypersensitivity to X-rays are Diamond-Blackfan anemia and aplastic anemia (Diemen, P.C., X-ray-sensitivity of lymphocytes of aplastic- and Diamond-Blackfan-anemia patients as detected by conventional cytogenetic and chromosome painting techniques. *Mutation Research* 373: 225-235, 1997). Recently evidence of several other genes responsible for DNA double strand break repair has been described. (Nicolas, N., Finnie, N.J., et al., *Eur. J. Immunol.* 26:1118-1122, 1996.) The above genes which, when defective, sensitize cells to toxic effects of DNA strand breaking agents would be amenable to the therapeutic strategy outlined above for the DNA-PK genes. Specifically, in a patient with two alternative alleles for such a gene and LOH at the relevant locus, an allele specific drug could be used to sensitize cancer cells to the action of strand breaking agents. Such drugs could then be used to treat cancer patients constitutionally heterozygous for two normal alleles at the relevant locus, in whom LOH had rendered cancer cells hemizygous or homozygous for one allele.

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Treatment would consist in the administration of the appropriate allele specific inhibitor plus a strand breaking agent or treatment to induce damage in all cells. Cancer cells (but not normal cells) would be rendered unable to respond by inhibition of expression of the relevant repair gene.

5

Alternatively, patients heterozygous for functional and defective copies of genes required for repair of strand breaks, and in whom LOH resulted in loss of the functional allele, could be treated by a strand break inducing procedure without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at the target locus and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to strand breaking agents or procedures (exposure to ionizing radiation) even though they might have cancers not traditionally treated with such measures.

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Example 49. Ataxia Telangiectasia Mutated (ATM) and c-Abl
Variagenics Target Gene _____

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The Ataxia Telangiectasia gene is essential for cell growth or survival in the presence of ionizing radiation or DNA damaging molecules

25

In order for cells to survive or proliferate in the presence of ionizing radiation (IR) or radiomimetic chemicals it is necessary that they are capable of efficiently repairing IR induced damage. Cells contain proteins necessary for such repair. One way such proteins can be identified is by their absence in specific patients who are particularly susceptible to the toxic effects of IR.

Ataxia Telangiectasia (AT) is a genetically transmitted autosomal recessive disorder characterized by variable degrees of immunodeficiency, telangiectasia (small blood vessels growing near the surface of the skin or eye), cerebellar ataxia (loss of balance due to abnormal development of the cerebellum) and increased sensitivity to both ionizing radiation and radiomimetic drugs, including bleomycin; AT cells are killed by lower doses of ionizing radiation or radiomimetic drugs than normal cells. Further, heterozygotes for mutant and normal AT alleles have radiation sensitivity close to that of homozygous normals. Therefore cancer cells from individuals heterozygous for null alleles of the AT gene (called ATM) should be highly susceptible to radiation therapy when only the deficient AT allele remains in cancer cells due to LOH, compared to normal cells from the same patients. Such patients could be treated by a DNA damage inducing procedure without the necessity for an allele specific inhibitor. Identification of such patients would require a test for heterozygosity at the target locus and a test for LOH which could show which allele is deleted in cancer cells. Such an approach would be expected to identify patients likely to respond well to strand breaking agents or procedures (such as exposure to ionizing radiation) even though they might have cancers not traditionally treated with such measures. In a related aspect, this approach is applicable to heterozygotes for other genes associated with ATM-mediated radiosensitivity. One such protein is the c-Abl protein tyrosine kinase, which binds to the ATM protein and regulates its function. c-Abl is known to be important in the stress response to ionizing radiation. One of its functions is activation of stress activated protein kinases (SAPKs) after irradiation or exposure to alkylating agents such as *cis*-platinum or mitomycin C, a response that is defective in ATM cells. Correction of the SAPK activation defect in ATM cells by non-mutant ATM cDNA suggests that the ATM - c-Abl interaction is necessary for the DNA damage response. (Kharbanda, S., et al. *Nature* 376: 785-788, 1995.)

In a cancer patient with two alternative functional alleles for a component of ATM and LOH at the ATM locus, an allele specific inhibitory drug could be used to sensitize

cancer cells to the action of DNA damage inducing treatments such as ionizing radiation or radiomimetic drugs. Such an allele specific drug could be used to treat cancer patients constitutionally heterozygous for two normal ATM alleles in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist of the administration of the appropriate allele specific inhibitor plus a DNA damage inducing treatment or procedure. The tumor cells would be unable to effectively the DNA damage, while the uninhibited allele in normal cells would be able to function. A similar approach could be taken to

The ATM gene is polymorphic

The ATM cDNA is 9.58 kb. Several likely polymorphisms have been identified, although population studies have not yet been performed to determine allele frequencies. One of the reported polymorphisms, an ATG to ATA change in codon 847, results in a methionine vs. isoleucine difference. Thus ATM is potentially targetable at the DNA, RNA and protein levels. It is likely that additional variances will be identified with broader population surveys and computational variance detection.

The ATM gene maps to chromosome 11q23 and the c-Abl gene maps to 9q34.1, two regions of high frequency LOH in different cancer types

Chromosome 9q34 is lost in a high fraction of bladder, esophagus, ovary, head & neck and testis cancers (17 - 76%) and in a lesser fraction of breast, liver and prostate cancers and leukemias. Chromosome 11q23 is lost in brain, cervix, esophagus, breast, kidney, colon, stomach, head & neck and lung cancers at frequencies ranging from 16% to 100%.

Other proteins required for repair of DNA damage are also candidates for allele specific therapy of cancer

It will be evident to one skilled in the art that strategies similar to those described above for ATM and c-Abl could be undertaken for other proteins required for the stress response to DNA damaging agents, such as other stress activated protein kinases or downstream effector proteins.

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Methylguanine Methyltransferase (MGMT)**Gene VARIA 1534**

The methylguanine methyltransferase gene is essential for cell growth or survival in the presence of alkylating agents

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Methylguanine methyltransferase (MGMT) is a suicide protein that repairs alkylating agent damage, specifically alkylation of the 6'O position of guanine. Alkyl groups are covalently bound to an active site cysteine (residue 145) of MGMT, thereby irreversibly inactivating the protein. 6'O-benzylguanine is an analog inhibitor of MGMT that, by inactivating MGMT, renders tumor cells more sensitive to the toxic effects of methylating and chloroethylating agents. MGMT is thus a conditionally essential gene in the presence of such drugs. 6'O-benzylguanine is being developed as a chemosensitizing agent.

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In a cancer patient with two alternative functional MGMT alleles an allele specific inhibitory drug could be used to sensitize cancer cells to the action of alkylating agents. Such an allele specific drug could be used to treat cancer patients constitutionally heterozygous for two normal MGMT alleles in whom LOH had rendered cancer cells hemizygous or homozygous for one allele. Treatment would consist of the administration of the appropriate allele specific inhibitor plus an alkylating agent. The tumor cells would be unable to effectively repair the alkylating agent induced DNA damage, while the uninhibited allele in normal cells would be able to function.

20

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The MGMT gene is polymorphic

Several variances have been reported in human MGMT, or discovered by Variagenics, including three protein polymorphisms. There is a silent C/T variance at position 255 (11% heterozygotes among 36 individuals surveyed), another C/T variance at nt. 346

which results in a L84F amino acid variance (5% heterozygotes), an A/G variance at nt. 523 which results in a I143V amino acid variance (24% heterozygotes). A variance has been reported in Japanese at codon 160, GGA vs. AGA, converting glycine to arginine. 15% of the population studied were heterozygotes.

5

The alteration of glycine 160 to arginine reduced the inactivation by O6-benzylguanine with an approximately 20 fold increase in the IC50 concentration. These results demonstrate variance-specific effects of a small molecule, O6-benzylguanine, on normal (non-mutant) alleles of the conditionally essential MGMT gene.

10

Administration of O6 benzylguanine to patients who are heterozygous for the residue 160 gly/arg variance in their normal cells, and contain only the form of the gene with a glycine residue at position 160 in their cancer cells, together with methylating or chloroethylating agents for chemotherapy, will be specifically toxic to cancer cells without increasing toxicity to normal cells.

15

References

1. Imai, Y, *Carcinogenesis* (1995), 16:2441-24445
2. Edara, S. (1996) Resistance of the human O6-alkylguanine-DNA alkyltransferase containing arginine at codon 160 to inactivation by O6-benzylguanine. *Cancer Research* 56, 5571-5575.

20

All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

25

One skilled in the art would readily appreciate that the present invention is well

adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The groups of genes and the particular genes described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. For example, those skilled in the art will readily recognize that the methods and inhibitors can utilize a variety of different target genes within the groups described. Thus, such additional embodiments are within the scope of the present invention and the following claims.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

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In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

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Thus, additional embodiments are within the scope of the invention and within the following claims.

CLAIMS

What we claim is:

5 1. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

10 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required for cell proliferation;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles; wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

20 2. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival;

25 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

 wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of

said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

5 3. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

10 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

15 wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

20 4. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

25 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

 wherein inhibition of expression of at least one but less than all of said alleles

or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

5 5. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

10 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

15 wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

20 6. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

25 (a) determining at least two alleles of a said gene, wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures;

 (b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

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7. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

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(a) determining at least two alleles of a said gene, wherein said gene is located on a high frequency LOH chromosomal region;

(b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

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wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

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8. The method of claim 7, wherein said gene is located on a chromosomal arm which has a frequency of allele loss of at least 15% in a cancer.

9. The method of claim 7, wherein said gene is located in proximity to a chromosomal marker which undergoes LOH at a frequency of at least 10% in a cancer.

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10. The method of claim 7, wherein said gene is located in proximity to a tumor suppressor gene which undergoes LOH at a frequency of at least 10% in a cancer.

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11. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a gene vital for cell growth or viability, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

5 (a) determining at least two alleles of a said gene, wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene;

(b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles;

10 wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

15 12. The method of claim 11, wherein said gene is located on a high frequency LOH chromosomal region.

20 13. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required for cell proliferation, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

25 14. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival, said gene has at least two alternative

alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

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15. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain organic compounds at levels
10 compatible with cell growth or survival, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

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16. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain cellular proteins at levels
compatible with cell growth or survival, said gene has at least two alternative alleles in a population, and

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wherein said inhibitor targets at least one but less than all of said alternative alleles.

17. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein
25 said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

18. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

19. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene is located on a high frequency LOH chromosomal arm region, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

20. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a gene vital for cell viability or cell growth, wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

21. A pharmaceutical composition, comprising

at least one allele specific inhibitor targeting at least one but less than all allelic forms of an essential gene in a population, wherein said gene encodes a product required for cell proliferation; and

a pharmaceutically acceptable carrier or excipient.

22. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain inorganic ions and vitamins at levels compatible with
cell growth or survival; and
a pharmaceutically acceptable carrier or excipient.

23. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain organic compounds at levels compatible with cell
growth or survival; and
a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain cellular proteins at levels compatible with cell growth
or survival; and
a pharmaceutically acceptable carrier or excipient.

25. A pharmaceutical composition, comprising
at least one allele specific inhibitor targeting at least one but less than all
allelic forms of an essential gene in a population, wherein said gene encodes a
product required to maintain cellular nucleotides at levels compatible with cell
growth or survival; and
a pharmaceutically acceptable carrier or excipient.

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26. A pharmaceutical composition, comprising

at least one allele specific inhibitor targeting at least one but less than all allelic forms of an essential gene in a population, wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures; and

a pharmaceutically acceptable carrier or excipient.

27. A pharmaceutical composition, comprising

at least one allele specific inhibitor targeting at least one but less than all allelic forms of an essential gene in a population, wherein said gene is located on a high frequency LOH chromosomal arm region; and

a pharmaceutically acceptable carrier or excipient.

28. A pharmaceutical composition, comprising

at least one allele specific inhibitor targeting at least one but less than all allelic forms of an essential gene in a population, wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene; and

a pharmaceutically acceptable carrier or excipient.

29. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required for cell proliferation;

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(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

30. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival;

(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

31. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival;

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(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

32. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival;

(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

33. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival;

(b) screening to identify an inhibitor which inhibits said at least one but less

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than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

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34. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

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(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures;

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(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

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35. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

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(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene is located on a high frequency LOH chromosomal arm region;

(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

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36. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a gene having at least two alternative alleles, comprising the steps of:

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(a) identifying a gene vital to cell viability or cell growth that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell, and wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene;

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(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

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(c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in which cancerous cells have only the allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene.

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37. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required for cell proliferation; and

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wherein cells of said precancerous condition have undergone LOH of said first gene.

38. The method of claim 37, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

39. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival; and

wherein cells of said precancerous condition have undergone LOH of said first gene.

40. The method of claim 39, wherein the cells of said precancerous condition are

not clonal from a single cell, further comprising the step of:

5 b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

10 41. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

15 a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival; and
20 wherein cells of said precancerous condition have undergone LOH of said first gene.

42. The method of claim 41, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

25 b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in

cells of said precancerous condition.

43. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

5 a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form
10 present in said normal somatic cells, and said first gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival; and
wherein cells of said precancerous condition have undergone LOH of said first gene.

15 44. The method of claim 43, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific
20 inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

25 45. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are

heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival; and

5 wherein cells of said precancerous condition have undergone LOH of said first gene.

46. The method of claim 45, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

10 b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for
15 each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

47. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

20 a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than
25 all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene encodes a product required to maintain the integrity and function of cellular and subcellular structures; and

 wherein cells of said precancerous condition have undergone LOH of said first gene.

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48. The method of claim 47, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

49. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene is located on a high frequency LOH chromosomal arm region; and

wherein cells of said precancerous condition have undergone LOH of said first gene.

50. The method of claim 49, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for

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each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

51. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of a first essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells, and said first gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene; and

wherein cells of said precancerous condition have undergone LOH of said first gene.

52. The method of claim 51, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

b. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different essential gene, and wherein said patient is heterozygous for each targeted essential gene and each targeted essential gene has undergone LOH in cells of said precancerous condition.

53. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of: administering a therapeutic amount of an allele specific inhibitor active on at

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least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required for cell proliferation, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

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54. The method of claim 53, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

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(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

55. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

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administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

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56. The method of claim 55, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

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(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

57. A method for treating a patient suffering from a cancer, wherein said patient

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is heterozygous for a gene vital for cell growth or viability, comprising the step of:

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

58. The method of claim 57, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

59. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

60. The method of claim 59, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

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(c) both (a) and (b).

61. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

5 administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic
10 form of said gene is present in cancer cells in said patient.

62. The method of claim 61, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

15 (b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

63. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

20 administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures, said allele specific inhibitor inhibits
25 only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

64. The method of claim 63, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are

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heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

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65. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

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wherein said gene is located on a high frequency LOH chromosomal arm region, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

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66. The method of claim 65, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

20

(c) both (a) and (b).

67. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a gene vital for cell growth or viability, comprising the step of:

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

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wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene, said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said

patient.

68. The method of claim 67, further comprising the steps of:

5 (a) determining whether non-cancerous cells of said patient are heterozygous for a particular gene essential for cell growth or viability; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

10 69. A method of inhibiting growth of a cell comprising the step of:

administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene encodes a product required for cell proliferation, and wherein said inhibitor is less active on at least one other allele of said gene.

15 70. A method of inhibiting growth of a cell comprising the step of:

administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

20 wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival, and wherein said inhibitor is less active on at least one other allele of said gene.

71. A method of inhibiting growth of a cell comprising the step of:

25 administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival, and wherein said inhibitor is less active on at least one other allele of said gene.

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72. A method of inhibiting growth of a cell comprising the step of:

administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene encodes a product required to maintain cellular proteins at levels compatible with cell growth or survival, and wherein said inhibitor is less active on at least one other allele of said gene.

73. A method of inhibiting growth of a cell comprising the step of:

administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival, and wherein said inhibitor is less active on at least one other allele of said gene.

74. A method of inhibiting growth of a cell comprising the step of:

administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures, and wherein said inhibitor is less active on at least one other allele of said gene.

75. A method of inhibiting growth of a cell comprising the step of:

administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene is located on a high frequency LOH chromosomal arm region, and wherein said inhibitor is less active on at least one other allele of said gene.

76. A method of inhibiting growth of a cell comprising the step of:

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administering at least one inhibitor active on an allele of a gene vital for cell viability or growth,

wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene, and wherein said inhibitor is less active on at least one other allele of said gene.

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77. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

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identifying a patient heterozygous for a said gene encoding a product required for cell proliferation,

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

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78. The method of claim 77, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

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79. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

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determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required for cell proliferation,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

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80. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

5 identifying a patient heterozygous for a said gene encoding a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival,

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

10 81. The method of claim 80, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

15 82. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

20 determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

25 83. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

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identifying a patient heterozygous for a said gene encoding a product required to maintain organic compounds at levels compatible with cell growth or survival;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

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84. The method of claim 83, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

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85. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

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determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required to maintain organic compounds at levels compatible with cell growth or survival,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

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86. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

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identifying a patient heterozygous for a said gene encoding a product required to maintain cellular proteins at levels compatible with cell growth or survival ;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

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87. The method of claim 86, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

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88. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

10 determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required to maintain cellular proteins at levels compatible with cell growth or survival ,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

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89. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

20 identifying a patient heterozygous for a said gene encoding a product required to maintain cellular nucleotides at levels compatible with cell growth or survival ;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

25

90. The method of claim 89, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

91. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

5 determining whether cancer cells in said patient have undergone LOH of a said gene encoding a product required to maintain cellular nucleotides at levels compatible with cell growth or survival,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

10 92. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

15 identifying a patient heterozygous for a said gene encoding a product required to maintain the integrity and function of cellular and subcellular structures ;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

20 93. The method of claim 91, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

25 94. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

determining whether cancer cells in said patient have undergone LOH of a

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said gene encoding a product required to maintain the integrity and function of cellular and subcellular structures,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

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95. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

10 identifying a patient heterozygous for a said gene located on a high frequency LOH chromosomal arm region ;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

15 96. The method of claim 95, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

20 97. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

25 determining whether cancer cells in said patient have undergone LOH of a said gene located on a high frequency LOH chromosomal arm region,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

98. A method of identifying a potential patient for treatment with an inhibitor

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active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the steps of:

identifying a patient heterozygous for a said gene which has at least two
5 sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene;

wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

10 99. The method of claim 98, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

15 100. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a gene vital for cell growth or viability, wherein said patient is suffering from a cancer, said method comprising the step of:

20 determining whether cancer cells in said patient have undergone LOH of a said gene which has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene,

wherein if said cells have undergone LOH of said gene, then said patient is a potential patient for said treatment.

25 101. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene encodes a product required for cell proliferation, wherein said portion comprises a sequence variance site, and wherein said probe

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hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

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102. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

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wherein said gene encodes a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

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103. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

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wherein said gene encodes a product required to maintain organic compounds at levels compatible with cell growth or survival, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

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104. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene encodes a product required to maintain cellular

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proteins at levels compatible with cell growth or survival, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

105. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene encodes a product required to maintain cellular nucleotides at levels compatible with cell growth or survival, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

106. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene encodes a product required to maintain the integrity and function of cellular and subcellular structures, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

107. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or

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viability,

wherein said gene is located on a high frequency LOH chromosomal arm region, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

108. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a gene vital for cell growth or viability,

wherein said gene has at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for said gene, wherein said portion comprises a sequence variance site, and wherein said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

109. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of any of claims 1, 13, 21, 29, 37, 53, 69, 77, and 101, wherein said gene is selected from the group consisting of 14-3-3 Protein TAU, CCNA(G2/Mitotic-Specific Cyclin A), CCNB1(G2/Mitotic-Specific Cyclin B1), CCND1(G1/S-Specific Cyclin D1), CCND2(G1/S-Specific Cyclin D2), CCND3(G1/S-Specific Cyclin D3), Cell division control protein 16, Cell division cycle 2, G1 to S and G2 to M, Cell division cycle 25A, Cell division cycle 25B, Cell division cycle 25C, Cell division cycle 27, Cell division-associated protein BIMB, Cyclin A1(G2/Mitotic-Specific Cyclin A1), Cyclin C(G1/S-Specific Cyclin C), Cyclin G1(G2/Mitotic-Specific Cyclin G), Cyclin G2(G2/Mitotic-Specific Cyclin G), Cyclin H, Cyclin H Assembly, GSPT1(G1 to S phase transition 1), Mitotic MAD2 Protein, MRNP7, RANBP1(RAN binding protein 1), WEE1, Cell Division Protein Kinase 4, CDC28 protein kinase 1, CDC28 protein

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kinase 2, M-Phase inducer phosphatase 2, M-phase phosphoprotein, mpp6, PPP1ca(Protein phosphatase 1, catalytic subunit, alpha isoform), STM7-LSB, CENP-F kinetochore protein, Centromere autoantigen C, Centromere protein B (80kD), Centromere protein E (312kD), CHC1(Chromosome condensation 1), Chromatin assembly factor-I p150 subunit, Chromatin assembly factor-I p60 subunit, Chromosome segregation gene homolog CAS, HMG1(High-mobility group (nonhistone chromosomal) protein 1), Minichromosome Maintenance (MCM7), Mitotic centromere-associated kinesin, RMSA1(Regulator of mitotic spindle assembly 1), and SUPT5h(Chromatin structural protein homolog (SUPT5H)).

110. The method ,inhibitor, pharmaceutical composition, or nucleic acid probe of any of claims 2, 14, 22, 30, 39, 55, 70, 80, and 102, wherein said gene is selected from the group consisting of PMCA1 (Calcium Pump), PMCA2 (Calcium Pump), PMCA3 (Calcium Pump), PMCA4 (Calcium Pump), ATP2b1 (Calcium-Transporting ATPase Plasma Membrane), ATP2b2 (Calcium-Transporting ATPase Plasma Membrane), ATP2b4 (Calcium-Transporting ATPase Plasma Membrane), ATP5b (ATP Synthase Beta Chain, Mitochondrial Precursor), Chloride Conductance Regulatory Protein ICLN, H-Erg (Potassium Channel Protein EAG), Nuclear Chloride Ion Channel Protein (NCC27), SCN1b(Sodium Channel, Voltage-Gated, Type I, Beta Polypeptide), Two P-Domain K⁺ Channel TWIK-1, VDAC2 (Voltage-Dependent Anion-Selective Channel Protein 2), ATP1b1 (Sodium/Potassium-Transporting ATPase Beta-1 Chain), ATP1b2 (Sodium/Potassium-Transporting ATPase Beta-2 Chain), ATPase, Ca⁺⁺ transporting, plasma membrane 4, ATPase, Ca⁺⁺ transporting, plasma membrane 2, ATPase, Na⁺/K⁺ transporting, alpha 1 polypeptide, ATPase, Na⁺/K⁺ transporting, alpha 3 polypeptide, ATPase, Na⁺/K⁺ transporting, beta 1 polypeptide, ATPase, Na⁺/K⁺ transporting, beta 2 polypeptide, Na⁺,K⁺ ATPase, 1 Subunit, Na⁺,K⁺ ATPase, 2 alpha, Na⁺,K⁺ ATPase, 3 beta, SLC9a1(Solute carrier family 9 (sodium/hydrogen exchanger)), Solute carrier family 4, anion exchanger, member 1, Solute carrier family 4, anion

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exchanger, member 2, Solute carrier family 9 (sodium/hydrogen exchanger), Passive transporters, MaxiK Potassium Channel Beta Subunit, Chloride Channel 2, Chloride Channel Protein (CLCN7), TRPC1 (Transient Receptor Potential Channel 1), Potassium Channel Kv2.1, ATP5d(ATP synthase, H⁺ transporting, mitochondrial F1 complex, delta subunit), ATP5f1(ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit b), ATP5o(ATP synthase, H⁺ transporting, mitochondrial F1 complex, O subunit), ETFa(Electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)), ETFb(Electron-transfer-flavoprotein, beta polypeptide), Nadh-ubiquinone oxidoreductase 13 kd-B subunit, Nadh-ubiquinone oxidoreductase 39 kD subunit precursor, NADH-Ubiquinone oxidoreductase 75 kD subunit precursor, NADH-Ubiquinone oxidoreductase MFWE subunit, NDUFV2(NADH dehydrogenase (ubiquinone) flavoprotein 2 (24kD)), Ubiquinol-cytochrome c reductase complex 11 kD, ATP Synthase Alpha Chain, NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit, Ascorbic Acid (transporter), Folate Binding Protein, Folate receptor 1 (adult), Nicotinamide (transporter), Pantothenic Acid transporter, Riboflavin (transporter), SCL19A1 (Solute Carrier Family 19, Member1), Solute carrier family 19 (folate transporter), member 1, Thiamine, B6, B12 (transporter), ATP7b (Copper-Transporting ATPase 2), Ceruloplasmin (ferroxidase), Ceruloplasmin receptor (Copper Transporter), Copper Transport Protein HAH1, Molybdenum, Selenium, Transferrin Receptor (Iron Transporter), Zinc Transporter, and mitochondrial import receptor subunit TOM20.

111. The method ,inhibitor, pharmaceutical composition, or nucleic acid probe of 3, 25, 23, 31, 41, 57, 71, 83, and 103, wherein said gene is selected from the group consisting of GLUT1, GLUT2, GLUT3, GLUT4, GLUT5, GLUT6, Solute carrier family 5 (sodium/glucose cotransporter), Solute carrier family 2 (facilitated glucose transporter), member 2, Solute carrier family 2 (facilitated glucose transporter) member 5, Solute carrier family 3 member 1, System b,(Na⁺ independent), System y,(Na⁺ independent), ATRC1(Catioinc), LEUT(Leucine Transporter),

SLC1A1(Solute Carrier Family 1, Member 1), Solute carrier family 16
 (monocarboxylic acid transporters), ACO1(Aconitase 1), ACO2(Aconitase 2,
 mitochondrial), Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain, Acyl-
 Coenzyme A dehydrogenase, C-4 to C-12 straight chain, Acyl-Coenzyme A
 5 dehydrogenase, long chain, Acyl-Coenzyme A dehydrogenase, very long chain,
 aKGD (alpha ketoglutaratedehydrogenase), ALD-a (Aldolase), ALD-b (Aldolase),
 ALD-c (Aldolase), CS (Citrate Synthetase), Dihydrolipoamide S-succinyltransferase,
 DLAT(Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate
 dehydrogenase complex)), DLD(Dihydrolipoamide dehydrogenase (E3 component
 10 of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto
 acid dehydrogenase complex)), E1k (Oxoglutarate dehydrogenase), E2k
 (Dihydrolipoamide S-succinyltransferase), E3 (Dihydrolipoyl Dehydrogenase),
 ENO1(Enolase 1,alpha), ENO2(Enolase 2), ENO3(Enolase 3), Enolase 2, (gamma,
 neuronal), Enolase 3, (beta, muscle), FH(Fumarate hydratase), G3PDH
 15 (Glyceraldehyde-3-Phosphate Dehydrogenase), G6PD (Glucose-6-Phosphate
 Dehydrogenase), Glucose-6-phosphate dehydrogenase, HK1 (Hexokinase 1), HK2
 (Hexokinase 2), HK3 (Hexokinase 3), IDH1(Isocitrate dehydrogenase 1 (NADP+),
 soluble), IDH2(Isocitrate dehydrogenase 2 (NADP+), mitochondrial),
 MDH1(Malate dehydrogenase 1, NAD (soluble)), MDH2(Malate dehydrogenase 1,
 20 NAD (mitochondrial)), NAD(H)-specific isocitrate dehydrogenase alpha subunit,
 Oxoglutarate dehydrogenase (lipoamide), PDHB (Pyruvate Dehydrogenase),
 PDHB(Pyruvate dehydrogenase (lipoamide) beta), PDK4 (Pyruvate dehydrogenase
 kinase, isoenzyme 4), PFKL(Phosphofructokinase), PGI (Phosphoglucoisomerase),
 PGKa (Phosphoglyceromutase), PGKb (Phosphoglyceromutase), PGM1
 25 (Phosphoglyceromutase), PGM2 (Phosphoglyceromutase), PGM3
 (Phosphoglyceromutase), PGM4 (Phosphoglyceromutase), Phosphofructokinase,
 muscle, Phosphoglucomutase 1, Phosphoglycerate kinase 1, PK1 (Pyruvate Kinase),
 PK2 (Pyruvate Kinase), PK3 (Pyruvate Kinase), Pyruvate dehydrogenase kinase
 isoenzyme 2 (PDK2), Pyruvate kinase, liver, Pyruvate kinase, muscle,

SDH1(Succinate dehydrogenase, iron sulphur (Ip) subunit), SDH2(Succinate dehydrogenase 2, flavoprotein (Fp) subunit), TKT(Transketolase (Wernicke-Korsakoff syndrome)), TPI (Trisephosphate Isomerase), Asparagine Synthetase, Aminoacylase-1, Aminoacylase-2, ACAC (Acetyl CoA Carboxylase Beta), ACAC (Acetyl CoA Carboxylase), ACADSB(Acyl-coA dehydrogenase), Mevalonate kinase, Phosphomevalonate kinase, Aspartoacylase, Ornithine decarboxylase 1, Short-acyl-CoA dehydrogenase, Medium acyl-CoA dehydrogenase, Long acyl-CoA dehydrogenase, Isovaleryl CoA dehydrogenase, 2-methyl branched chain, Adenosine Deaminase, Purine-nucleoside phosphorylase, Guanine Deaminase, Xanthine Oxidase, ITM1 (Integral Transmembrane Protein), GFPT (Glutamine-Fructose-6-Phosphate Transaminase), Heparan, Polypeptide N-Acetyltransferase, ACAA(Acetyl-Coenzyme A acyltransferase), Lysophosphatidic acid acyltransferase-alpha, Lysophosphatidic acid acyltransferase-beta, FNTa (Farnesyltransferase Alpha Subunit), FNTb (Farnesyltransferase Beta Subunit), NMT1 (N-myristoyltransferase), Calcineurin A, Calcineurin B, Calreticulin Precursor, Phosphatase 2b, PPP3ca(Protein phosphatase 3 , catalytic subunit), SNK Interacting 2-28(Calcineurin B Subunit), Protein Kinase C, PRKCA(Protein kinase C, alpha), PRKCB1(Protein kinase C, beta 1), PRKCD(Protein kinase C, delta), PRKCM(Protein kinase C, mu), PRKCQ(Protein kinase C-theta), PRKCSH(Protein kinase C substrate 80K-H), Geranylgeranyl, Geranylgeranyltransferase (Type I Beta), GGTB (Geranylgeranyltransferase), Geranylgeranyltransferase (Type II Beta-Subunit), Gdp Dissociation Inhibitors, GDI Alpha (RAB GDP Dissociation Inhibitor Alpha), and Rab Gdp (RAB GDP Dissociation Inhibitor Alpha).

112. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of any of claims 4, 16, 24, 32, 43, 59, 72, 86, and 104, wherein said gene is selected from the group consisting of GOT(Glutamic-oxaloacetic transaminase 2), GOT1(Glutamic-oxaloacetic transaminase 1), PYCS(Pyrroline-5-carboxylate synthetase), Tyrosine aminotransferase, AARS, CARS, DARS, EPRS, FARS,

GARS, HARS, IARS, KARS, LARS, MARS, NARS, QARS , RARS, SARS, TARS, VARS, WRS, YARS, Ribosomal Protein L11, Ribosomal Protein L12, Ribosomal Protein L17, Ribosomal Protein L18, Ribosomal Protein L18a, Ribosomal Protein L19, Ribosomal Protein L21, Ribosomal Protein L22, Ribosomal Protein L23, Ribosomal Protein L23a, Ribosomal Protein L25, Ribosomal Protein L26, Ribosomal Protein L27, Ribosomal Protein L27a, Ribosomal Protein L28, Ribosomal Protein L29, Ribosomal Protein L30, Ribosomal Protein L31, Ribosomal Protein L32, Ribosomal Protein L35, Ribosomal Protein L35a, Ribosomal Protein L36a, Ribosomal Protein L39, Ribosomal Protein L4, Ribosomal Protein L41, Ribosomal Protein L44, Ribosomal Protein L6, Ribosomal Protein L7, Ribosomal Protein L7a, Ribosomal Protein L8, Ribosomal Protein L9, Ribosomal Protein P1, Ribosomal Protein S10, Ribosomal Protein S11, Ribosomal Protein S13, Ribosomal Protein S14, Ribosomal Protein S15, Ribosomal Protein S15A, Ribosomal Protein S16, Ribosomal Protein S17, Ribosomal Protein S17A, Ribosomal Protein S17B, Ribosomal Protein S18, Ribosomal Protein S20, Ribosomal Protein S20A, Ribosomal Protein S20B, Ribosomal Protein S21, Ribosomal Protein S23, Ribosomal Protein S25, Ribosomal Protein S26, Ribosomal Protein S28, Ribosomal Protein S29, Ribosomal Protein S3, Ribosomal Protein S3A, Ribosomal Protein S4, Ribosomal Protein S4X, Ribosomal Protein S4Y, Ribosomal Protein S5, Ribosomal Protein S6, Ribosomal Protein S7, Ribosomal Protein S8, Ribosomal Protein S9, Initiation of polypeptide polymerization, eIF-2 (Eukaryotic initiation factor), eIF-2-associated p67(Eukaryotic initiation factor), eIF-2A(Eukaryotic initiation factor), eIF-2Alpha(Eukaryotic initiation factor), eIF-2B(Eukaryotic initiation factor), eIF-2B-Gamma(Eukaryotic initiation factor), eIF-2Beta(Eukaryotic initiation factor), eIF-3 p110(Eukaryotic initiation factor), eIF-3 p36(Eukaryotic initiation factor), eIF-4A(Eukaryotic initiation factor), eIF-4C(Eukaryotic initiation factor), eIF-4E(Eukaryotic initiation factor), eIF-4Gamma(Eukaryotic initiation factor), eIF-5(Eukaryotic initiation factor), eIF-5A, Eukaryotic peptide chain release factor subunit 1, P97(Eukaryotic initiation factor), eEF1A2(Eukaryotic elongation factor),

eEF1D(Eukaryotic elongation factor), eEF2(Eukaryotic elongation factor), eIF4A2 (Eukaryotic initiation factor), KIAA0031(Elongation factor 2), KIAA0219(Putative translational activator C18G6.05C), Factor 1-Alpha 2(Eukaryotic translation elongation factor 1 alpha 2), Cis-Trans Isomerase, DNAJ Protein Homolog 1, DNAJ Protein Homolog 2, DNAJ Protein homolog HSJ1, T-Complex, Aspartylglucosaminidase, T-Complex 1, Alpha, T-Complex 1, Epsilon, T-Complex 1, Gamma, T-Complex 1, Theta, T-Complex 1, Zeta, 26S Protease regulatory subunit 4, Alpha-2-Macroglobulin, Calpain 1, Large, CLPP(ATP-Dependent CLP protease proteolytic subunit), KIAA0123 (Mitochondrial processing peptidase alpha subunit), MMP7, Proteasome Beta 6, Proteasome Beta 7, Proteasome C13, Proteasome C2, Proteasome C7-1, Proteasome inhibitor hPI31 subunit, Proteasome P112, Proteasome P27, Proteasome P55, Enzyme E2-17 Kd(Cyclin-selective ubiquitin carrier protein), ISOT-3(Ubiquitin carboxyl-terminal hydrolase T), ORF (Ubiquitin carboxyl-terminal hydrolase 14), PGP(Ubiquitin carboxyl-terminal hydrolase isozyme L1), UBA52(Ubiquitin A-52 residue ribosomal protein fusion product 1), Ubiquitin carboxyl-terminal hydrolase 3, Ubiquitin carboxyl-terminal hydrolase isozyme L3, Ubiquitin carboxyl-terminal hydrolase T, Ubiquitin carrier protein (E2-EPF), Ubiquitin fusion-degradation protein (UFD1L), Ubiquitin Hydrolase, Ubiquitin-conjugating enzyme E2I, SEC23(Protein transport protein SEC23), SEC23A(Protein transport protein SEC23), SEC7(Protein transport protein SEC7), SEC61 (Beta Subunit), and LDLR (LDL receptor).

113. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of any of claims 5, 17, 25, 33, 45, 73, 89, and 105, wherein said gene is selected from the group consisting of Adenylate Kinase-2, Adenylosuccinate synthetase, Adenylosuccinate Lyase, DPRT (ADP-Ribosyltransferase), ADSL (Adenylosuccinate lyase/AMP synthetase), ADSS (Adenylosuccinate Synthetase), CAD PROTEIN, CTP Synthetase, CTPS(CTP synthetase), Cytidine Triphosphate Synthetase, GARS (Phosphoribosylglycinamide synthetase), GART (Phosphoribosylglycinamide

formyltransferase), GART(Phosphoribosylglycinamide formyltransferase,
 phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase),
 GMP Synthetase, IMP Cyclohydrolase, IMP dehydrogenase, IMPDH1(IMP (inosine
 monophosphate) dehydrogenase 1), IMPDH2(IMP (inosine monophosphate)
 5 dehydrogenase 2), Phosphoribosyl diphosphotransferase,
 Phosphoribosylaminoimidazolecarboxamide formyltransferase,
 Phosphoribosylformylglycinamide synthetase, Phosphoribosylglycinamide
 carboxylase, Phosphoribosylglycinamide-succinocarboxamide synthetase, PPAT
 (Amidophosphoribosyltransferase), PPAT(Phosphoribosyl pyrophosphate
 10 amidotransferase), Ribonucleoside-diphosphate reductase M1 chain, Ribonucleoside-
 diphosphate reductase M2 chain, Thymidine Kinase, Thymidylate Synthase,
 UMK(Uridine kinase), UMPK (Uridine monophosphate kinase), UMPS(Uridine
 monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-
 decarboxylase)), Uridine Phosphorylase, DNA Origin Recognition Complex, ORC1,
 15 ORC2, ORC3, ORC4, ORC5, ORC6, ORC Regulators, CDC6, CDC7, CDC1,
 DNA Polymerization, DNA Polymerases, Adprt (NAD(+) ADP-
 Ribosyltransferase), DNA Polymerase Alpha-Subunit, DNA Polymerase Delta,
 POLa(DNA Polymerase Alpha/Primase Associated Subunit), POLb(DNA
 Polymerase Beta Subunit), POLd1(Polymerase (DNA directed), Delta 1, Catalytic
 20 Subunit), POLd2(Polymerase (DNA directed), Delta 2), POLE(Polymerase (DNA
 directed)), POLg (DNA Polymerase Gamma Subunit), Terminal Transferase (DNA
 Nucleotidylexotransferase), Activator 1 36 Kd, CDC46 (DNA Replication Licensing
 Factor), CDC47 (DNA Replication Licensing Factor CDC47), DNA Topoisomerase
 III, DRAP1 (DNA Replication Licensing Factor MCM3), KIAA0030 Gene (Cell
 25 Division Control Protein 19), KIAA0083 Gene (DNA Replication Helicase DNA2
), MCM3 (DNA Replication Licensing Factor MCM3), PCNA (Proliferating Cell
 Nuclear Antigen), PRIM1 (DNA Primase 49 kD Subunit), PRIM2 (DNA Primase),
 PRIM2a (DNA Primase 58 kD Subunit), PRIM2b (DNA Primase), RECa
 (Replication Protein A 14 kD Subunit), RFC1 (Replication Factor C (activator 1) 1),

RFC2 (Replication Factor C 2), RFC3 (Replication Factor C (activator 1) 3), RFC4
 (Replication Factor C, 37-kD subunit), RFC5 (Replication Factor C), RPA1
 (Replication protein A1 (70kD)), RPA2 (Replication protein A2 (32kD)), RPA3
 (Replication protein A3 (14kD)), TOP1 (DNA Topoisomerase I), TOP2a
 5 (Topoisomerase (DNA) II Alpha (170kD)), TOP2b (Topoisomerase (DNA) II Beta
 (180kD)), CHL1(CHL1-Related Helicase), DNA Helicase II, Mi-2(Chromodomain-
 Helicase- DNA-Binding Protein CHD-1), RECQL (ATP-Dependent DNA Helicase
 Q1), Smbp2 (DNA-Binding Protein SMUBP-2), H1(0) (Histone H5A), Histone H1d,
 Histone H1x, Histone H2a.1, Histone H2a.2, Histone H2b.1, Histone H4, SLBP
 10 (Histone Hairpin-Binding Protein), TATA-binding Complex, Small Nuclear RNA-
 Activating Complex, Polypeptide 1, 43KD (SNAPC1), Small Nuclear RNA-
 Activating Complex, Polypeptide 2, (SNAPC2), Small Nuclear RNA_Activating
 Complex, Polypeptide 3, 50KD (SNAPC3), TAF2D(TBP-associated factor),
 TAFII100(TBP-associated factor), TAFII130(TBP-associated factor), TAFII20(TBP-
 15 associated factor), TAFII250(TBP-associated factor), TAFII28(TBP-associated
 factor), TAFII30(TBP-associated factor), TAFII32(TBP-associated factor),
 TAFII40(TBP-associated factor), TAFII55(TBP-associated factor), TAFII80(TBP-
 associated factor), TBP(TATA Binding Protein), TMF1 (TATA Element Modulatory
 Factor 1), RPB 7.0, RPB 7.6, RPB 17, RPB 14.4, RNA polymerase I subunit
 20 hRPA39, 13.6 Kd Polypeptide (DNA-Directed RNA Polymerase II 13.6 kD
 Polypeptide), POLR2C(RNA polymerase II, polypeptide C (33kD)), Polypeptide A
 (220kd), RNA Polymerase II 23k, RNA polymerase II holoenzyme component
 (SRB7), RNA polymerase II subunit (hsRPB10), RNA polymerase II subunit
 (hsRPB8), RNA polymerase II subunit hsRPB4, RNA polymerase II subunit
 25 hsRPB7, RNA Polymerase II Subunit(DNA- Directed RNA Polymerases I, II, and
 III 7.3 kD polypeptide), TCEB1L(Transcription elongation factor B (SIII),
 polypeptide 1-like), RNA polymerase III subunit (RPC39), RNA polymerase III
 subunit (RPC62), Elongation Factor 1-Beta, Elongation Factor S-II, TCEA (110kD),
 TCEB1, TCEB (18kD), TCEB1L, TCEB3, TCEC (15kDa), TFIIS (Transcription

Elongation Factor IIS), E2F1 (E2F Transcription Factor), TFAP2A (Transcription
 Factor A2 Alpha), TFCP2 (Transcription Factor CP2), TFC12 (Transcription Factor
 12), PRKDC (Protein Kinase, DNA activated catalytic subunit), SUPT6H, TFIIA
 gamma subunit, TFIIA delta, TFIIB related factor hBRF (HBRF), TFIIE Alpha
 5 Subunit, TFIIE Beta Subunit, TFIIF, Beta Subunit, GTF2F1 (TFIIF), GTF2F2
 (TFIIF), General Transcription Factor IIIA, TFIIH(52 kD subunit of transcription
 factor), TFIIH(p89), TFIIH(p80), TFIIH(p62), TFIIH(p44), TFIIH(p34),
 Transcription Factor IIf(General transcription factor IIF, polypeptide 1 (74kD
 subunit))Transcription Factor IIf(General transcription factor IIF, polypeptide 1
 10 (74kD subunit)), BTf 62 kDSubunit (Basic transcription factor 62 kD subunit),
 CAMP-dependent transcription factor ATF-4, CCAAT box-binding transcription
 factor 1, CRM1(Negative regulator CRM1), Cyclic-AMP-dependent transcription
 factor ATF-1, GABPA(GA-binding protein transcription factor, alpha subunit
 (60kD)), ISGF-3(Signal transducer and activator of transcription 1-alpha/beta),
 15 NFIX(Nuclear factor I/X (CCAAT-binding transcription factor)), NFYA(Nuclear
 transcription factor Y, alpha), NTF97(Nuclear factor p97), Nuclear factor I-B2
 (NFIB2), Nuclear factor NF45, Nuclear factor NF90, POU2F1(POU domain, class
 2, transcription factor 1), Sp2 transcription factor, TCF12(Transcription factor 12
 (HTF4, helix-loop-helix transcription factors 4)), TCF3(Transcription factor 3 (E2A
 20 immunoglobulin enhancer binding factors E12/E47)), TCF6L1(Transcription factor
 6-like 1), TF P65(Transcription factor p65), TFCOUP2(Transcription factor COUP
 2 (a.k.a. ARP1)), Transcription factor IL-4 Stat, Transcription Factor S-II
 (Transcription factor S-II-related protein), Transcription factor Stat5b, Transcription
 Factor, Transcription factor (CBFB), 9G8 Splicing Factor (Pre-mRNA Splicing
 25 factor SRP20), CC1.3(Splicing factor (CC1.3)), HnRNP F protein,
 HNRPA2B1(Heterogeneous nuclear ribonucleoproteins A2/B1),
 HNRPG(Heterogeneous nuclear ribonucleoprotein G), HNRPK(Heterogeneous
 nuclear ribonucleoprotein K), Pre-mRNA splicing factor helicase, Pre-mRNA
 splicing factor SF2, P33 subunit, Pre-mRNA splicing factor SRP20, Pre-mRNA

splicing factor SRP75, PRP4(Serine/threonine-protein kinase PRP4), PTB-Associated
 Splicing Factor, Ribonucleoprotein A', Ribonucleoprotein A1, Ribonucleoprotein
 C1/C2, RNP Protein, L (Heterogeneous nuclear ribonucleoprotein L), RNP-Specific
 C(U1 small nuclear ribonucleoprotein C), SAP 145(Spliceosome associated protein
 5), SAP 61(Splicesomal protein), SC35(Splicing factor), SF3a120, SFRS2(Splicing
 factor, arginine/serine-rich 2), SFRS5(Splicing factor, arginine/serine-rich 5),
 SFRS7(Splicing factor, arginine/serine-rich 7), Small nuclear ribonucleoprotein SM
 D1, SnRNP core protein Sm D2, SnRNP core protein Sm D3, SNRP70(U1 snRNP
 70K protein), SNRPB(Small nuclear ribonucleoprotein polypeptides B and B1),
 10 SNRPE(Small nuclear ribonucleoprotein polypeptide E), SNRPN(Small nuclear
 ribonucleoprotein polypeptide N), Splicing factor SF3a120, Splicing factor U2AF
 35 kD subunit, Splicing factor U2AF 65 kD subunit, SRP30C(Pre-mRNA splicing
 factor SF2, p33 subunit), SRP55-2(Pre-mRNA splicing factor SRP75), Transcription
 factor BTEB, Transcription initiation factor TFIID 250 kD subunit, Cleavage and
 15 polyadenylation specificity factor, Cleavage stimulation factor, 3' pre-RNA, subunit
 1, 50kD, Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD, HNRNP
 Methyltransferase, PABPL1(Poly(A)-binding protein-like 1), Pap mRNA(Poly(A)
 Polymerase), RNA unwinding, RNA Helicase, GU Protein (ATP-Dependent RNA
 helicase dead), KIAA0224 Gene(Putative ATP-dependent RNA helicase), RNA
 20 Helicase A, RNA Helicase P110, and Ste13(Nuclear RNA Helicase).

114. The method, inhibitor, pharmaceutical composition, or nucleic acid probe of
 any of claims 6, 18, 26, 34, 47, 63, 92, and 106, wherein said gene is selected from
 the group consisting of AP47(Clathrin Coat Assembly AP47), AP50(Clathrin Coat
 25 Assembly Protein AP50), Cell Surface Protein (Clathrin Heavy Polypeptide-Like
 Protein), Cltb(Clathrin Light Chain B), Cltc (Clathrin Heavy Chain), Adenylate
 Cyclase, Adenylate Cyclase, Adenylate Cyclase, II, Adenylate Cyclase,IV, Complex
 I, MTND1 (Subunit ND1), MTND2 (Subunit ND2), MTND3 (Subunit ND3),
 MTND4 (Subunit ND4), MTND4L (Subunit ND4L), MTND5 (Subunit ND5),

MTND6 (Subunit ND6), Complex II, Complex III, Cytochrome b subunit, Complex
 IV, CO1 (Cytochrome c Oxidase Subunit I), CO2 (Cytochrome c Oxidase Subunit
 2), CO3 (Cytochrome c Oxidase Subunit 3), Complex V, ATP Synthase Subunit
 ATPase 6, Kinesin Heavy Chain, Kinesin Light Chain, Syntaxin 1a, Syntaxin 1b,
 5 Syntaxin 3, Syntaxin 5a, Syntaxin 7, CANX (Calnexin), ER Lumen Protein 1, ER
 Lumen Protein 2, Ribophorin I, Ribophorin II, Signal recognition particle receptor,
 SRP Protein, TIM17 preprotein translocase, Golgin-245, TGN46 (Trans-Golgi
 Network Integral Membrane Protein TGN38 Precursor), Beta-Cop, Coatomer Beta'
 Subunit, Coatomer Delta Subunit, Gp36b Glycoprotein (Vesicular integral-membrane
 10 protein VIP36 precursor), Homologue of yeast sec7, Protein transport protein SEC13
 (Chromosome 3p25), SEC14 (*S. Cerevisiae*), Synaptic vesicle membrane protein
 VAT-1, Synaptobrevin-3, Synaptotagmin I, Transmembrane(COP-coated vesicle
 membrane protein p24 precursor), Vacuolar-Type (Clathrin-coated vesicle/synaptic
 vesicle proton pump 116 kd subunit), 140 kD Nucleolar phosphoprotein,
 15 Autoantigen p542, Export protein Rae1 (RAE1), Heterogeneous nuclear
 ribonucleoprotein A1, Nuclear pore complex protein hnup153, Nuclear pore complex
 protein NUP214, Nuclear pore glycoprotein p62, Nuclear Transport Factor 2,
 Nucleoporin 98 (NUP98), NUP88, Ribonucleoprotein A, Ribonucleoprotein B",
 Karyopherin, Importin Alpha Subunit, TRN (Transportin), Actin, Beta-Contractin,
 20 Capping Protein Alpha, CFL1 (Cofilin, Non-Muscle Isoform), Desmin, Dystrophin,
 Gelsolin, hOGG1(Myosin Light Chain Kinase), IC Heavy Chain, Itga2 (Integrin,
 Alpha 2 (CD49B, alpha 2 Subunit of VLA-2 receptor)), Itga3 (Integrin Alpha-3
 Precursor), Keratin 19, Keratin, Type II, Lamin A, LBR(Lamin B Receptor), Light
 Chain Alkali, MacMarcks mRNA, MAP1a (Microtubule-Associated Protein 1A),
 25 MAP2(Microtubule-Associated Protein 2), MEG1(Protein-Tyrosine Phosphatase
 MEG1), Microtubule-Associated Protein TAU, Suppressor Of Tubulin STU2, TUBg
 (Tubulin Gamma Chain), Tubulin Alpha-4 Chain, USH1b (Myosin II Heavy Chain),
 Villin, Villin 2 (Ezrin), Actin Depolymerizing, Capping (Actin Filament),
 MYH9(Myosin, Heavy Polypeptide 9, Non-Muscle), MYL5(Myosin Regulatory

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Light Chain 2), Myosin Heavy Chain 95F, Myosin Heavy Chain IB, Myosin IB, Sh3p17(Myosin IC Heavy Chain), Sh3p18(Myosin IC Heavy Chain), KIAA0059(Dematin:Actin-Bundling Protein), TTN (Titin:Myosin Light Chain Kinase), ATP6c(Vacuolar H⁺ ATPase proton channel subunit), ATP6a1 (ATPase, H⁺ Transporting, Lysosomal (Vacuolar Proton Pump), Alpha Polypeptide, 70kD), ATP6b1(ATPase, H⁺ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD), ATP6d(ATPase, H⁺ transporting, lysosomal (vacuolar proton pump) 42kD), ATP6e(ATPase, H⁺ transporting, lysosomal (vacuolar proton pump) 31kD), ATPase, H⁺ transporting, lysosomal (vacuolar proton pump) 31kD, and Superoxide Dismutase.

115. A method for identifying an inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on a conditionally essential gene, and wherein said gene is subject to loss of heterozygosity in a cancer, said method comprising the steps of:

(a) determining at least two alleles of a said gene;

(b) testing a potential allele specific inhibitor to determine whether said potential allele specific inhibitor is active on at least one but less than all of said alleles; wherein inhibition of expression of at least one but less than all of said alleles or reduction of the level of activity of a product of at least one but less than all of said alleles in the presence of said potential allele specific inhibitor is indicative that said potential allele specific inhibitor is a said inhibitor.

116. An inhibitor potentially useful for treatment of cancer, wherein said inhibitor is active on an allelic form of a conditionally essential gene, said gene has at least two alternative alleles in a population, and

wherein said inhibitor targets at least one but less than all of said alternative alleles.

117. A pharmaceutical composition, comprising

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at least one allele specific inhibitor targeting at least one but less than all allelic forms of a conditionally essential gene in a population; and
a pharmaceutically acceptable carrier or excipient.

5 118. A method for producing an inhibitor potentially useful for cancer treatment, wherein said inhibitor is active on at least one but less than all alternative alleles of a conditionally essential gene having at least two alternative alleles, comprising the steps of:

10 (a) identifying a conditionally essential gene that has alternative allelic forms in a noncancerous cell, wherein one of said alternative allelic forms is deleted in a cancer cell;

(b) screening to identify an inhibitor which inhibits said at least one but less than all of said at least two alternative alleles; and

15 (c) synthesizing said inhibitor in an amount sufficient to produce a therapeutic effect when administered to a patient suffering from a cancer in whom cancerous cells have only an allele of said gene inhibited by said inhibitor and in whom normal cells are heterozygous for said gene and contain an allelic form not inhibited by said inhibitor.

20 119. A method for preventing the development of cancer in a patient having a precancerous condition, comprising the steps of:

a. subjecting cells of said precancerous condition to an altered condition such that a first conditionally essential becomes essential;

25 b. administering to said patient a therapeutic amount of a first allele specific inhibitor targeted to an allele of said first conditionally essential gene present in cells of said precancerous condition, wherein the normal somatic cells of said patient are heterozygous for said first gene, said inhibitor is active on at least one but less than all allelic forms of said gene present in a population and targets only one allelic form present in said normal somatic cells; and

wherein cells of said precancerous condition have undergone LOH of said first gene.

120. The method of claim 119, wherein the cells of said precancerous condition are not clonal from a single cell, further comprising the step of:

c. serially administering to said patient at least one additional allele specific inhibitor, wherein each of said at least one additional allele specific inhibitors targets a different allele of a conditionally essential gene or an essential gene than is targeted by said first allele specific inhibitor, wherein said different allele may be a different allele of said first gene or an allele of a different gene, and wherein said patient is heterozygous for each targeted gene and each targeted gene has undergone LOH in cells of said precancerous condition.

121. A method for treating a patient suffering from a cancer, wherein said patient is heterozygous for a conditionally essential gene, comprising the steps of:

a) subjecting cells of said cancer to altered conditions such that said gene is essential; and

administering a therapeutic amount of an allele specific inhibitor active on at least one but less than all allelic forms of said gene present in a population,

wherein said allele specific inhibitor inhibits only one allelic form of said gene present in said patient, and said only one allelic form of said gene is present in cancer cells in said patient.

122. The method of claim 121, further comprising the steps of:

(a) determining whether non-cancerous cells of said patient are heterozygous for a particular conditionally essential gene; or

(b) determining whether cancerous cells of said patient have only one allele of said particular gene; or

(c) both (a) and (b).

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123. A method of inhibiting growth of a cell comprising the steps of:

- a) subjecting said cell to conditions such that said gene is essential; and
- b) administering at least one inhibitor active on an allele of said

conditionally essential gene,

5 wherein said inhibitor is less active on at least one other allele of said gene.

124. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a conditionally essential gene, wherein said patient is suffering from a cancer, said method comprising the step of:

10 identifying a patient heterozygous for a said gene,

 wherein if said patient is heterozygous for said gene, then said patient is a potential patient for said treatment.

125. The method of claim 124, further comprising the step of determining whether cancer cells in said patient contain only a single allele of said gene,

15 wherein if said cancer cells contain only a single allele of said gene, then said patient is a potential patient for said treatment.

126. A method of identifying a potential patient for treatment with an inhibitor active on at least one but less than all alleles of a conditionally essential gene, wherein said patient is suffering from a cancer, said method comprising the step of:

20 determining whether cancer cells in said patient have undergone LOH of a said gene,

 wherein if said cells have undergone LOH of said gene, then said patient is
25 a potential patient for said treatment.

126. A nucleic acid probe at least 12 nucleotides in length which is perfectly complementary to a portion of a first allelic form of a conditionally essential gene, wherein said portion comprises a sequence variance site, and wherein

said probe hybridizes under stringent hybridization conditions to said portion and not to a corresponding portion of a second allelic form having at least one different nucleotide at said sequence variance site.

5 127. A method for selecting a patient for treatment with an antiproliferative treatment, comprising the steps of:

a) determining whether normal somatic cells in a potential patient are heterozygous for an essential or conditionally essential gene, wherein a first allelic form of said gene is more active than a second allelic form, and wherein a reduction
10 in the activity of said gene in a cell increases the sensitivity of said cell to a said antiproliferative treatment; and

b) determining whether cancer cells of said patient have only said second allelic form of said gene,

wherein if said somatic cells are heterozygous and said cancer cells have only
15 said second allelic form, it is indicative that said patient is suitable for treatment with said antiproliferative treatment.

128. A method for selecting an antiproliferative treatment for a patient suffering from a cancer, comprising the steps of:

20 a) determining whether normal somatic cells in a potential patient are heterozygous for an essential or conditionally essential gene which reduces the sensitivity of cells to an antiproliferative treatment, wherein a first allelic form of said gene is more active than a second allelic form, and wherein a reduction in the activity of said gene in a cell increases the sensitivity of said cell to a said antiproliferative
25 treatment; and

b) determining whether cancer cells of said patient have only said second allelic form of said gene,

wherein if said somatic cells are heterozygous for said gene and said cancer cells have only said second allelic form, it is indicative that said antiproliferative

treatment is suitable for said patient.

129. The method of any of claims 115-129, wherein said gene is selected from the group consisting of:

5 galactose-1-phosphate uridylyltransferase, galactose kinase, UDP galactose-4-epimerase, methionine synthase, asparagine synthase, glutamine synthetase, multidrug resistance gene/Pglycoprotein, multidrug resistance associated proteins 1-5, bleomycin hydrolase, dihydropyrimidine dehydrogenase, β -ureidopropionase, β -alanine synthetase, cytidine deaminase, thiopurine methyltransferase, CYP1A1, CYP1A2, 10 CYP2A6, CYP2A7, CYP2B6, CYP2B7, CYP2C8, CYP2C9, CYP2C17, CYP2C18, CYP2C19, CYP2D6, CYP2E1, CYP2F1, CYP3A3, CYP3A4, CYP3A5, CYP3A7, CYP4B1, CYP7, CYP11, CYP17, CYP19, CYP21, CYP27, glutathione transferase alpha, glutathione transferase theta, glutathione transferase mu, glutathione transferase pi, methylguanine methyltransferase, 3-alkylguanine alkyltransferase, 3-methyladenine 15 DNA glucosylase, DNA dependent protein kinase, catalytic subunit of DNA-PK, DNA binding subunit of DNA-PK Ku-70 or Ku-80 subunit, KARP-1, Poly(ADP-ribose) polymerase, Fanconi Anemia genes A, B, C, D, E, F, G, and H, ERCC-1, ERCC2/XPD, ERCC3/XPB, ERCC4, ERCC5, ERCC6, XPA, XPC, XPE, HHR23A, HHR23B, uracil glycosylase, 3-methyl adenine DNA glycosylase, NF-kappa B, 20 XRCC4, XRCC5/Ku80, XRCC6, XRCC7, glutathione-S-transferase, I-kappa B alpha, HSP70, HSP27, and 9-oxoguanine DNA glycosylase.

131. A method for identifying a potential patient undergoing transplantation for treatment with an inhibitor active on at least one but less than all alleles of an 25 essential gene, comprising the step of:

identifying a patient undergoing an allogenic bone marrow transplantation in which the donor tissue contains at least one alternative allele of an essential gene different from the alleles in somatic cells of said patient.

132. The method of claim 131, wherein said donor or said recipient is homozygous for an alternative allelic form of an essential gene that is not present in the other of said donor or said recipient.

5 133. A method for treating graft versus host disease in a patient receiving allogenic bone marrow transplantation, said method comprising the step of

administering to said patient at least one allele specific inhibitor specific for at least one but less than all of the allelic forms of an essential gene in a population, wherein said inhibitor inhibits stimulation of the donor immune system, and cells of
10 the said patient comprise an allelic form of said gene not present in the donor bone marrow.

134. The method of claim 133, wherein said allele specific inhibitor is selected by identifying at least one alternative alleles of an essential gene present in the donor
15 tissues but absent in the normal somatic cells of said patient; and

selecting a said inhibitor active on a said alternative allele of an essential gene present in said donor tissues but absent in the normal somatic cells of said patient.

20 135. The method of claim 134, wherein said at least one inhibitor recognizes both alleles of said essential gene that are present in said donor, but not both alleles of said gene that are present in said patient.

25 136. A method for enhancing engraftment of an allogenic bone marrow transplant, comprising the step of administering to a patient receiving said transplant an allele specific inhibitor which kills or suppresses the patient's bone marrow but not the donor bone marrow, thereby providing space for engraftment of the donor cells within the marrow cavity.

137. The method of claim 136, wherein the allele specific inhibitor is selected by

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identifying alternative alleles of an essential gene that are present in the recipient but not the donor marrow.

5 138. The method of claim 137, wherein said allele specific inhibitor recognizes both allelic forms of the essential gene that are present in the recipient, but not both allelic forms of the same gene that are present in the recipient.

10 139. A method for treating or preventing chimerism in allogenic bone marrow transplantation, comprising
selectively killing or suppressing proliferation of the patient's own cells without toxicity to the donor cells by
administering to a patient receiving said transplantation at least one allele specific inhibitor active on at least one but less than all alternative alleles of a gene vital for cell growth or viability, wherein said inhibitor targets the allelic form or
15 forms of a gene in bone marrow of said patient but does not target at least one allelic form of said gene in the donor bone marrow.

20 140. A method for treating cancer in a patient receiving allogenic or autologous transplantation, comprising the step of
administering to said patient at least one allele specific inhibitor which kills or inhibits the growth of cancer cells without toxicity to the transplanted marrow.

25 141. The method of claim 141, wherein said transplantation is autologous transplantation and said at least one allele specific inhibitor is selected to be active on the allele of an essential gene remaining in the cancer cells due to LOH in patients whose normal somatic cells are heterozygous for said essential gene, but not on the alternative allele of said gene present in said normal somatic cells,
whereby said administration enables continuing therapy of cancer without suppression of the transplanted marrow.

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142. The method of claim 140, wherein said transplantation is allogenic transplantation and said allele specific inhibitor recognizes both alleles of said essential gene that are present in the recipient, but not both forms of the said gene that are present in said patient.

5

143. A method for eliminating malignant cells from transplanted marrow during autologous transplantation of a patient heterozygous for an essential gene, comprising

10 contacting cells from harvested autologous bone marrow *ex vivo* with at least one allele specific inhibitor active on at least one but less than all alternative alleles of said essential gene, wherein said inhibitor targets an allelic form of said gene present in cancer cells of said patient but does not target an alternative allele of said gene present in normal cells from said autologous bone marrow,

 wherein said gene has undergone LOH in cancer cells of said patient.

15

144. The method of claim 143, wherein said autologous bone marrow is harvested from said patient prior to high dose radiation or chemotherapy.

145. The method of claim 143, further comprising the steps of:

20

a. identifying one alternative allele of an essential gene remaining in the cancer cell due to LOH in patients who are heterologous with two different alternative forms of the essential gene in normal cells of the autologous bone marrow;

25

b. cultivating said autologous bone marrow *ex vivo* in the presence of an allele specific inhibitor that inhibits the allele that is present in the cancer cells, but not the heterologous allele that is present in the normal bone marrow. .

146. The method of claim 143, wherein said autologous bone marrow is contacted with a plurality of said allele specific inhibitors.

147. A method for separating a first cell from a mixture of cells, comprising the steps of:

5 a) providing an allele specific binding compound which binds to at least one but less than all alleles of a gene, wherein a said allele of said gene expressed in said first cell is not expressed in other cells of said mixture of cells or is expressed in other cells in said mixture of cells and not in said first cell;

b) contacting said mixture of cells with said binding compound under conditions such that said binding compound binds to said allele and not to non-target alleles; and

10 c) separating bound cells from unbound cells.

148. The method of claim 147, wherein said mixture of cells comprises normal somatic cells and cancer cells from a patient, said first cells are said normal somatic cells, and said first cells express a said allele deleted in said cancer cells due to LOH of said gene, comprising

15 separating said normal somatic cells from said cancer cells.

149. The method of claim 147, wherein said allele specific binding compound is an antibody or antibody fragment.

20

150. The method of claim 147, wherein said binding compound is attached to a solid support.

Target Gene Summary Table
Dihydropyrimidine Dehydrogenase
Chromosome 1p22-1q21
VARIA950

Fig. 1

| | | | Genotypes of 36 unrelated individuals | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | Protein | | Race Specific heterozygosity | | | |
|--------------|----------|------|---------------------------------------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----------|------|------------------------------|---------------------------------|----------------------------|--|
| Primer Pair | Location | Base | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | Comments | Het% | | | | |
| DPD1a-DPD2b | bp 166 | T/C | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | 11% | Cys/Arg | | |
| DPD1c-DPD2a | bp 577 | A/G | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | AA | 9% | Met/Val | |
| DPD2a-DPD10b | bp 3925 | G/A | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | 35% | These are separated by 11 bases | 50 % in blacks and chinese | |
| DPD2a-DPD10b | bp 3937 | C/T | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | CC | 38% | | |
| | | | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | TT | 56% | Locus Heterozygosity | |

Ethnic & Racial Groups Surveyed:

a=Asian (other)
ar=Arab
ash=Ashkenazi
b=Black
c=Chinese
cu=Cuban
g=Greek
h=Hispanic
i=Indian
it=Italian
j=Japanese
pr=Puerto Rican
w=White
*empty box = genotype not determined

Other SSCP polymorphisms: # %

Sequence nomenclature and numbering from:
Yokota,H., Fernandez-Salguero,P., Funaya,H., Un,K., McBride,O.W., Podschun,B., Schnackertz,K.D., and Gonzalez, F.J. "cDNA Cloning and Chromosome Mapping of Human Dihydropyrimidine Dehydrogenase, an Enzyme Associated With 5-Fluorouracil Toxicity and Congenital Thymine Uraciluria." Journal of Biological Chemistry, 269 (37) 23192-23195 (1994)

Validation Status:

Other populations genotyped:
None

*bold nucleotide is the polymorphic base

| ID# | Allele | Sequence around polymorphism* |
|--------------|--------|-------------------------------|
| VARIA500.2.1 | 166 T | TGCAACTCTGTGTCCACTTC |
| VARIA500.2.2 | 166 C | TGCAACTCTGGGTCCACTTC |
| VARIA500.3.1 | 577 A | ATTCAAAGCAATGAGTATCCC |
| VARIA500.3.2 | 577 G | ATTCAAAGCAGTGAGTATCCC |
| VARIA500.1.1 | 3925 G | CCCCTCTTTTGTGTGCACAT |
| VARIA500.1.2 | 3925 A | CCCCTCTTTTACTGTGTGCACAT |
| VARIA500.4.1 | 3937 C | TGTGCACATACGGGCTCTGAC |
| VARIA500.4.2 | 3937 T | TGTGCACATATGGGCTCTGAC |

| | | Genotypes of 36 unrelated individuals | | | | | | | | | | | | | | | | | | | | | | | | | | | | Race Specific heterozygosity 50% of Blacks, all Hispanics | | | | | | | | | | | | | |
|--|-------------|---------------------------------------|------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|---|----|----|----|----|----|----|----|----|----|--------------------------|----------|------------------------------|--|
| | Primer Pair | Location | Base | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | Comments | Location | Race Specific heterozygosity | |
| | TAF6-TAF2 | 554 | G A | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | GG | GA | 22% | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | 22% Locus Heterozygosity | | | |

Ethnic & Racial Groups Surveyed:
 a=Asian (other)
 ar=Arab
 ash=Ashkenazi
 b=Black
 c=Chinese
 cu=Cuban
 g=Greek
 h=Hispanic
 i=Indian
 it=Italian
 j=Japanese
 pr=Puerto Rican
 w=White
 *empty box = genotype not determined

Other SSCP polymorphisms: # %

Sequence from:
 GenBank accession # U13991
 Jacq. X., Brou, C., Lutz, Y., Davidson, I., Chambon, P.
 and L. Tora (1994) Human TAFII30 is present in a
 distinct TFIIID complex and is required for
 transcriptional activation by the estrogen receptor.
 Cell 79: 107-117. (Note: the numbering in the GenBank
 accession and the Cell 79:107-117 paper differ by two nucleotides, the
 cytosine at nucleotide 556 using the number in the latter.)

Validation:
 Other TATA associated factors (TAFs) have been
 proven essential for cell growth.

Other populations genotyped:

| ID# | Allele | Sequence around polymorphism |
|-------------|--------|------------------------------|
| VARIA20 1.1 | 554 | TGAAGGCACAGCCTCCGCA |
| VARIA20 1.2 | 554 | TGAAGGCACAGCCTCCGCA |

*Bold nucleotide is the polymorphic base

[illegible]

[illegible]

Target Gene Summary Table
Replication Protein A, 70 kDa Subunit
Chromosome 17p13.3
VARIA401

[illegible]

Target Gene Summary Table
Alanyl-tRNA Synthetase
Chromosome 16q22
VARIA304

Ethnic & Racial Groups Surveyed:

| 注 | % |
|-----|-----|
| 1 | 100 |
| 2 | 100 |
| 3 | 100 |
| 4 | 100 |
| 5 | 100 |
| 6 | 100 |
| 7 | 100 |
| 8 | 100 |
| 9 | 100 |
| 10 | 100 |
| 11 | 100 |
| 12 | 100 |
| 13 | 100 |
| 14 | 100 |
| 15 | 100 |
| 16 | 100 |
| 17 | 100 |
| 18 | 100 |
| 19 | 100 |
| 20 | 100 |
| 21 | 100 |
| 22 | 100 |
| 23 | 100 |
| 24 | 100 |
| 25 | 100 |
| 26 | 100 |
| 27 | 100 |
| 28 | 100 |
| 29 | 100 |
| 30 | 100 |
| 31 | 100 |
| 32 | 100 |
| 33 | 100 |
| 34 | 100 |
| 35 | 100 |
| 36 | 100 |
| 37 | 100 |
| 38 | 100 |
| 39 | 100 |
| 40 | 100 |
| 41 | 100 |
| 42 | 100 |
| 43 | 100 |
| 44 | 100 |
| 45 | 100 |
| 46 | 100 |
| 47 | 100 |
| 48 | 100 |
| 49 | 100 |
| 50 | 100 |
| 51 | 100 |
| 52 | 100 |
| 53 | 100 |
| 54 | 100 |
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| 56 | 100 |
| 57 | 100 |
| 58 | 100 |
| 59 | 100 |
| 60 | 100 |
| 61 | 100 |
| 62 | 100 |
| 63 | 100 |
| 64 | 100 |
| 65 | 100 |
| 66 | 100 |
| 67 | 100 |
| 68 | 100 |
| 69 | 100 |
| 70 | 100 |
| 71 | 100 |
| 72 | 100 |
| 73 | 100 |
| 74 | 100 |
| 75 | 100 |
| 76 | 100 |
| 77 | 100 |
| 78 | 100 |
| 79 | 100 |
| 80 | 100 |
| 81 | 100 |
| 82 | 100 |
| 83 | 100 |
| 84 | 100 |
| 85 | 100 |
| 86 | 100 |
| 87 | 100 |
| 88 | 100 |
| 89 | 100 |
| 90 | 100 |
| 91 | 100 |
| 92 | 100 |
| 93 | 100 |
| 94 | 100 |
| 95 | 100 |
| 96 | 100 |
| 97 | 100 |
| 98 | 100 |
| 99 | 100 |
| 100 | 100 |

2

Fig. 2

SSCP Overview

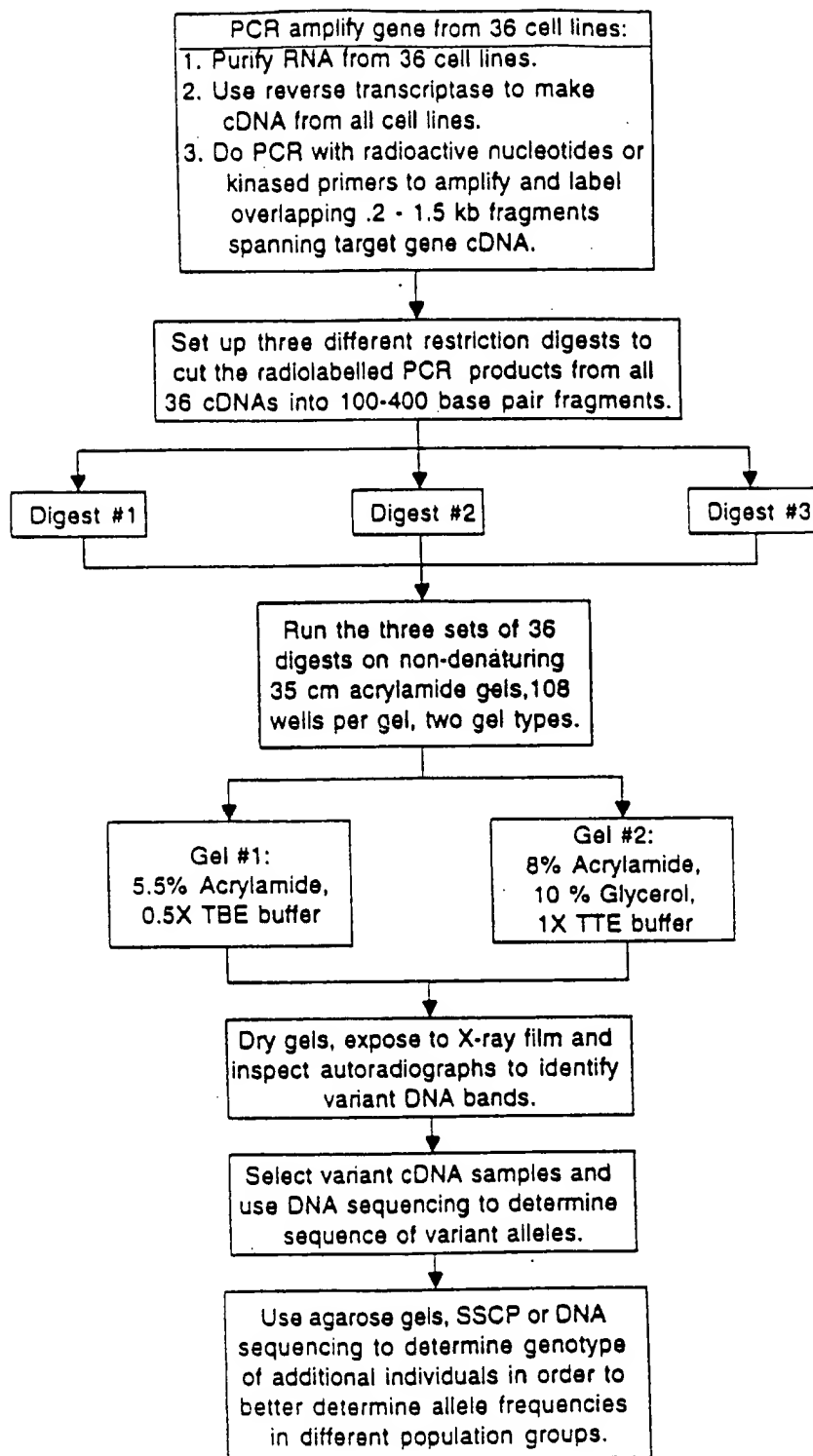


Fig. 3

Chromosome 1 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|--------|-------|-------------|-----------|--------------|--------------|
| 36 | D1Z2 | 110 | 24 | 0.22 | Breast | GCC 5:310 |
| 36 | D1Z2 | 37 | 15 | 0.41 | Breast | AJHG 45:73 |
| 36 | D1Z2 | 18 | 9 | 0.5 | Endocrine | CR 52:770 |
| 36 | D1Z2 | 20 | 1 | 0.05 | Endocrine | CR 52:770 |
| 36 | D1Z2 | 7 | 7 | 1 | Neuroblastom | CR 55:5366 |
| 36 | D1S243 | 43 | 10 | 0.23 | Breast | CR 55:1752 |
| 36 | D1S243 | 20 | 6 | 0.3 | Endocrine | Unknown |
| 36 | D1S243 | 14 | 14 | 1 | Neuroblastom | CR 55:5366 |
| 36 | D1S243 | 36 | 9 | 0.25 | Neuroblastom | CR 55:5681 |
| 36 | D1S243 | 8 | 7 | 0.88 | Neuroblastom | GCC 10:275 |
| 36-35 | D1S80 | 9 | 0 | 0 | Brain | CR 54:1397 |
| 36-35 | D1S80 | 14 | 1 | 0.07 | Brain | CR 54:1397 |
| 36-35 | D1S80 | 34 | 16 | 0.47 | Brain | AJP 145:1175 |
| 36-35 | D1S80 | 17 | 4 | 0.24 | Breast | GCC 12:16 |
| Unknown | D1S80 | 74 | 22 | 0.3 | Breast | CR 53:1990 |
| 36-35 | D1S80 | 63 | 20 | 0.32 | Breast | CR 54:4274 |
| 36-35 | D1S80 | 40 | 8 | 0.2 | Endocrine | GCC 13:9 |
| 36-35 | D1S80 | 13 | 10 | 0.77 | Neuroblastom | GCC 10:275 |
| 36-35 | D1S80 | 38 | 9 | 0.24 | Neuroblastom | CR 55:5681 |
| Unknown | D1S80 | 19 | 2 | 0.11 | Testis | CR 54:6265 |
| Unknown | D1S80 | 17 | 2 | 0.12 | Testis | CR 9:2245 |
| 36.3-35 | D1S76 | 34 | 16 | 0.47 | Brain | AJP 145:1175 |
| 36.3-35 | D1S76 | 41 | 4 | 0.1 | Breast | CR 53:4356 |
| 36.3-35 | D1S76 | 19 | 3 | 0.16 | Breast | GCC 12:16 |
| 36.3-35 | D1S76 | 38 | 13 | 0.34 | Breast | CR 54:4274 |
| 36.3-35 | D1S76 | 17 | 15 | 0.88 | Neuroblastom | GCC 10:275 |
| Unknown | D1S77 | 21 | 10 | 0.48 | Brain | AJP 145:1175 |
| Unknown | D1S77 | 19 | 3 | 0.16 | Breast | GCC 12:16 |
| Unknown | D1S77 | 18 | 4 | 0.22 | Esophageal | GCC 10:177 |
| Unknown | D1S77 | 6 | 2 | 0.33 | Stomach | BJC 73:424 |
| Unknown | D1S253 | 17 | 3 | 0.18 | Leukemia | CR 55:5377 |
| 36 | D1S47 | 32 | 3 | 0.09 | Breast | CR 51:1020 |
| 36 | D1S47 | 15 | 1 | 0.07 | Colon | CR 52:285 |
| 36 | D1S47 | 17 | 12 | 0.71 | Colon | CR 50:7232 |
| 36 | D1S47 | 24 | 7 | 0.29 | Melanoma | PNAS 86:1614 |
| 36 | D1S47 | 31 | 7 | 0.23 | Neuroblastom | GCC 10:30 |
| 36 | D1S214 | 43 | 6 | 0.14 | Breast | CR 55:1752 |
| 36 | D1S214 | 11 | 10 | 0.91 | Neuroblastom | GCC 10:275 |

Chromosome 1 - p Arm

| | | | | | | |
|-----------|--------|----|----|------|-------------------|--------------|
| 36 | D1S214 | 13 | 0 | 0 | Stomach | BJC 73:424 |
| Unknown | D1S160 | 17 | 9 | 0.53 | Brain | AJP 11145:11 |
| Unknown | D1S160 | 21 | 5 | 0.24 | Liver | CR 54:4188 |
| Unknown | D1S160 | 34 | 8 | 0.24 | Neuroblastom a | CR 55:5681 |
| Unknown | D1S160 | 41 | 22 | 0.54 | Ovary | BJC 75:1105 |
| Unknown | D1S244 | 36 | 9 | 0.25 | Neuroblastom a | CR 55:5681 |
| 36 | D1S450 | 37 | 8 | 0.22 | Breast | CR 55:1752 |
| Unknown | NPPA | 1 | 0 | 0 | Testis | GCC 13:249 |
| Unknown | EGD | 10 | 1 | 0.1 | Testis | GCC 13:249 |
| 36 | D1S228 | 40 | 5 | 0.12 | Breast | CR 55:1752 |
| 36 | D1S228 | 7 | 5 | 0.71 | Neuroblastom a | GCC 10:275 |
| 36 | D1S228 | 31 | 7 | 0.23 | Neuroblastom a | CR 55:5681 |
| 36 | D1S228 | 8 | 1 | 0.12 | Stomach | BJC 73:424 |
| Unknown | D1S170 | 19 | 5 | 0.26 | Liver | CR 54:4188 |
| Unknown | D1S170 | 36 | 7 | 0.19 | Neuroblastom a | CR 55:5681 |
| Unknown | D1S170 | 33 | 16 | 0.48 | Ovary | BJC 75:1105 |
| Unknown | D1S94 | 19 | 12 | 0.63 | Colon | CR 50:7232 |
| Unknown | D1S94 | 8 | 4 | 0.5 | Neuroblastom a | 0 7:1185 |
| Unknown | D1S94 | 36 | 9 | 0.25 | Neuroblastom a | GCC 10:30 |
| 35 | D1S199 | 50 | 9 | 0.18 | Breast | CR 55:1752 |
| 35 | D1S199 | 30 | 4 | 0.13 | Cervix | CR 56:197 |
| 35 | D1S199 | 14 | 13 | 0.93 | Neuroblastom a | CR 55:5366 |
| 35 | D1S199 | 4 | 2 | 0.5 | Neuroblastom a | GCC 10:275 |
| 35 | D1S199 | 9 | 0 | 0 | Stomach | BJC 73:424 |
| 36.1-p34 | ALPL | 17 | 2 | 0.12 | Colon | CR 52:285 |
| 36.1-p34 | ALPL | 2 | 1 | 0.5 | Endocrine | CR 52:770 |
| 36.1-p34 | ALPL | 17 | 4 | 0.24 | Melanoma | PNAS 86:4614 |
| 36.11 | D1S112 | 1 | 1 | 1 | Neuroblastom a | CR 55:5366 |
| Unknown | D1S112 | 20 | 1 | 0.05 | Neuroblastom a | GCC 10:275 |
| Unknown | FUCA1 | 15 | 5 | 0.33 | Brain | AJP 1145:117 |
| Unknown | FUCA1 | 13 | 6 | 0.46 | Melanoma | PNAS 86:4614 |
| Unknown | FUCA1 | 14 | 0 | 0 | Testis | GCC 13:249 |
| Unknown | D1S234 | 10 | 8 | 0.8 | Neuroblastom a | GCC 10:275 |
| 36.2-36.1 | FGR | 12 | 2 | 0.17 | Brain | CR 54:1397 |
| 36.2-36.1 | FGR | 7 | 0 | 0 | Brain | CR 54:1397 |
| 36.2-36.1 | FGR | 4 | 2 | 0.5 | Endocrine | CR 52:770 |
| 36.2-36.1 | FGR | 14 | 6 | 0.43 | Ovary | BJC 75:1105 |

Chromosome 1 - p Arm

| | | | | | | |
|------------|----------|-----|----|------|--------------|--------------|
| Unknown | D1S63 | 39 | 4 | 0.1 | Testis | CR 54:6265 |
| Unknown | D1S247 | 2 | 1 | 0.5 | Neuroblastom | GCC 10:275 |
| 36.2-34 | D1S95-96 | 74 | 20 | 0.27 | Breast | CR 53:1990 |
| Unknown | D1S96 | 17 | 11 | 0.65 | Colon | CR 50:7232 |
| 36.2-36.12 | D1S95 | 19 | 2 | 0.11 | Neuroblastom | 0 7:1185 |
| Unknown | D1S96 | 18 | 0 | 0 | Neuroblastom | 0 7:1185 |
| 32 | D1S7 | 105 | 43 | 0.41 | Breast | CR 54:4274 |
| 32 | D1S7 | 46 | 13 | 0.28 | Breast | GCC 10:275 |
| 32 | D1S7 | 28 | 26 | 0.93 | Colon | CR 50:7232 |
| 32 | D1S7 | 14 | 7 | 0.5 | Endocrine | N 328:524 |
| 32 | D1S7 | 13 | 1 | 0.08 | Liver | BJC 64:1083 |
| 32 | D1S7 | 50 | 15 | 0.3 | Liver | JJCR 87:169 |
| 32 | D1S7 | 6 | 6 | 1 | Neuroblastom | CR 55:5366 |
| 32 | D1S7 | 14 | 5 | 0.36 | Pancreas | BJC 65:100 |
| 32 | D1S7 | 31 | 3 | 0.1 | Stomach | HG 92:244 |
| 32 | D1S7 | 45 | 14 | 0.31 | Stomach | CR 51:2926 |
| 32 | D1S7 | 31 | 3 | 0.1 | Stomach | BJC 73:424 |
| 32 | D1S7 | 30 | 1 | 0.03 | Testis | GCC 10:275 |
| Unknown | D1S233 | 19 | 5 | 0.26 | Head&Neck | CR 54:1152 |
| Unknown | D1S233 | 4 | 2 | 0.5 | Neuroblastom | GCC 10:275 |
| Unknown | D1S241 | 4 | 3 | 0.75 | Neuroblastom | GCC 10:275 |
| Unknown | D1S201 | 35 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D1S201 | 19 | 1 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D1S201 | 8 | 3 | 0.38 | Neuroblastom | GCC 10:275 |
| Unknown | D1S201 | 12 | 3 | 0.25 | Stomach | BJC 73:424 |
| 35-32 | D1S57 | 15 | 1 | 0.07 | Brain | CR 50:5784 |
| 32 | D1S57 | 26 | 12 | 0.46 | Brain | AJP 1145:117 |
| 35-32 | D1S57 | 11 | 0 | 0 | Brain | CR 469:6572 |
| 35-32 | D1S57 | 18 | 1 | 0.06 | Breast | GCC 2:191 |
| 35-32 | D1S57 | 73 | 15 | 0.21 | Breast | GCC 2:191 |
| 35-32 | D1S57 | 43 | 4 | 0.09 | Breast | CR 50:7184 |
| 35-32 | D1S57 | 81 | 36 | 0.44 | Breast | CR 50:7271 |
| 35-32 | D1S57 | 3 | 2 | 0.67 | Breast | CR 53:3804 |
| 35-32 | D1S57 | 44 | 6 | 0.14 | Breast | CR 51:6194 |
| 35-32 | D1S57 | 19 | 6 | 0.32 | Breast | CR 51:6194 |
| 35-32 | D1S57 | 23 | 5 | 0.22 | Breast | GCC 10:275 |
| 32 | D1S57 | 74 | 23 | 0.31 | Breast | CR 53:1990 |
| 32 | D1S57 | 52 | 1 | 0.02 | Cervix | CR 54:4181 |
| 35-32 | D1S57 | 6 | 0 | 0 | Cervix | GCC 9:119 |
| 35-32 | D1S57 | 180 | 40 | 0.22 | Colon | BJC 61:475 |
| 35-32 | D1S57 | 22 | 2 | 0.09 | Colon | CCG 48:167 |

Chromosome 1 - p Arm

| | | | | | | |
|---------|--------|-----|----|------|--------------|-------------|
| 35-32 | D1S57 | 16 | 6 | 0.38 | Colon | CR 54:217 |
| 35-32 | D1S57 | 12 | 0 | 0 | Colon | N 331:273 |
| 32 | D1S57 | 16 | 1 | 0.06 | Endocrine | CR 54:270 |
| 32 | D1S57 | 12 | 8 | 0.67 | Endocrine | CR 52:770 |
| 35-32 | D1S57 | 15 | 6 | 0.4 | Endocrine | GGC 12:120 |
| 32 | D1S57 | 27 | 8 | 0.3 | Esophageal | CR 54:2996 |
| 32 | D1S57 | 14 | 1 | 0.07 | Kidney | CR 51:820 |
| 35-32 | D1S57 | 22 | 1 | 0.05 | Liver | CR 51:89 |
| 35-32 | D1S57 | 28 | 5 | 0.18 | Lung | CR 52:2478 |
| 32 | D1S57 | 2 | 2 | 1 | Neuroblastom | CR 55:5366 |
| 32 | D1S57 | 14 | 1 | 0.07 | Ovary | CR 54:511 |
| 35-32 | D1S57 | 18 | 7 | 0.39 | Ovary | O 7:1059 |
| 35-32 | D1S57 | 4 | 0 | 0 | Pancreas | CR 54:261 |
| 35-32 | D1S57 | 20 | 2 | 0.1 | Sarcoma | CR 52:2419 |
| 32 | D1S57 | 5 | 3 | 0.6 | Stomach | GGC 12:121 |
| 35-32 | D1S57 | 17 | 0 | 0 | Testis | G 5:134 |
| 32 | D1S57 | 12 | 2 | 0.05 | Testis | O 9:275 |
| 32 | D1S57 | 37 | 2 | 0.05 | Testis | CR 54:6265 |
| 35-32 | D1S57 | 8 | 2 | 0.25 | Uterus | GGC 9:119 |
| 32 | D1S57 | 11 | 1 | 0.09 | Uterus | CR 51:5632 |
| Unknown | D1S255 | 14 | 7 | 0.6 | Neuroblastom | GGC 10:275 |
| Unknown | D1S255 | 5 | 4 | 0.8 | Stomach | BJC 73:424 |
| Unknown | D1S186 | 25 | 7 | 0.28 | Liver | CR 54:1188 |
| 32 | MYCL1 | 74 | 26 | 0.35 | Breast | CR 53:1990 |
| 32 | MYCL1 | 81 | 36 | 0.44 | Breast | GGC 12:128 |
| 32 | MYCL1 | 152 | 55 | 0.36 | Breast | HG 85:101 |
| 32 | MYCL1 | 59 | 23 | 0.39 | Breast | CR 54:4294 |
| 32 | MYCL1 | 17 | 2 | 0.12 | Breast | AJHG 45:73 |
| 32 | MYCL1 | 16 | 10 | 0.62 | Colon | CR 50:7232 |
| 32 | MYCL1 | 20 | 2 | 0.1 | Colon | CR 52:285 |
| 32 | MYCL1 | 20 | 5 | 0.25 | Colon | GGC 12:1382 |
| 32 | MYCL1 | 9 | 1 | 0.11 | Endocrine | CR 52:770 |
| 32 | MYCL1 | 20 | 4 | 0.2 | Endocrine | GGC 12:139 |
| 32 | MYCL1 | 12 | 8 | 0.67 | Endocrine | CR 52:770 |
| 32 | MYCL1 | 11 | 0 | 0 | Esophageal | CR 54:2996 |
| 32 | MYCL1 | 18 | 2 | 0.11 | Liver | JJCR 81:108 |
| 32 | MYCL1 | 27 | 0 | 0 | Liver | CR 54:1188 |
| 32 | MYCL1 | 5 | 0 | 0 | Lung | CR 54:5643 |
| 32 | MYCL1 | 12 | 1 | 0.09 | Lung | CR 54:5643 |
| 32 | MYCL1 | 57 | 12 | 0.21 | Lung | O 10:937 |
| 32 | MYCL1 | 20 | 2 | 0.1 | Lung | CR 54:5643 |
| 32 | MYCL1 | 2 | 1 | 0.5 | Lung | CR 54:5643 |
| Unknown | MYCL1 | 9 | 2 | 0.22 | Neuroblastom | CR 55:5366 |
| 32 | MYCL1 | 41 | 9 | 0.22 | Ovary | BJC 75:1105 |

Chromosome 1 - p Arm

| | | | | | | |
|-----------|--------|----|----|------|--------------|--------------|
| 32 | MYCL1 | 13 | 4 | 0.31 | Ovary | GO 55:245 |
| 32 | MYCL1 | 17 | 4 | 0.24 | Ovary | GO 55:245 |
| 32 | MYCL1 | 27 | 3 | 0.11 | Ovary | GO 55:245 |
| 32 | MYCL1 | 9 | 0 | 0 | Sarcoma | CR 52:2419 |
| 32 | MYCL1 | 4 | 0 | 0 | Testis | CCG 52:72 |
| 32 | MYCL1 | 1 | 0 | 0 | Testis | CCG 52:72 |
| 32 | MYCL1 | 1 | 0 | 0 | Testis | CCG 52:72 |
| 32 | MYCL1 | 20 | 1 | 0.05 | Uterus | CR 54:4294 |
| Unknown | GDUT1 | 23 | 3 | 0.13 | Testis | CR 54:4294 |
| 34.2-32.2 | D1S190 | 23 | 3 | 0.13 | Cervix | CR 56:197 |
| 34.2-32.2 | D1S190 | 3 | 1 | 0.33 | Neuroblastom | GCC 10:275 |
| Unknown | D1S193 | 7 | 2 | 0.29 | Neuroblastom | GCC 10:275 |
| 37 | D1S211 | 42 | 6 | 0.14 | Breast | CR 53:1990 |
| Unknown | D1S211 | 5 | 3 | 0.6 | Neuroblastom | GCC 10:275 |
| Unknown | D1S197 | 12 | 7 | 0.58 | Neuroblastom | GCC 10:275 |
| Unknown | D1S197 | 16 | 5 | 0.31 | Stomach | BJC 73:424 |
| 32 | D1S62 | 74 | 19 | 0.26 | Breast | CR 53:1990 |
| 32 | D1S62 | 15 | 0 | 0 | Colon | CCG 48:167 |
| 32 | D1S62 | 2 | 2 | 1 | Stomach | BJC 73:424 |
| Unknown | D1S162 | 0 | 5 | 0 | Breast | Unknown |
| Unknown | D1S162 | 19 | 5 | 0.26 | Liver | CR 54:4188 |
| Unknown | D1S200 | 12 | 7 | 0.58 | Neuroblastom | GCC 10:275 |
| Unknown | D1S200 | 33 | 5 | 0.15 | Neuroblastom | CR 55:5681 |
| Unknown | D1S15 | 74 | 22 | 0.3 | Breast | CR 53:1990 |
| Unknown | D1S15 | 4 | 1 | 0.25 | Endocrine | CR 52:770 |
| Unknown | D1S15 | 24 | 6 | 0.25 | Testis | CR 54:6266 |
| pter-22 | D1S21 | 18 | 9 | 0.5 | Brain | AJP 1145:117 |
| pter-22 | D1S21 | 74 | 20 | 0.27 | Breast | CR 53:1990 |
| 31-pter | D1S21 | 10 | 0 | 0 | Breast | CR 53:1990 |
| 31-pter | D1S21 | 12 | 1 | 0.08 | Endocrine | CR 52:770 |
| 31-pter | D1S21 | 1 | 3 | 0.13 | Endocrine | CR 52:770 |
| 31-pter | D1S17 | 19 | 8 | 0.42 | Brain | AJP 1145:117 |
| 31-pter | D1S17 | 8 | 1 | 0.12 | Breast | CR 53:1990 |
| 31-pter | D1S17 | 5 | 0 | 0 | Breast | CR 51:1020 |
| pter-22 | D1S17 | 73 | 22 | 0.5 | Breast | CR 53:1990 |
| pter-22 | D1S17 | 4 | 3 | 0.75 | Endocrine | CR 52:770 |
| pter-22 | D1S17 | 9 | 2 | 0.27 | Endocrine | CR 52:770 |
| 31-pter | D1S17 | 13 | 2 | 0.15 | Endocrine | GCC 13:9 |
| pter-22 | D1S17 | 19 | 4 | 0.21 | Melanoma | CR 53:1990 |
| pter-22 | D1S18 | 74 | 20 | 0.27 | Breast | CR 53:1990 |
| pter-22 | D1S18 | 6 | 4 | 0.67 | Endocrine | CR 52:770 |

Chromosome 1 - p Arm

| | | | | | | |
|---------|--------|----|----|------|--------------|-----------------|
| Unknown | D1S203 | 14 | 6 | 0.43 | Neuroblastom | GCC 10:275 a |
| Unknown | D1S246 | 11 | 0 | 0 | Stomach | BJC 74:424 |
| Unknown | D1S209 | 15 | 7 | 0.47 | Neuroblastom | GCC 10:275 a |
| Unknown | D1S159 | 16 | 3 | 0.19 | Liver | CR 54:4188 |
| Unknown | D1S219 | 8 | 0 | 0 | Stomach | BJC 73:424 |
| 31 | D1S461 | 14 | 11 | 0.25 | Breast | CR 53:1990 |
| 21 | D1S216 | 14 | 13 | 0.93 | Neuroblastom | CR 55:5366 a |
| 21 | D1S216 | 8 | 4 | 0.5 | Neuroblastom | GCC 10:275 a |
| pter-31 | D1S2 | 12 | 7 | 0.58 | Brain | AJP 145:1175 |
| pter-31 | D1S2 | 1 | 0 | 0 | Breast | GCC 12:16 |
| pter-31 | D1S2 | 74 | 19 | 0.26 | Breast | CR 53:1990 |
| pter-31 | D1S2 | 16 | 3 | 0.19 | Melanoma | PNAS 86:4614 |
| 31 | D1S500 | 33 | 8 | 0.24 | Breast | CR 55:1752 |
| 31 | D1S480 | 39 | 11 | 0.28 | Breast | CR 55:1752 |
| Unknown | D1S207 | 15 | 8 | 0.53 | Neuroblastom | GCC 10:275 a |
| Unknown | D1S207 | 14 | 2 | 0.14 | Stomach | BJC 74:424 |
| pter-22 | D1S16 | 74 | 22 | 0.3 | Breast | CR 53:1990 |
| pter-22 | D1S16 | 11 | 0 | 0 | Cervix | CR 54:4188 |
| pter-22 | D1S16 | 6 | 2 | 0.33 | Endocrine | CR 52:770 |
| pter-22 | D1S16 | 24 | 4 | 0.17 | Melanoma | PNAS 86:4614 |
| pter-22 | D1S16 | 13 | 5 | 0.38 | Testis | CR 54:6266 |
| 31 | D1S225 | 36 | 7 | 0.19 | Breast | CR 55:1752 |
| Unknown | D1S167 | 9 | 1 | 0.11 | Liver | CR 54:4188 |
| Unknown | AF3 | 10 | 0 | 0 | Breast | AJHG 115:73 |
| Unknown | AF3 | 26 | 6 | 0.23 | Testis | CR 54:6265 |
| Unknown | D1S236 | 11 | 5 | 0.45 | Neuroblastom | GCC 10:275 a |
| 22-13 | D1S10 | 74 | 19 | 0.26 | Breast | CR 53:1990 |
| Unknown | AMY2A | 17 | 0 | 0 | Testis | CR 54:6265 |
| 21 | AMY2B | 16 | 5 | 0.31 | Liver | CR 54:4188 |
| 21 | AMY2B | 16 | 3 | 0.19 | Ovary | CR 54:4188 |
| 21 | AMY2B | 12 | 0 | 0 | Uterus | CR 54:4294 |
| 22-13 | D1S14 | 74 | 24 | 0.32 | Breast | CR 53:1990 |
| 22-13 | D1S14 | 18 | 3 | 0.17 | Endocrine | GCC 13:9 |
| 22-13 | D1S14 | 23 | 4 | 0.17 | Testis | CR 54:6265 |
| 21-13 | D1S73 | 13 | 6 | 0.46 | Brain | AJP 145:1175 |
| 21-13 | D1S73 | 74 | 23 | 0.31 | Breast | CR 53:1990 |
| 21-13 | D1S73 | 22 | 6 | 0.27 | Breast | GCC 12:16 |
| 21-13 | D1S73 | 23 | 6 | 0.26 | Testis | CR 54:6265 |
| 22-13 | D1S9 | 8 | 6 | 0.75 | Brain | AJP 145:1175 |
| 22-13 | D1S9 | 74 | 23 | 0.31 | Breast | CR 53:1990 |
| 22-13 | D1S9 | 25 | 0 | 0 | Testis | CR 54:6265 |
| 12 | RAP1A | 18 | 1 | 0.06 | Colon | CR 54:4188 |

Chromosome 1 - p Arm

| | | | | | | |
|---------|-----------------|----|----|------|--------------|--------------|
| 13 | DIS418 | 39 | 8 | 0.21 | Breast | CR 55:1752 |
| 13 | NRAS | 74 | 21 | 0.28 | Breast | CR 53:1990 |
| 13 | NRAS | 10 | 5 | 0.5 | Endocrine | CR 52:770 |
| 13 | NRAS | 6 | 1 | 0.17 | Endocrine | CR 52:770 |
| 13 | NGFB | 32 | 13 | 0.41 | Brain | AJP 145:1175 |
| 13 | NGFB | 6 | 0 | 0 | Breast | CCG 52:72 |
| 13 | NGFB | 13 | 2 | 0.15 | Breast | AJHG 45:73 |
| 13 | NGFB | 13 | 9 | 0.69 | Breast | CR 53:1990 |
| 13 | NGFB | 18 | 3 | 0.17 | Colon | IJC 53:382 |
| 13 | NGFB | 5 | 1 | 0.2 | Testis | CCG 52:72 |
| 13 | NGFB | 16 | 0 | 0 | Testis | CR 54:6266 |
| 13 | NGFB | 1 | 0 | 0 | Testis | CCG 52:72 |
| 13 | NGFB | 3 | 0 | 0 | Testis | CCG 52:72 |
| 13 | NGFB | 6 | 0 | 0 | Uterus | CR 53:1990 |
| 22-13 | DIS11 | 74 | 19 | 0.26 | Breast | CR 53:1990 |
| 21-Nov | DIS36 | 17 | 2 | 0.12 | Breast | CR 53:1990 |
| 22-13 | DIS13 | 74 | 16 | 0.22 | Breast | CR 53:1990 |
| 22-13 | DIS13 | 7 | 6 | 0.86 | Endocrine | CR 52:770 |
| 22-13 | DIS13 | 7 | 6 | 0.86 | Endocrine | CR 52:770 |
| 22-13 | DIS64 | 18 | 10 | 0.36 | Brain | JNCI 84:506 |
| 31-pter | Unknown | 36 | 1 | 0.03 | Breast | CR 53:1990 |
| 32 | DIS100-101 | 74 | 20 | 0.27 | Breast | CR 53:1990 |
| Unknown | DIS33 | 9 | 4 | 0.44 | Breast | CR 51:1020 |
| 3-35-5 | Unknown | 37 | 6 | 0.16 | Colon | CCG 48:167 |
| Unknown | Unknown | 14 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | DIS188 | 23 | 1 | 0.17 | Endocrine | CR 52:770 |
| Unknown | DIS19 | 4 | 2 | 0.5 | Endocrine | CR 52:770 |
| Unknown | PND | 3 | 2 | 0.67 | Endocrine | CR 52:770 |
| Unknown | DIS252 | 19 | 3 | 0.16 | Head&Neck | CR 54:1152 |
| Unknown | DIS57-NGFB | 21 | 4 | 0.19 | Head&Neck | CR 54:1152 |
| Unknown | DIS243-DIS228 | 22 | 1 | 0.05 | Kidney | PNAS 92:2854 |
| Unknown | DIS243-DIS228 | 6 | 0 | 0 | Kidney | CR 55:6189 |
| Unknown | DIS:243-228 | 33 | 3 | 0.09 | Kidney | CR 55:6189 |
| 33-35 | Unknown | 14 | 2 | 0.14 | Liver | CR 54:4188 |
| Unknown | DIS187 | 19 | 4 | 0.21 | Liver | CR 54:4188 |
| Unknown | ISO1 | 27 | 6 | 0.22 | Liver | CR 54:4188 |
| Unknown | ISO2 | 13 | 4 | 0.31 | Liver | CR 54:4188 |
| Unknown | DIS19 | 21 | 6 | 0.29 | Melanoma | CR 56:589 |
| Unknown | DIS:214-201-255 | 20 | 1 | 0.05 | Melanoma | CR 56:589 |
| Unknown | PND | 13 | 3 | 0.36 | Melanoma | CR 56:589 |
| Unknown | DIS220 | 20 | 10 | 0.5 | Neuroblastom | GCC 10:275 |
| Unknown | DIS232 | 11 | 1 | 0.61 | Neuroblastom | GCC 10:275 |
| Unknown | DIS252 | 8 | 2 | 0.25 | Neuroblastom | GCC 10:275 |

Chromosome 1 - p Arm

| | | | | | | |
|---------|---------------|------|------|------|--------------|-------------|
| Unknown | D1S97 | 18 | 0 | 0 | Neuroblastom | 0 7:1185 |
| Unknown | GGAT2A07 | 28 | 3 | 0.11 | Neuroblastom | CR 55:5681 |
| Unknown | D1S80 | 18 | 1 | 0.06 | Ovary | BJC 54:546 |
| Unknown | D1S:162-175 | 14 | 1 | 0.07 | Ovary | BJC 72:1330 |
| Unknown | F3-AMY | 25 | 6 | 0.24 | Ovary | BJC 53:2393 |
| Unknown | MTHFR | 28 | 16 | 0.57 | Ovary | BJC 75:1105 |
| 13-36 | PND-D1S2-NGEB | 11 | 0 | 0 | Prostate | GND:530 |
| 3.3-.5 | Unknown | 9 | 3 | 0.33 | Stomach | BJC 59:750 |
| SOM | | 7135 | 1886 | 0.26 | | |

Chromosome 1 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|------------|-------|-------------|-----------|---------------|--------------|
| Unknown | D1S305 | 30 | 7 | 0.23 | Cervix | CR 55:199 |
| CENTR | D1S305 | 14 | 1 | 0.07 | Neuroblastoma | CR 55:5366 |
| Unknown | D1S67 | 30 | 1 | 0.03 | Brain | AJP 145:1175 |
| 21 | D1S67 | 74 | 7 | 0.09 | Breast | CR 53:1990 |
| Unknown | D1S67 | 15 | 2 | 0.13 | Breast | CR 50:2184 |
| Unknown | D1S67 | 7 | 2 | 0.29 | Cervix | GCC 9:119 |
| Unknown | D1S67 | 26 | 3 | 0.12 | Esophageal | GCC 10:147 |
| Unknown | D1S67 | 14 | 1 | 0.07 | Kidney | CR 51:820 |
| Unknown | D1S67 | 6 | 1 | 0.17 | Lung | CR 52:2478 |
| Unknown | D1S67 | 3 | 3 | 1 | Lung | CR 52:2478 |
| Unknown | D1S67 | 1 | 1 | 1 | Lung | CR 52:2478 |
| Unknown | D1S67 | 17 | 5 | 0.29 | Lung | CR 52:2478 |
| Unknown | D1S67 | 14 | 4 | 0.29 | Ovary | CR 51:4118 |
| 21 | D1S67 | 23 | 2 | 0.09 | Ovary | IJC 54:546 |
| Unknown | D1S67 | 26 | 3 | 0.12 | Testis | CR 51:5265 |
| Unknown | D1S67 | 22 | 4 | 0.18 | Uterus | GCC 9:119 |
| 21-23 | MUC1 | 74 | 9 | 0.12 | Breast | CR 53:1990 |
| 21-23 | MUC1 | 7 | 0 | 0 | Breast | CR 53:3804 |
| 21-23 | MUC1 | 44 | 13 | 0.3 | Breast | GCC 12:16 |
| 21-23 | MUC1 | 43 | 7 | 0.16 | Breast | CR 51:1020 |
| 21-23 | MUC1 | 21 | 7 | 0.33 | Head&Neck | CR 52:1494 |
| 21-23 | MUC1 | 16 | 4 | 0.25 | Stomach | CR 51:2926 |
| 21-23 | MUC1 | 25 | 2 | 0.08 | Testis | GCC 13:249 |
| 21 | PEM-pMUC10 | 89 | 14 | 0.16 | Breast | GCC 5:311 |
| 21 | SPTA1 | 74 | 9 | 0.12 | Breast | CR 53:1990 |
| 21 | SPTA1 | 6 | 2 | 0.33 | Breast | GCC 12:16 |
| 21 | SPTA1 | 6 | 2 | 0.33 | Breast | PN 86:7204 |
| 21 | SPTA1 | 22 | 2 | 0.09 | Colon | CR 52:285 |
| 21 | SPTA1 | 29 | 3 | 0.1 | Colon | CR 52:285 |
| Unknown | D1S176 | 17 | 1 | 0.06 | Liver | CR 54:4188 |
| 22-25 | ATP1B1 | 74 | 9 | 0.12 | Breast | CR 53:1990 |
| 21-23 | APOA2 | 6 | 0 | 0 | Breast | GCC 2:191 |
| 21-23 | APOA2 | 18 | 4 | 0.22 | Ovary | HT 65:229 |
| 21-23 | APOA2 | 5 | 0 | 0 | Testis | GCC 13:249 |
| 21-23 | APOA2 | 26 | 2 | 0.08 | Uterus | CR 51:4294 |
| 21-31 | D1S61 | 74 | 10 | 0.14 | Breast | CR 53:1990 |
| 21-31 | D1S61 | 52 | 12 | 0.23 | Breast | CR 51:1020 |
| 21-31 | D1S61 | 39 | 8 | 0.21 | Breast | GCC 12:16 |
| 21-31 | D1S61 | 21 | 2 | 0.1 | Endocrine | GCC 13:249 |
| Unknown | D1S75 | 14 | 0 | 0 | Brain | AJP 145:1175 |
| Unknown | D1S75 | 18 | 1 | 0.06 | Testis | CR 51:2265 |
| Unknown | D1S66 | 14 | 4 | 0.29 | Esophageal | CR 54:2996 |
| Unknown | D1S66 | 11 | 0 | 0 | Sarcoma | CR 52:2419 |
| 23-25 | AT3 | 19 | 0 | 0 | Brain | CR 54:1397 |
| 23-25 | AT3 | 14 | 0 | 0 | Brain | CR 54:1397 |

Chromosome 1 - q Arm

| | | | | | | |
|----------|--------|----|----|------|--------------|--------------|
| 23-25 | AT3 | 14 | 1 | 0.07 | Breast | AJHG 45:73 |
| 23-25 | AT3 | 2 | 0 | 0 | Breast | GCC 24:101 |
| 23-25 | AT3 | 14 | 0 | 0 | Colon | CR 52:285 |
| 23-25 | AT3 | 4 | 0 | 0 | Liver | GCC 46:72 |
| 23-25 | AT3 | 22 | 1 | 0.05 | Ovary | IJC 54:546 |
| 23-25.1 | AT3 | 5 | 0 | 0 | Ovary | CR 54:6265 |
| 23-25 | AT3 | 27 | 0 | 0 | Testis | CR 54:6265 |
| 23-25 | AT3 | 8 | 2 | 0.25 | Testis | GCC 43:249 |
| Unknown | D1S238 | 22 | 4 | 0.18 | Cervix | CR 56:197 |
| 31-32.1 | F13B | 9 | 0 | 0 | Brain | CR 54:1397 |
| 31-32.1 | F13B | 15 | 0 | 0 | Brain | CR 54:1397 |
| 31-32.1 | F13B | 12 | 1 | 0.08 | Endocrine | GCC 43:249 |
| 31-32.1 | F13B | 13 | 0 | 0 | Uterus | CR 54:4294 |
| Unknown | D1S65 | 18 | 0 | 0 | Brain | AJP 145:1175 |
| Unknown | D1S65 | 18 | 5 | 0.28 | Breast | GCC 12:16 |
| Unknown | D1S65 | 6 | 0 | 0 | Esophagus | CR 54:2113 |
| Unknown | D1S65 | 16 | 2 | 0.12 | Head&Neck | CR 52:1494 |
| Unknown | D1S65 | 15 | 3 | 0.2 | Testis | CR 54:6265 |
| 32 or 42 | REN | 11 | 0 | 0 | Brain | AJP 145:1175 |
| 32 or 42 | REN | 12 | 3 | 0.25 | Breast | CR 54:1020 |
| 32 | REN | 21 | 7 | 0.33 | Breast | GCC 12:16 |
| 32 or 42 | REN | 6 | 1 | 0.17 | Breast | CR 54:990 |
| 32 or 42 | REN | 12 | 2 | 0.17 | Cervix | CR 49:3598 |
| 32 | REN | 16 | 1 | 0.06 | Colon | CR 52:285 |
| 32 or 42 | REN | 19 | 7 | 0.37 | Colon | IJC 53:382 |
| 32 or 42 | REN | 8 | 0 | 0 | Liver | PNAS 86:8852 |
| 32 or 42 | REN | 14 | 0 | 0 | Liver | JJCR 81:108 |
| 32 or 42 | REN | 4 | 0 | 0 | Neuroblastom | CR 49:1095 |
| 32 or 42 | REN | 21 | 1 | 0.05 | Ovary | IJC 54:546 |
| 32 or 42 | REN | 8 | 0 | 0 | Prostate | GCC 43:249 |
| 32 or 42 | REN | 15 | 4 | 0.27 | Stomach | CR 52:3099 |
| 32 or 42 | REN | 11 | 3 | 0.27 | Testis | CR 54:6265 |
| 32 or 42 | REN | 6 | 0 | 0 | Uterus | CR 51:5632 |
| 32 | D1S249 | 12 | 0 | 0 | Neuroblastom | CR 54:5366 |
| Unknown | LAMB2 | 13 | 1 | 0.08 | Testis | CR 54:6265 |
| Unknown | D1S58 | 24 | 1 | 0.46 | Breast | GCC 12:16 |
| Unknown | D1S58 | 27 | 7 | 0.26 | Cervix | CR 54:4481 |
| Unknown | D1S58 | 15 | 0 | 0 | Colon | GCC 46:72 |
| Unknown | D1S58 | 21 | 4 | 0.19 | Testis | CR 54:6265 |
| Unknown | D1S58 | 23 | 5 | 0.22 | Testis | CR 54:6265 |
| Unknown | D1S81 | 32 | 0 | 0 | Brain | AJP 145:1175 |
| Unknown | D1S81 | 39 | 12 | 0.31 | Breast | GCC 12:16 |
| Unknown | D1S81 | 41 | 5 | 0.12 | Breast | CR 53:4356 |
| Unknown | D1S81 | 20 | 1 | 0.05 | Liver | CR 54:89 |
| Unknown | D1S213 | 30 | 6 | 0.2 | Cervix | CR 56:197 |

Chromosome 1 - q Arm

| | | | | | | |
|---------|-------------------|------|----|------|-----------|-------------|
| Unknown | D1S251 | 51 | 4 | 0.04 | Kidney | CR 54:4481 |
| Unknown | D1S74 | 11 | 4 | 0.36 | Breast | GCC 12:16 |
| Unknown | D1S8 | 51 | 15 | 0.29 | Breast | GCC 12:16 |
| Unknown | D1S74 | 39 | 7 | 0.18 | Cervix | CR 54:4481 |
| Unknown | D1S8 | 9 | 0 | 0 | Endocrine | CR 54:4481 |
| 32-44 | D1S103 | 18 | 2 | 0.11 | Ovary | BJC 69:429 |
| Unknown | D1S74 | 4 | 0 | 0 | Testis | CR 54:4481 |
| Unknown | D1S74 | 50 | 3 | 0.06 | Testis | CR 54:3983 |
| Unknown | D1S74 | 54 | 3 | 0.06 | Testis | CR 54:3983 |
| Unknown | D1S8 | 31 | 2 | 0.06 | Testis | GCC 13:249 |
| Unknown | D1S8 | 31 | 2 | 0.06 | Testis | GCC 13:249 |
| 21-23 | Unknown | 70 | 18 | 0.26 | Breast | JNCI 84:506 |
| 21-24 | Unknown | 75 | 16 | 0.21 | Breast | JNCI 84:506 |
| Unknown | DF3 | 43 | 6 | 0.14 | Breast | IJC 61:1 |
| 4.2-.3 | Unknown | 34 | 4 | 0.12 | Colon | BJC 59:750 |
| 2.1-.4 | Unknown | 27 | 3 | 0.11 | Colon | BJC 59:750 |
| Unknown | D1S102 | 12 | 1 | 0.08 | Endocrine | GCC 12:16 |
| Unknown | D1S215 | 11 | 2 | 0.18 | Endocrine | CR 56:599 |
| Unknown | D1S259 | 27 | 5 | 0.21 | Head&Neck | CR 54:4756 |
| Unknown | D1S304-212 | 43 | 6 | 0.14 | Head&Neck | CR 54:4756 |
| Unknown | D1S304-212 | 17 | 2 | 0.12 | Head&Neck | CR 54:4756 |
| Unknown | Unknown | 8 | 3 | 0.38 | Liver | BJC 64:1083 |
| 42-43 | Unknown | 13 | 3 | 0.23 | Liver | BJC 64:1083 |
| Unknown | Unknown | 4 | 1 | 0.25 | Liver | BJC 64:1083 |
| Unknown | D1S:237-212 | 27 | 2 | 0.07 | Melanoma | CR 56:589 |
| Unknown | APOA2-D1S:158-103 | 14 | 0 | 0 | Ovary | BJC 72:1330 |
| Unknown | REN-D1981 | 23 | 9 | 0.39 | Ovary | CR 54:2393 |
| Unknown | Unknown | 13 | 2 | 0.15 | Pancreas | BJC 65:809 |
| 32-44 | Unknown | 7 | 0 | 0 | Pancreas | CR 54:2761 |
| 4.2-.3 | Unknown | 6 | 1 | 0.17 | Stomach | BJC 59:750 |
| 2.1-.4 | Unknown | 10 | 5 | 0.5 | Stomach | BJC 59:750 |
| Unknown | AGT | 52 | 3 | 0.06 | Testis | CR 54:3983 |
| Unknown | AGT | 7 | 0 | 0 | Testis | CR 54:3983 |
| Unknown | CR2 | 21 | 3 | 0.14 | Testis | CR 54:6265 |
| Unknown | D1S180 | 3 | 0 | 0 | Testis | CR 54:3983 |
| Unknown | D1S180 | 50 | 7 | 0.14 | Testis | CR 54:3983 |
| Unknown | D1S235 | 2 | 0 | 0 | Testis | CR 54:3983 |
| Unknown | D1S235 | 39 | 4 | 0.1 | Testis | CR 54:3983 |
| STUD | | 2869 | 41 | 0.15 | | |

Chromosome 2 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------------|-------|-------------|-----------|------------|--------------|
| Unknown | D2S44 | 7 | 1 | 0.14 | Uterus | GCC 9:119 |
| Unknown | Unknown | 11 | 1 | 0.09 | Brain | CR 50:5784 |
| Unknown | D2S44 | 7 | 1 | 0.14 | Breast | CR 53:3804 |
| Unknown | D2S44 | 74 | 6 | 0.08 | Breast | CR 53:4356 |
| Unknown | D2S47 | 23 | 0 | 0 | Breast | CR 50:7184 |
| 23-15 | D2S6 | 27 | 3 | 0.11 | Breast | GCC 2:191 |
| 23-15 | D2S6 | 22 | 2 | 0.09 | Breast | JNCI 84:506 |
| 23-15 | D2S6 | 42 | 5 | 0.12 | Breast | CR 53:4356 |
| 23-PTER | TPO | 50 | 21 | 0.42 | Breast | BCRT 32:5 |
| Unknown | D2S139 | 27 | 4 | 0.15 | Cervix | CR 56:197 |
| Unknown | D2S177 | 18 | 2 | 0.11 | Cervix | CR 56:197 |
| Unknown | D2S44 | 7 | 0 | 0 | Cervix | GCC 9:119 |
| Unknown | D2S44 | 48 | 6 | 0.12 | Cervix | CR 54:4481 |
| Unknown | D2S48 | 26 | 3 | 0.12 | Cervix | CR 54:4481 |
| Unknown | APOB | 7 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D2S44 | 236 | 37 | 0.16 | Colon | BJC 64:475 |
| Unknown | D2S45 | 14 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D2S155 | 11 | 2 | 0.18 | Endocrine | CR 56:599 |
| Unknown | D2S44 | 60 | 10 | 0.17 | Esophageal | GCC 10:177 |
| Unknown | D2S44 | 20 | 4 | 0.2 | Esophageal | CR 54:2996 |
| Unknown | D2S47 | 41 | 10 | 0.24 | Esophageal | GCC 10:177 |
| Unknown | D2S47 | 30 | 2 | 0.07 | Esophageal | CR 54:2996 |
| Unknown | D2S162 | 21 | 4 | 0.19 | Head&Neck | CR 54:1152 |
| Unknown | D2S166-149 | 15 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D2S166-149 | 20 | 1 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D2S207-D2S131 | 21 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D2S207-D2S131 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D2S47 | 11 | 2 | 0.18 | Kidney | CR 51:820 |
| Unknown | D2S207-131 | 32 | 0 | 0 | Kidney | CR 55:6189 |
| Unknown | D2S48 | 9 | 0 | 0 | Liver | CR 51:89 |
| 13 | TGFA | 5 | 0 | 0 | Liver | PNAS 86:8852 |
| Unknown | Unknown | 27 | 6 | 0.22 | Lung | CR 54:2322 |
| Unknown | D2S44 | 7 | 2 | 0.29 | Lung | CR 54:5643 |
| Unknown | D2S44 | 4 | 2 | 0.5 | Lung | CR 54:5643 |
| Unknown | D2S44 | 22 | 11 | 0.5 | Lung | CR 54:5643 |
| Unknown | D2S47 | 19 | 1 | 0.05 | Lung | CR 522478 |
| 12 | CD8A | 20 | 3 | 0.15 | Ovary | BJC 69:429 |
| Unknown | D2S44 | 23 | 9 | 0.39 | Ovary | CR 53:2393 |
| Unknown | D2S47 | 11 | 0 | 0 | Ovary | CR 51:5118 |
| 23-15 | D2S6 | 31 | 7 | 0.23 | Ovary | IJC 54:546 |
| 23-PTER | TPO | 14 | 2 | 0.14 | Ovary | BJC 69:429 |
| Unknown | D2S1 | 14 | 1 | 0.07 | Prostate | G 11:530 |
| Unknown | D2S3-D2S6 | 6 | 0 | 0 | Prostate | G 11:530 |
| Unknown | D2S47 | 10 | 2 | 0.2 | Sarcoma | CR 52:2419 |
| Unknown | D2S123 | 13 | 1 | 0.08 | Stomach | CR 55:1933 |
| Unknown | D2S44 | 45 | 12 | 0.27 | Testis | O 9:2245 |

Chromosome 2 - p Arm

| | | | | | | |
|---------|--------|------|-----|------|--------|------------|
| Unknown | D2S48 | 31 | 5 | 0.16 | Testis | O 9:2245 |
| 24 | MYCN | 2 | 0 | 0 | Testis | CCG 52:72 |
| 24 | MYCN | 2 | 0 | 0 | Testis | CCG 52:72 |
| 24 | MYCN | 2 | 0 | 0 | Testis | CCG 52:72 |
| 13 | D2S101 | 21 | 0 | 0 | Uterus | CR 54:4294 |
| Unknown | D2S44 | 7 | 1 | 0.14 | Uterus | GCC 9:119 |
| SUM | | 1272 | 191 | 0.15 | | |

Chromosome 2 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|--------|-------|-------------|-----------|---------------|--------------|
| 13 | TL1A | 20 | 0 | 0 | Uterus | CR 54:4294 |
| Unknown | D2S44 | 17 | 0 | 0 | Brain | CR 49:6572 |
| Unknown | D2S44 | 17 | 0 | 0 | Brain | CR 50:5784 |
| Unknown | CRYG | 8 | 1 | 0.12 | Breast | GCC 2:191 |
| Unknown | D2S44 | 51 | 7 | 0.14 | Breast | GCC 4:113 |
| Unknown | D2S44 | 31 | 3 | 0.1 | Breast | GCC 2:191 |
| Unknown | D2S44 | 49 | 5 | 0.1 | Breast | CR 50:7184 |
| Unknown | CRYG | 9 | 1 | 0.11 | Cervix | CR 49:3598 |
| Unknown | D2S122 | 28 | 4 | 0.14 | Cervix | CR 56:197 |
| Unknown | D2S172 | 29 | 7 | 0.24 | Cervix | CR 56:197 |
| Unknown | CRYG | 21 | 0 | 0 | Colon | N 331:273 |
| 35-37 | D2S3 | 16 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D2S44 | 32 | 1 | 0.03 | Colon | CCG 48:167 |
| Unknown | D2S54 | 8 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D2S125 | 20 | 2 | 0.1 | Endocrine | CR 56:599 |
| Unknown | D2S44 | 14 | 1 | 0.07 | Esophageal | CR 51:2113 |
| Unknown | D2S55 | 13 | 0 | 0 | Esophageal | CR 54:3996 |
| Unknown | D2S111 | 20 | 3 | 0.15 | Head&Neck | CR 54:1152 |
| Unknown | D2S163 | 10 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D2S163 | 20 | 4 | 0.2 | Head&Neck | CR 54:4756 |
| Unknown | D2S125 | 28 | 1 | 0.04 | Kidney | PNAS 92:2854 |
| Unknown | D2S44 | 38 | 5 | 0.13 | Kidney | CR 51:820 |
| 33-35 | CRYP1 | 1 | 0 | 0 | Liver | CR 51:89 |
| Unknown | D2S44 | 18 | 0 | 0 | Liver | CR 51:89 |
| Unknown | D2S44 | 4 | 0 | 0 | Liver | PNAS 86:8852 |
| p16-15 | D2S5 | 4 | 0 | 0 | Liver | CCG 48:72 |
| Unknown | D2S44 | 40 | 11 | 0.28 | Lung | CR 52:478 |
| p16-15 | D2S5 | 1 | 0 | 0 | Neuroblastoma | CR 49:1095 |
| Unknown | D2S3 | 23 | 9 | 0.39 | Ovary | CR 53:2393 |
| Unknown | D2S44 | 29 | 4 | 0.14 | Ovary | CR 51:5118 |
| p16-15 | D2S5 | 5 | 1 | 0.2 | Ovary | CR 50:2724 |
| Unknown | D2S50 | 10 | 0 | 0 | Ovary | CR 50:2724 |
| Unknown | D2S55 | 19 | 2 | 0.11 | Ovary | IJC 54:546 |
| Unknown | D2S72 | 16 | 6 | 0.38 | Ovary | BJC 69:429 |
| Unknown | D2S44 | 4 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | D2S44 | 26 | 7 | 0.27 | Sarcoma | CR 52:2419 |
| Unknown | D2S44 | 18 | 1 | 0.06 | Stomach | HG 92:244 |
| Unknown | D2S44 | 27 | 0 | 0 | Testis | LI 73:606 |
| 13 | TL1A | 20 | 0 | 0 | Uterus | CR 54:4294 |
| SUM | | 744 | 86 | 0.12 | | |

Chromosome 3 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------|-------|-------------|-----------|------------|-------------|
| 26 | D3S17 | 12 | 10 | 0.83 | Kidney | CR 51:1071 |
| 26 | D3S17 | 7 | 7 | 1 | Lung | GCC 1:240 |
| Unknown | D3S1307 | 36 | 2 | 0.06 | Esophageal | BJC 73:366 |
| Unknown | D3S1317 | 31 | 10 | 0.32 | Kidney | BJC 69:230 |
| Unknown | D3S1317 | 12 | 3 | 0.25 | Stomach | CR 55:1933 |
| 25 | D3S18 | 19 | 9 | 0.47 | Kidney | CR 51:1071 |
| 25 | D3S18 | 1 | 1 | 1 | Lung | GCC 1:240 |
| 14 | D3S1038 | 21 | 6 | 0.29 | Esophageal | CR 54:6484 |
| 14 | D3S1038 | 37 | 5 | 0.14 | Esophageal | BJC 73:366 |
| 14 | D3S1038 | 5 | 0 | 0 | Kidney | GCC 12:76 |
| 14 | D3S1038 | 40 | 19 | 0.47 | Kidney | BJC 69:230 |
| 14 | D3S1038 | 6 | 5 | 0.83 | Lung | JAMA 273:55 |
| 14 | D3S1038 | 1 | 1 | 1 | Lung | JAMA 273:55 |
| 14 | D3S1038 | 25 | 3 | 0.12 | Uterus | CR 54:4294 |
| Unknown | D3S1263 | 22 | 7 | 0.32 | Cervix | CR 56:197 |
| Unknown | D3S651 | 6 | 4 | 0.67 | Kidney | CR 51:4707 |
| Unknown | D3S651 | 18 | 3 | 0.17 | Lung | CR 52:873 |
| Unknown | D3S651 | 8 | 8 | 1 | Lung | CR 52:873 |
| 24-25 | RAF1 | 4 | 1 | 0.25 | Breast | CR 53:3804 |
| 24-25 | RAF1 | 3 | 1 | 0.33 | Cervix | CR 49:3598 |
| 25 | RAF1 | 10 | 10 | 1 | Head&Neck | CGC 54:91 |
| 25 | RAF1 | 1 | 0 | 0 | Kidney | CR 51:4707 |
| 25 | RAF1 | 22 | 20 | 0.91 | Kidney | CR 51:1071 |
| 25 | RAF1 | 12 | 9 | 0.75 | Kidney | CR 51:1544 |
| 25 | RAF1 | 2 | 2 | 1 | Kidney | CR 51:1071 |
| 25 | RAF1 | 22 | 10 | 0.45 | Kidney | G 11:537 |
| 24-25 | RAF1 | 17 | 9 | 0.53 | Kidney | CR 49:1390 |
| 24-25 | RAF1 | 4 | 2 | 0.5 | Lung | GCC 1:95 |
| 24-25 | RAF1 | 15 | 14 | 0.93 | Lung | GCC 1:95 |
| 25 | RAF1 | 1 | 1 | 1 | Lung | CR 49:5130 |
| 24-25 | RAF1 | 1 | 0 | 0 | Lung | GCC 1:95 |
| 25 | RAF1 | 5 | 5 | 1 | Lung | O 4:451 |
| 25 | RAF1 | 12 | 2 | 0.17 | Prostate | G 11:530 |
| 25 | RAF1 | 1 | 1 | 1 | Uterus | CR 51:5632 |
| 24-25 | D3S1286 | 37 | 12 | 0.32 | Esophageal | BJC 69:1 |
| Unknown | D3S1293 | 33 | 5 | 0.15 | Esophageal | BJC 73:366 |
| Unknown | D3S1293 | 40 | 2 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D3S1293 | 39 | 10 | 0.26 | Head&Neck | CR 54:4756 |
| Unknown | D3S1020 | 5 | 5 | 1 | Lung | CR 52:873 |
| Unknown | D3S1020 | 7 | 3 | 0.43 | Lung | CR 52:873 |
| Unknown | D3S1002 | 5 | 5 | 1 | Lung | CR 52:873 |
| Unknown | D3S1002 | 12 | 3 | 0.25 | Lung | CR 52:873 |
| 25.1 | D3S669 | 22 | 3 | 0.14 | Breast | CR 51:5794 |
| 25.1 | D3S669 | 10 | 7 | 0.7 | Kidney | CR 51:4707 |
| Unknown | D3S669 | 5 | 5 | 1 | Lung | CR 52:873 |
| Unknown | D3S669 | 12 | 2 | 0.17 | Lung | CR 52:873 |

Chromosome 3 - p Arm

| | | | | | | |
|---------|---------|----|----|------|------------|-------------|
| Unknown | THRB | 54 | 15 | 0.28 | Breast | GCC 12:128 |
| 21-PTER | THRB | 30 | 4 | 0.13 | Breast | AJP 140:215 |
| 22-24.1 | THRB | 71 | 32 | 0.45 | Breast | CR 54:3021 |
| Unknown | THRB | 24 | 9 | 0.38 | Cervix | IJC 58:787 |
| 22-24.1 | THRB | 7 | 3 | 0.43 | Cervix | CR 49:3598 |
| 24 | THRB | 9 | 1 | 0.11 | Colon | IJC 53:382 |
| 24 | THRB | 44 | 10 | 0.23 | Esophageal | BJC 73:366 |
| 24 | THRB | 9 | 3 | 0.33 | Head&Neck | C 72:881 |
| 22-24.1 | THRB | 23 | 6 | 0.26 | Head&Neck | CR 54:1152 |
| 22-24.1 | THRB | 3 | 0 | 0 | Head&Neck | CGC 54:91 |
| 22-24.1 | THRB | 5 | 5 | 1 | Kidney | CR 51:949 |
| 24 | THRB | 34 | 18 | 0.53 | Kidney | G 11:537 |
| 22-24.1 | THRB | 11 | 11 | 1 | Lung | CR 49:5130 |
| 21-PTER | THRB | 1 | 0 | 0 | Lung | GCC 1:95 |
| 24 | THRB | 7 | 3 | 0.43 | Lung | GCC 3:358 |
| 22-24.1 | THRB | 2 | 2 | 1 | Lung | GCC 1:95 |
| 22-24.1 | THRB | 3 | 1 | 0.33 | Lung | GCC 1:95 |
| 22-24.1 | THRB | 5 | 3 | 0.6 | Lung | GCC 1:95 |
| 24 | THRB | 6 | 5 | 0.83 | Lung | O 4:451 |
| 22-24.1 | THRB | 10 | 2 | 0.2 | Lung | GCC 11:15 |
| 22-24.1 | THRB | 22 | 17 | 0.77 | Lung | GCC 1:95 |
| Unknown | THRB | 38 | 22 | 0.58 | Melanoma | GCC 15:102 |
| 24 | THRB | 22 | 5 | 0.23 | Ovary | IJC 52:575 |
| 22-24.1 | THRB | 7 | 4 | 0.57 | Ovary | O 5:219 |
| Unknown | THRB | 22 | 6 | 0.27 | Ovary | IJC 54:546 |
| 22-24.1 | THRB | 17 | 5 | 0.29 | Ovary | BJC 69:429 |
| Unknown | THRB | 16 | 0 | 0 | Pediatric | CR 50:3279 |
| 24 | THRB | 11 | 0 | 0 | Prostate | GCC 11:119 |
| Unknown | THRB | 2 | 0 | 0 | Uterus | CR 51:5632 |
| 24 | THRB | 4 | 1 | 0.25 | Uterus | CR 51:5632 |
| 24 | THRB | 5 | 3 | 0.6 | Kidney | G 11:537 |
| 24.2-25 | D3S1266 | 52 | 15 | 0.29 | Esophageal | IJC 69:1 |
| 23 | D3S647 | 24 | 2 | 0.08 | Breast | CR 51:5794 |
| 23 | D3S647 | 21 | 8 | 0.38 | Esophageal | CR 54:6484 |
| 23 | D3S647 | 30 | 4 | 0.13 | Esophageal | BJC 73:366 |
| 23 | D3S647 | 22 | 8 | 0.36 | Kidney | BJC 69:230 |
| 23 | D3S647 | 11 | 5 | 0.45 | Kidney | CR 51:4707 |
| pter-21 | D3S12 | 5 | 0 | 0 | Stomach | HG 89:445 |
| 22-24.2 | D3S1211 | 17 | 4 | 0.24 | Esophageal | IJC 69:1 |
| 21.3 | D3S1029 | 23 | 4 | 0.17 | Esophageal | CR 54:6484 |
| 21.3 | D3S1029 | 1 | 1 | 1 | Lung | JAMA 273:55 |
| 21.3 | D3S1029 | 6 | 5 | 0.83 | Lung | JAMA 273:55 |
| Unknown | D3S867 | 18 | 5 | 0.28 | Lung | CR 52:873 |
| Unknown | D3S867 | 7 | 7 | 1 | Lung | CR 52:873 |
| Unknown | D3S1298 | 24 | 8 | 0.33 | Cervix | CR 56:197 |
| 13 | D3S685 | 54 | 6 | 0.11 | Breast | CR 51:5794 |

Chromosome 3 - p Arm

| | | | | | | |
|---------|---------|----|----|------|------------|-------------|
| Unknown | D3S685 | 6 | 3 | 0.5 | Cervix | GCC 9:119 |
| 21.3-22 | D3S1007 | 17 | 9 | 0.53 | Esophageal | CR 54:6484 |
| 21.3-22 | D3S1007 | 33 | 6 | 0.18 | Esophageal | BJC 73:366 |
| Unknown | D3S685 | 47 | 15 | 0.32 | Esophageal | GCC 10:177 |
| 21.3-22 | D3S1007 | 3 | 0 | 0 | Kidney | GCC 12:76 |
| Unknown | D3S685 | 27 | 18 | 0.67 | Kidney | CR 51:4707 |
| 21.3-22 | D3S1007 | 50 | 37 | 0.74 | Lung | IJC 64:373 |
| Unknown | D3S685 | 31 | 14 | 0.45 | Lung | CR 52:873 |
| Unknown | D3S685 | 10 | 10 | 1 | Lung | CR 52:873 |
| 13 | D3S685 | 1 | 1 | 1 | Lung | CR 52:2478 |
| 13 | D3S685 | 7 | 7 | 1 | Lung | CR 52:2478 |
| 13 | D3S685 | 3 | 3 | 1 | Lung | CR 52:2478 |
| 13 | D3S685 | 26 | 9 | 0.35 | Lung | CR 52:2478 |
| 13 | D3S685 | 18 | 3 | 0.17 | Ovary | CR 51:5118 |
| Unknown | D3S685 | 18 | 3 | 0.17 | Ovary | CR 51:5118 |
| Unknown | D3S685 | 11 | 2 | 0.18 | Uterus | GCC 9:119 |
| 22-24.2 | D3S1260 | 63 | 25 | 0.4 | Esophageal | IJC 69:1 |
| 22-24.2 | D3S1260 | 3 | 0 | 0 | Melanoma | GCC 15:102 |
| 21 | D3S11 | 16 | 0 | 0 | Endocrine | CR 56:599 |
| 21 | D3S11 | 7 | 4 | 0.57 | Kidney | CR 49:1390 |
| 21 | D3S2-S3 | 1 | 1 | 1 | Breast | GCC 2:191 |
| 21 | D3S2-S3 | 20 | 1 | 0.05 | Breast | GCC 2:191 |
| 21 | D3S2-S3 | 1 | 0 | 0 | Breast | PN 84:2372 |
| 21 | D3S2-S3 | 2 | 0 | 0 | Breast | PN 84:2372 |
| 21 | D3S2-S3 | 3 | 0 | 0 | Breast | PN 84:2372 |
| 21.3 | D3S686 | 34 | 2 | 0.06 | Breast | CR 51:5794 |
| 21 | D3S2 | 22 | 4 | 0.18 | Cervix | CR 54:4481 |
| Unknown | D3S2 | 16 | 6 | 0.38 | Cervix | IJC 58:787 |
| 21 | D3S2 | 9 | 9 | 1 | Cervix | CR 49:3598 |
| 21 | D3S2 | 16 | 3 | 0.19 | Colon | IJC 53:382 |
| 21 | D3S2 | 9 | 0 | 0 | Colon | N 331:273 |
| Unknown | D3S2 | 12 | 0 | 0 | Endocrine | GCC 13:9 |
| 21 | D3S2 | 22 | 8 | 0.36 | Esophageal | CR 54:2996 |
| Unknown | D3S2 | 10 | 1 | 0.1 | Esophageal | CR 51:2113 |
| 21.3 | D3S686 | 38 | 11 | 0.29 | Esophageal | BJC 73:366 |
| 21 | D3S2 | 4 | 3 | 0.75 | Head&Neck | CGC 54:91 |
| 21 | D3S2 | 14 | 6 | 0.43 | Kidney | CR 51:949 |
| Unknown | D3S2 | 2 | 0 | 0 | Kidney | CR 51:1544 |
| Unknown | D3S2 | 23 | 18 | 0.78 | Kidney | CR 51:1071 |
| Unknown | D3S2 | 2 | 1 | 0.5 | Kidney | CGC 32:281 |
| Unknown | D3S2 | 11 | 2 | 0.18 | Kidney | PNAS 85:157 |
| 21 | D3S2 | 14 | 8 | 0.57 | Kidney | G 11:537 |
| Unknown | D3S2 | 20 | 9 | 0.45 | Kidney | CR 51:1544 |
| 14-21 | D3S2 | 8 | 7 | 0.88 | Kidney | CR 49:1390 |
| 21 | D3S2 | 8 | 7 | 0.88 | Kidney | N 327:721 |
| 21.3 | D3S686 | 10 | 6 | 0.6 | Kidney | CR 51:4707 |

Chromosome 3 - p Arm

| | | | | | | |
|---------|--------|----|----|------|-------------------|-------------|
| Unknown | D3S2 | 4 | 1 | 0.25 | Leukemia | CGC 61:42 |
| 21 | D3S2 | 15 | 12 | 0.8 | Lung | PNAS 84:925 |
| 21 | D3S2 | 1 | 0 | 0 | Lung | PNAS 84:925 |
| 21 | D3S2 | 5 | 1 | 0.2 | Lung | GCC 11:15 |
| 21 | D3S2 | 5 | 2 | 0.4 | Lung | GCC 1:95 |
| Unknown | D3S2 | 1 | 0 | 0 | Lung | N 329:451 |
| 21 | D3S2 | 1 | 0 | 0 | Lung | PNAS 84:925 |
| 21 | D3S2 | 7 | 7 | 1 | Lung | PNAS 84:925 |
| 21 | D3S2 | 8 | 6 | 0.75 | Lung | PNAS 86:509 |
| Unknown | D3S2 | 9 | 8 | 0.89 | Lung | N 329:451 |
| Unknown | D3S2 | 1 | 0 | 0 | Lung | N 329:451 |
| 21 | D3S2 | 6 | 6 | 1 | Lung | GCC 1:240 |
| 21 | D3S2 | 6 | 5 | 0.83 | Lung | PNAS 84:925 |
| Unknown | D3S2 | 20 | 8 | 0.4 | Lung | JJCR 80:924 |
| Unknown | D3S2 | 6 | 5 | 0.83 | Lung | NEJ 317:110 |
| Unknown | D3S2 | 4 | 3 | 0.75 | Lung | NEJ 317:110 |
| Unknown | D3S2 | 2 | 1 | 0.5 | Lung | NEJ 317:110 |
| Unknown | D3S2 | 12 | 0 | 0 | Lung | PNAS 84:925 |
| 21 | D3S2 | 9 | 4 | 0.44 | Lung | PNAS 86:509 |
| 21 | D3S2 | 12 | 8 | 0.67 | Lung | JJCR 80:924 |
| 21 | D3S2 | 3 | 1 | 0.33 | Lung | GCC 1:95 |
| 21 | D3S2 | 11 | 8 | 0.73 | Lung | GCC 1:95 |
| 21 | D3S2 | 8 | 8 | 1 | Lung | CR 49:5130 |
| 14-21 | D3S2 | 5 | 5 | 1 | Lung | GCC 5:119 |
| 21.3 | D3S686 | 6 | 6 | 1 | Lung | CR 52:873 |
| 21.3 | D3S686 | 11 | 7 | 0.64 | Lung | CR 52:873 |
| Unknown | D3S2 | 11 | 6 | 0.55 | Melanoma | GCC 15:102 |
| Unknown | D3S2 | 6 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| 21 | D3S2 | 16 | 1 | 0.06 | Ovary | IJC 54:546 |
| 21 | D3S2 | 6 | 4 | 0.67 | Sarcoma | CGC 53:45 |
| 21 | D3S2 | 12 | 4 | 0.33 | Sarcoma | CR 52:2419 |
| Unknown | D3S2 | 10 | 0 | 0 | Stomach | CR 48:2988 |
| Unknown | D3S2 | 19 | 1 | 0.05 | Testis | O 9:2245 |
| 21 | D3S2 | 12 | 4 | 0.33 | Testis | G 5:134 |
| Unknown | D3S2 | 5 | 0 | 0 | Uterus | CR 51:5632 |
| 14.2 | D3S3 | 1 | 0 | 0 | Breast | GCC 2:191 |
| 14.2 | D3S3 | 9 | 9 | 1 | Head&Neck | CGC 54:91 |
| 14.2 | D3S3 | 4 | 3 | 0.75 | Kidney | CR 51:1071 |
| 14.2 | D3S3 | 1 | 1 | 1 | Kidney | CR 49:1390 |
| 14.2 | D3S3 | 9 | 0 | 0 | Kidney | PNAS 85:157 |
| 14.2 | D3S3 | 2 | 1 | 0.5 | Kidney | N 327:721 |
| 14.2 | D3S3 | 3 | 1 | 0.33 | Kidney | G 11:537 |
| 14.2 | D3S3 | 5 | 3 | 0.6 | Lung | GCC 1:95 |
| 14.2 | D3S3 | 1 | 1 | 1 | Lung | GCC 1:95 |
| 14.2 | D3S3 | 4 | 4 | 1 | Lung | GCC 1:240 |
| 14.2 | D3S3 | 1 | 0 | 0 | Lung | N 329:451 |

Chromosome 3 - p Arm

| | | | | | | |
|-------------|---------|----|----|------|------------|-------------|
| 14.2 | D3S3 | 9 | 6 | 0.67 | Lung | N 329:451 |
| 14.2 | D3S3 | 3 | 3 | 1 | Lung | GCC 1:95 |
| 14.2 | D3S3 | 1 | 0 | 0 | Lung | N 329:451 |
| 14.2 | D3S3 | 2 | 1 | 0.5 | Lung | NEJ 317:110 |
| 14.2 | D3S3 | 4 | 3 | 0.75 | Lung | NEJ 317:110 |
| 14.2 | D3S3 | 4 | 0 | 0 | Lung | GCC 11:15 |
| 14.2 | D3S3 | 1 | 1 | 1 | Lung | GCC 1:95 |
| 21.2-14.2 | D3S32 | 8 | 0 | 0 | Brain | CR 49:6572 |
| 21.2-14.2 | D3S32 | 16 | 2 | 0.11 | Brain | CR 50:5784 |
| 21.2-14.2 | D3S32 | 16 | 3 | 0.19 | Breast | CR 50:7184 |
| 21.2-14.2 | D3S32 | 44 | 9 | 0.2 | Breast | CR 51:5794 |
| 21.2-14.2 | D3S32 | 30 | 12 | 0.4 | Cervix | CR 54:4481 |
| 14.2-21.2 | D3S32 | 3 | 3 | 1 | Cervix | GCC 9:119 |
| 21.2-14.2 | D3S32 | 17 | 7 | 0.41 | Cervix | IJC 58:787 |
| 14.2-21.2 | D3S32 | 4 | 1 | 0.25 | Cervix | IJC 67:71 |
| 14.2-21.2 | D3S32 | 19 | 8 | 0.42 | Esophageal | CR 54:2996 |
| 21.2-14.2 | D3S32 | 28 | 10 | 0.36 | Esophageal | IJC 73:366 |
| 21.2-14.2 | D3S32 | 7 | 0 | 0 | Head&Neck | C 72:881 |
| 21.2-14.2 | D3S32 | 15 | 8 | 0.53 | Kidney | CR 51:820 |
| 14.2-21.2 | D3S32 | 15 | 9 | 0.6 | Kidney | CR 51:4707 |
| 14.2-21.2 | D3S32 | 21 | 17 | 0.81 | Kidney | CR 51:1071 |
| 21.2-14.2 | D3S32 | 18 | 8 | 0.44 | Kidney | CR 51:949 |
| 21.2-14.2 | D3S32 | 20 | 2 | 0.1 | Liver | CR 51:89 |
| 21.2-14.2 | D3S32 | 11 | 6 | 0.55 | Lung | GCC 3:358 |
| 21.2-14.2 | D3S32 | 17 | 11 | 0.65 | Lung | CR 52:873 |
| 21.2-14.2 | D3S32 | 6 | 6 | 1 | Lung | O 4:451 |
| 21.2-14.2 | D3S32 | 5 | 1 | 0.2 | Lung | GCC 11:15 |
| 21.2-14.2 | D3S32 | 4 | 4 | 1 | Lung | CR 52:873 |
| 21.2-14.2 | D3S32 | 17 | 10 | 0.59 | Melanoma | GCC 15:102 |
| 21.2-14.2 | D3S32 | 13 | 2 | 0.15 | Ovary | IJC 54:546 |
| 21.2-14.2 | D3S32 | 17 | 3 | 0.18 | Ovary | CR 51:5118 |
| 21.2-14.2 | D3S32 | 17 | 3 | 0.18 | Ovary | CR 51:5118 |
| 21.2-14.2 | D3S32 | 3 | 1 | 0.33 | Pancreas | CR 54:2761 |
| 21.2-14.2 | D3S32 | 10 | 1 | 0.1 | Prostate | PNAS 87:875 |
| 21.2-14.2 | D3S32 | 10 | 1 | 0.1 | Prostate | CSurveys 11 |
| 21.2-14.2 | D3S32 | 33 | 15 | 0.45 | Testis | O 9:2245 |
| 21.2-14.2 | D3S32 | 4 | 2 | 0.5 | Uterus | GCC 9:119 |
| 21.2-21.1 | D3S1289 | 15 | 5 | 0.33 | Melanoma | GCC 15:102 |
| 21.32-21.33 | D3S643 | 14 | 4 | 0.29 | Breast | CR 51:5794 |
| 21.32-21.33 | D3S643 | 19 | 0 | 0 | Esophageal | CR 54:6484 |
| 21.32-21.33 | D3S643 | 3 | 3 | 1 | Kidney | CR 51:4707 |
| 21.32-21.33 | D3S643 | 17 | 4 | 0.24 | Leukemia | B 83:3449 |
| 21.32-21.33 | D3S643 | 6 | 3 | 0.5 | Lung | CR 52:873 |
| 21.32-21.33 | D3S643 | 3 | 3 | 1 | Lung | CR 52:873 |
| 21 | D3F15S2 | 15 | 7 | 0.47 | Breast | GE 5:554 |
| 21 | D3F15S2 | 33 | 5 | 0.15 | Breast | CR 53:4356 |

Chromosome 3 - p Arm

| | | | | | | |
|---------|---------|----|----|------|------------|-------------|
| 21 | D3F15S2 | 2 | 0 | 0 | Cervix | CR 49:3598 |
| 21 | D3F15S2 | 5 | 3 | 0.6 | Cervix | IJC 58:787 |
| 21 | D3F15S2 | 21 | 17 | 0.81 | Esophageal | EJC 30B:248 |
| 21 | D3F15S2 | 12 | 9 | 0.75 | Head&Neck | C 72:881 |
| 21 | D3F15S2 | 4 | 2 | 0.5 | Head&Neck | CGC 54:91 |
| 21 | D3F15S2 | 3 | 3 | 1 | Kidney | CGC 32:281 |
| 21 | D3F15S2 | 3 | 0 | 0 | Kidney | |
| 21 | D3F15S2 | 14 | 14 | 0.58 | Kidney | G 11:537 |
| 21 | D3F15S2 | 7 | 1 | 0.14 | Kidney | |
| 21 | D3F15S2 | 13 | 10 | 0.77 | Kidney | CR 49:1390 |
| 21 | D3F15S2 | 21 | 16 | 0.76 | Kidney | PNAS 85:157 |
| 21 | D3F15S2 | 9 | 9 | 1 | Kidney | N 327:721 |
| 21 | D3F15S2 | 2 | 1 | 0.5 | Kidney | CR 51:949 |
| 21 | D3F15S2 | 16 | 12 | 0.75 | Kidney | |
| 21 | D3F15S2 | 12 | 0 | 0 | Lung | N 329:451 |
| 21 | D3F15S2 | 9 | 9 | 1 | Lung | N 329:451 |
| 21 | D3F15S2 | 7 | 3 | 0.43 | Lung | GCC 11:15 |
| 21 | D3F15S2 | 1 | 0 | 0 | Lung | N 329:451 |
| 21 | D3F15S2 | 7 | 2 | 0.29 | Lung | CL 51:133 |
| 21 | D3F15S2 | 8 | 3 | 0.38 | Lung | PNAS 86:509 |
| 21 | D3F15S2 | 8 | 2 | 0.25 | Lung | GCC 3:358 |
| 21 | D3F15S2 | 6 | 3 | 0.5 | Lung | PNAS 86:509 |
| 21 | D3F15S2 | 2 | 0 | 0 | Lung | PNAS 86:509 |
| 21 | D3F15S2 | 2 | 0 | 0 | Lung | CL 51:133 |
| 21 | D3F15S2 | 2 | 0 | 0 | Lung | O 4:451 |
| 21 | D3F15S2 | 5 | 4 | 0.8 | Lung | |
| 21 | D3F15S2 | 1 | 0 | 0 | Lung | GCC 1:95 |
| 21 | D3F15S2 | 1 | 3 | 0.6 | Lung | NEJ 317:110 |
| 21 | D3F15S2 | 5 | 4 | 0.57 | Lung | GCC 1:95 |
| 21 | D3F15S2 | 7 | 4 | 0 | Lung | GCC 1:95 |
| 21 | D3F15S2 | 1 | 0 | 0 | Lung | CR 49:5130 |
| 21 | D3F15S2 | 2 | 2 | 1 | Lung | |
| 21 | D3F15S2 | 16 | 11 | 0.69 | Lung | GCC 1:95 |
| 21 | D3F15S2 | 12 | 7 | 0.58 | Melanoma | GCC 15:102 |
| 21 | D3F15S2 | 8 | 1 | 0.12 | Ovary | O 5:219 |
| 21 | D3F15S2 | 22 | 4 | 0.18 | Ovary | IJC 52:575 |
| 21 | D3F15S2 | 22 | 4 | 0.18 | Ovary | IJC 54:546 |
| 21 | D3F15S2 | 12 | 2 | 0.17 | Ovary | BJC 69:429 |
| 21 | D3F15S2 | 3 | 0 | 0 | Testis | CCG 52:72 |
| 21 | D3F15S2 | 1 | 0 | 0 | Testis | CCG 52:72 |
| 21 | D3F15S2 | 2 | 0 | 0 | Testis | CCG 52:72 |
| 21 | D3F15S2 | 18 | 2 | 0.11 | Testis | GCC 13:249 |
| 21 | D3F15S2 | 2 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | D3S1076 | 29 | 2 | 0.07 | Esophageal | BJC 73:366 |
| Unknown | D3S1076 | 14 | 4 | 0.29 | Esophageal | CR 54:6484 |
| Unknown | D3S1076 | 22 | 13 | 0.59 | Kidney | BJC 69:230 |
| Unknown | D3S965 | 4 | 0 | 0 | Lung | CR 52:873 |
| Unknown | D3S965 | 1 | 1 | 1 | Lung | CR 52:873 |

Chromosome 3 - p Arm

| | | | | | | |
|-----------|---------|----|----|------|------------|-------------|
| 21.2 | D3S660 | 33 | 6 | 0.18 | Breast | CR 51:5794 |
| Unknown | D3S660 | 6 | 2 | 0.33 | Kidney | CR 51:4707 |
| Unknown | D3S660 | 12 | 5 | 0.42 | Lung | CR 52:873 |
| Unknown | D3S660 | 8 | 8 | 1 | Lung | CR 52:873 |
| Unknown | D3S717 | 6 | 3 | 0.5 | Kidney | CR 51:4707 |
| Unknown | D3S717 | 4 | 2 | 0.5 | Lung | CR 52:873 |
| Unknown | D3S717 | 4 | 4 | 1 | Lung | CR 52:873 |
| Unknown | D3S936 | 11 | 4 | 0.36 | Kidney | CR 51:4708 |
| Unknown | D3S936 | 12 | 5 | 0.42 | Lung | CR 52:873 |
| Unknown | D3S936 | 4 | 4 | 1 | Lung | CR 52:873 |
| 14.2-21.1 | D3S1313 | 54 | 11 | 0.2 | Esophageal | IJC 69:1 |
| 14.2-21.1 | D3S1300 | 53 | 19 | 0.36 | Esophageal | IJC 69:1 |
| 14.2-14.3 | D3S678 | 50 | 19 | 0.38 | Breast | CR 51:5794 |
| 14.2-14.3 | D3S678 | 10 | 7 | 0.7 | Kidney | CR 51:4707 |
| Unknown | D3S687 | 25 | 8 | 0.32 | Breast | CR 51:5794 |
| Unknown | D3S687 | 13 | 8 | 0.62 | Kidney | CR 51:4707 |
| Unknown | D3S687 | 4 | 4 | 1 | Lung | CR 52:873 |
| Unknown | D3S687 | 15 | 3 | 0.2 | Lung | CR 52:873 |
| Unknown | D3S1228 | 31 | 4 | 0.13 | Esophageal | BJC 73:366 |
| 25 | D3S1228 | 18 | 8 | 0.44 | Esophageal | CR 54:6484 |
| 25 | D3S1228 | 26 | 12 | 0.46 | Kidney | BJC 69:230 |
| 25 | D3S1228 | 6 | 4 | 0.67 | Lung | JAMA 273:55 |
| 25 | D3S1228 | 1 | 1 | 1 | Lung | JAMA 273:55 |
| 14.1-14.2 | D3S1285 | 47 | 18 | 0.38 | Esophageal | IJC 69:1 |
| 14.1-14.2 | D3S1285 | 10 | 7 | 0.7 | Melanoma | GCC 15:102 |
| Unknown | D3S714 | 24 | 1 | 0.04 | Breast | CR 51:5794 |
| Unknown | D3S714 | 9 | 3 | 0.33 | Lung | CR 52:873 |
| 14-13 | D3S1217 | 28 | 18 | 0.64 | Esophageal | C 73:2472 |
| 14-13 | D3S1217 | 28 | 18 | 0.64 | Head&Neck | CA 73:2472 |
| Unknown | D3S1079 | 25 | 4 | 0.16 | Esophageal | BJC 73:366 |
| Unknown | D3S1079 | 11 | 4 | 0.36 | Esophageal | CR 54:6484 |
| Unknown | D3S1261 | 20 | 8 | 0.4 | Cervix | CR 56:197 |
| Unknown | D3S13 | 2 | 0 | 0 | Stomach | RG 89:445 |
| 12-14.2 | D3S1296 | 57 | 17 | 0.3 | Esophageal | IJC 69:1 |
| Unknown | D3S659 | 54 | 23 | 0.43 | Breast | CR 51:5794 |
| Unknown | D3S659 | 7 | 6 | 0.86 | Cervix | GCC 9:119 |
| Unknown | D3S659 | 28 | 10 | 0.36 | Esophageal | GCC 10:177 |
| Unknown | D3S659 | 36 | 6 | 0.17 | Esophageal | BJC 73:366 |
| Unknown | D3S659 | 17 | 7 | 0.41 | Esophageal | CR 54:6484 |
| Unknown | D3S659 | 11 | 8 | 0.73 | Kidney | CR 51:4707 |
| Unknown | D3S659 | 40 | 18 | 0.45 | Kidney | BJC 69:230 |
| Unknown | D3S659 | 17 | 5 | 0.29 | Lung | CR 52:873 |
| Unknown | D3S659 | 10 | 3 | 0.9 | Lung | CR 52:873 |
| Unknown | D3S659 | 6 | 0 | 0 | Ovary | CR 51:5118 |
| Unknown | D3S659 | 6 | 0 | 0 | Ovary | CR 51:5118 |
| Unknown | D3S659 | 11 | 5 | 0.45 | Uterus | GCC 9:119 |

Chromosome 3 - p Arm

| | | | | | | |
|---------|---------------|----|----|------|------------|-------------|
| Unknown | D3S659 | 14 | 1 | 0.07 | Uterus | CR 54:4294 |
| 13 | D3S693 | 6 | 0 | 0 | Breast | CR 51:5794 |
| 13 | D3S693 | 1 | 0 | 0 | Lung | CR 52:5735 |
| 14 | D3S6 | 32 | 11 | 0.34 | Breast | CR 54:499 |
| 14 | D3S6 | 5 | 2 | 0.4 | Kidney | CR 49:1390 |
| 14 | D3S6 | 3 | 0 | 0 | Kidney | PNAS 85:157 |
| 14 | D3S6 | 3 | 1 | 0.33 | Kidney | GCC 11:95 |
| 14 | D3S6 | 8 | 7 | 0.88 | Lung | GCC 11:95 |
| 14 | D3S6 | 6 | 2 | 0.33 | Lung | GCC 11:15 |
| 14 | D3S6 | 4 | 2 | 0.5 | Lung | GCC 11:15 |
| 21-3 | ITIH1-2H3 | 66 | 55 | 0.83 | Lung | ITC 10:497 |
| Unknown | D3S30 | 37 | 15 | 0.41 | Breast | CR 54:3021 |
| 13 | D3S30 | 18 | 0 | 0 | Breast | CR 48:165 |
| Unknown | D3S30 | 17 | 6 | 0.35 | Cervix | IJC 58:787 |
| Unknown | D3S30 | 19 | 6 | 0.32 | Esophageal | CR 51:2468 |
| 13 | D3S30 | 32 | 12 | 0.38 | Esophageal | BJC 73:366 |
| Unknown | D3S30 | 16 | 8 | 0.5 | Kidney | CR 51:820 |
| 13 | D3S30 | 18 | 9 | 0.5 | Kidney | CR 51:820 |
| Unknown | D3S30 | 12 | 3 | 0.25 | Lung | CR 52:273 |
| 13 | D3S30 | 7 | 1 | 0.14 | Lung | GCC 11:15 |
| Unknown | D3S30 | 11 | 11 | 1 | Lung | CR 52:273 |
| 13 | D3S30 | 7 | 7 | 1 | Lung | GCC 11:240 |
| Unknown | D3S30 | 11 | 8 | 0.73 | Melanoma | GCC 15:102 |
| 13 | D3S30 | 14 | 1 | 0.07 | Ovary | CR 51:5118 |
| 13 | D3S30 | 14 | 1 | 0.07 | Ovary | CR 51:5118 |
| Unknown | D3S30 | 12 | 1 | 0.08 | Ovary | BJC 69:429 |
| 13 | D3S30 | 18 | 0 | 0 | Testis | G 5:134 |
| 13-14 | D3S1284 | 19 | 12 | 0.63 | Head&Neck | CR 54:1152 |
| 13-14 | D3S1284 | 3 | 0 | 0 | Kidney | GCC 12:76 |
| Unknown | D3S738 | 3 | 3 | 1 | Lung | GCC 5:119 |
| Unknown | D3S625 | 2 | 2 | 1 | Lung | GCC 5:119 |
| Unknown | D3S742 | 4 | 3 | 0.75 | Lung | GCC 5:119 |
| Unknown | D3S739 | 5 | 3 | 0.6 | Lung | GCC 5:119 |
| Unknown | D3S740 | 5 | 4 | 0.8 | Lung | GCC 5:119 |
| Unknown | D3S216 | 1 | 1 | 1 | Lung | GCC 5:119 |
| Unknown | D3S733 | 3 | 3 | 1 | Lung | GCC 5:119 |
| 13 | D3S4 | 16 | 7 | 0.44 | Kidney | CR 51:949 |
| 13 | D3S4 | 17 | 4 | 0.24 | Kidney | CR 51:1071 |
| 13 | D3S4 | 14 | 8 | 0.57 | Kidney | CR 49:1390 |
| 13 | D3S4 | 6 | 5 | 0.83 | Lung | GCC 1:240 |
| Unknown | D3S743 | 5 | 4 | 0.8 | Lung | GCC 5:119 |
| Unknown | D3S759 | 7 | 6 | 0.86 | Lung | GCC 5:119 |
| Unknown | D3S640 | 5 | 3 | 0.6 | Lung | GCC 5:119 |
| Unknown | D3S1090 | 2 | 2 | 1 | Lung | GCC 5:119 |
| Unknown | D3S1090 | 2 | 2 | 1 | Lung | GCC 5:119 |
| Unknown | D3S:1067-1228 | 29 | 9 | 0.31 | Bladder | CR 55:5213 |

Chromosome 3 - p Arm

| | | | | | | |
|-----------|-------------------------|----|----|------|------------|-------------|
| Unknown | RAF1-DNF15S2 | 25 | 12 | 0.48 | Bladder | CR 51:5405 |
| 24-26 | Unknown | 28 | 13 | 0.46 | Breast | JNCI 84:506 |
| Unknown | D3S2-H3H2 | 37 | 12 | 0.32 | Breast | CR 54:3021 |
| Unknown | DNF15S2 | 4 | 1 | 0.25 | Breast | CR 53:3804 |
| 24 | EABMD | 67 | 26 | 0.39 | Breast | CR 54:499 |
| Unknown | RAF1-DNF15S2 | 15 | 7 | 0.47 | Breast | GE 5:554 |
| Unknown | D3S663 | 6 | 3 | 0.5 | Cervix | GCC 9:119 |
| 21.1-14.2 | D3S1067 | 20 | 7 | 0.35 | Esophageal | CR 54:6484 |
| Unknown | D3S1110 | 17 | 7 | 0.41 | Esophageal | CR 54:6484 |
| Unknown | D3S1111 | 11 | 1 | 0.09 | Esophageal | CR 54:6484 |
| Unknown | D3S192 | 34 | 8 | 0.24 | Esophageal | BJC 73:366 |
| Unknown | D3S656 | 19 | 8 | 0.42 | Esophageal | CR 54:6484 |
| Unknown | D3S663 | 22 | 2 | 0.09 | Esophageal | CR 54:6484 |
| Unknown | D3S966 | 38 | 9 | 0.24 | Esophageal | BJC 73:366 |
| Unknown | D3S966 | 19 | 5 | 0.26 | Esophageal | CR 54:6484 |
| 21.1-14.2 | D3S1067 | 41 | 20 | 0.49 | Kidney | BJC 69:230 |
| 25-26 | D3S1085 | 3 | 3 | 1 | Kidney | CR 51:4707 |
| Unknown | D3S1110 | 15 | 11 | 0.73 | Kidney | BJC 69:230 |
| Unknown | D3S1263-D3S1307-D3S1297 | 22 | 9 | 0.41 | Kidney | PNAS 92:285 |
| Unknown | D3S1263-D3S1307-D3S1297 | 6 | 0 | 0 | Kidney | PNAS 92:285 |
| Unknown | D3S22 | 9 | 7 | 0.78 | Kidney | CR 51:1071 |
| 25 | D3S649 | 11 | 7 | 0.64 | Kidney | CR 51:4707 |
| Unknown | D3S654 | 13 | 4 | 0.31 | Kidney | CR 51:4707 |
| Unknown | D3S656 | 7 | 4 | 0.57 | Kidney | CR 51:4707 |
| 25 | D3S689 | 1 | 0 | 0 | Kidney | CR 51:4707 |
| 25-26 | D3S858 | 11 | 5 | 0.45 | Kidney | CR 51:4707 |
| 21.1-21.2 | D3S898 | 8 | 7 | 0.88 | Kidney | CR 51:4707 |
| 14.1-14.2 | D3S907 | 6 | 2 | 0.33 | Kidney | CR 51:4707 |
| 12 | D3S960 | 2 | 2 | 1 | Kidney | CR 51:4707 |
| Unknown | D3S:1263-1307-1297 | 33 | 10 | 0.3 | Kidney | CR 55:6189 |
| Unknown | DNF15S2 | 28 | 25 | 0.89 | Kidney | CR 51:1071 |
| Unknown | DNF15S2 | 19 | 9 | 0.47 | Kidney | CR 51:1544 |
| Unknown | ERBA-B | 18 | 17 | 0.94 | Kidney | CR 51:1071 |
| Unknown | ERBA-B | 2 | 0 | 0 | Kidney | CR 51:1071 |
| Unknown | RAF1-DNF15S2 | 13 | 7 | 0.54 | Kidney | CR 51:949 |
| 25-26 | VHL | 19 | 16 | 0.84 | Kidney | CR 54:2852 |
| Unknown | Unknown | 27 | 25 | 0.93 | Lung | CR 54:2322 |
| 21.3 | D3S1339 | 12 | 11 | 0.92 | Lung | IJC 64:371 |
| 21 | D3S48 | 5 | 5 | 1 | Lung | GCC 5:119 |
| Unknown | D3S654 | 9 | 7 | 0.78 | Lung | CR 52:873 |
| Unknown | D3S654 | 22 | 8 | 0.36 | Lung | CR 52:873 |
| Unknown | DNF15S2 | 5 | 1 | 0.2 | Lung | NEJ 317:110 |
| Unknown | DNF15S2 | 2 | 1 | 0.5 | Lung | NEJ 317:110 |
| Unknown | DNF15S2 | 5 | 5 | 1 | Lung | NEJ 317:110 |

Chromosome 3 - p Arm

| | | | | | | |
|-----------|--------------------|------|------|------|----------|-------------|
| Unknown | IT1H1-D3S1339-1007 | 7 | 7 | 1 | Lung | CR 55:5133 |
| Unknown | RAF1-DNF15S2 | 4 | 4 | 1 | Lung | GCC 5:119 |
| Unknown | RAF1-DNF15S2 | 6 | 3 | 0.5 | Lung | PNAS 86:509 |
| Unknown | RAF1-DNF15S2 | 5 | 3 | 0.6 | Lung | PNAS 86:509 |
| Unknown | RAF1-DNF15S2 | 17 | 8 | 0.47 | Lung | GCC 3:358 |
| 25-24 | D3S1252 | 5 | 1 | 0.2 | Melanoma | GCC 15:102 |
| all | 7 loci | 46 | 11 | 0.24 | Ovary | CR 53:4456 |
| 21 | D3S2-D3S86 | 23 | 0 | 0 | Ovary | CR 53:2393 |
| Unknown | D3S1270-11 | 14 | 2 | 0.14 | Ovary | BJC 72:1330 |
| Unknown | Unknown | 19 | 2 | 0.11 | Testis | G 5:134 |
| 21-1-14-2 | D3S1067 | 25 | 3 | 0.12 | Uterus | CR 54:4294 |
| Unknown | D3S663 | 10 | 2 | 0.2 | Uterus | GCC 9:119 |
| SDM | | 5933 | 2353 | 0.4 | | |

Chromosome 3 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Refers |
|-----------|---------|-------|-------------|-----------|--------------|--------|
| 11.0-12.0 | GPX1 | 19 | 17 | 0.89 | Kidney | Cr 15 |
| 11.0-12.0 | GPX1 | 6 | 6 | 1 | Lung | Cr 15 |
| 11.0-12.0 | GPX1 | 3 | 3 | 1 | Lung | Cr 15 |
| 12 | D3S1 | 7 | 0 | 0 | Head&Neck | CGC 5 |
| 12 | D3S1 | 2 | 0 | 0 | Kidney | CGC 3 |
| 12 | D3S1 | 4 | 0 | 0 | Lung | NEJ 3 |
| 12 | D3S1 | 4 | 0 | 0 | Lung | O 444 |
| 12 | D3S1 | 1 | 0 | 0 | Lung | N 329 |
| 12 | D3S1 | 9 | 2 | 0.22 | Lung | N 329 |
| 12 | D3S1 | 1 | 0 | 0 | Lung | N 329 |
| 12 | D3S1 | 19 | 2 | 0.11 | Ovary | UTC 9 |
| 12 | D3S1 | 8 | 1 | 0.12 | Testis | GCC 1 |
| Unknown | D3S1764 | 24 | 1 | 0.04 | Esophageal | BJC 7 |
| Unknown | D3S196 | 31 | 3 | 0.1 | Esophageal | BJC 7 |
| Unknown | D3S196 | 19 | 9 | 0.47 | Head&Neck | CR 54 |
| Unknown | D3S196 | 19 | 5 | 0.26 | Ovary | BJC 6 |
| Unknown | D3S196 | 22 | 2 | 0.09 | Uterus | CR 54 |
| Unknown | CP | 7 | 1 | 0.14 | Lung | N 329 |
| Unknown | CP | 1 | 0 | 0 | Lung | N 329 |
| Unknown | CP | 1 | 0 | 0 | Lung | N 329 |
| Unknown | D3S1268 | 24 | 2 | 0.08 | Head&Neck | CR 54 |
| Unknown | D3S1268 | 34 | 0 | 0 | Head&Neck | CR 54 |
| Unknown | D3S1268 | 35 | 5 | 0.14 | Melanoma | CR 56 |
| Unknown | D3S1262 | 37 | 8 | 0.22 | Cervix | CR 56 |
| Unknown | D3S1262 | 18 | 1 | 0.06 | Esophageal | CR 54 |
| 28 | SST | 6 | 0 | 0 | Cervix | CR 49 |
| 28 | SST | 6 | 0 | 0 | Liver | CCG |
| 28 | SST | 9 | 2 | 0.22 | Lung | N 329 |
| 28 | SST | 12 | 0 | 0 | Lung | PNAS |
| 28 | SST | 1 | 0 | 0 | Lung | N 329 |
| 28 | SST | 7 | 0 | 0 | Lung | CR 49 |
| 28 | SST | 1 | 0 | 0 | Melanoma | N 329 |
| 28 | SST | 3 | 0 | 0 | Neuroblastom | CR 49 |
| Unknown | D3S1314 | 26 | 1 | 0.04 | Kidney | PNAS |
| Unknown | D3S42 | 4 | 1 | 0.25 | Breast | CR 53 |
| Unknown | D3S42 | 26 | 3 | 0.12 | Breast | GCC 4 |
| Unknown | D3S42 | 28 | 9 | 0.32 | Cervix | CR 54 |
| Unknown | D3S42 | 12 | 0 | 0 | Stomach | HG 92 |
| Unknown | D3S42 | 34 | 9 | 0.26 | Testis | O 972 |
| Unknown | D3S42 | 16 | 0 | 0 | Testis | LI 73 |
| Unknown | D3S44 | 35 | 6 | 0.17 | Ovary | CR 53 |
| Unknown | D3S46 | 19 | 5 | 0.26 | Esophageal | CR 54 |
| Unknown | D3S46 | 0 | 3 | 0 | Esophageal | Unkno |
| Unknown | D3S46 | 44 | 13 | 0.3 | Esophageal | GCC 1 |
| Unknown | D3S46 | 16 | 3 | 0.19 | Kidney | CR 54 |

Chromosome 3 - q Arm

| | | | | | | |
|-----------|----------------|------|-----|------|------------|-------|
| Unknown | D3S46 | 7 | 0 | 0 | Liver | CR 51 |
| Unknown | D3S46 | 40 | 6 | 0.15 | Lung | CR 52 |
| Unknown | D3S46 | 18 | 1 | 0.06 | Ovary | CR 51 |
| Unknown | D3S46 | 18 | 1 | 0.06 | Ovary | CR 51 |
| Unknown | D3S46 | 3 | 0 | 0 | Pancreas | CR 54 |
| Unknown | D3S46 | 12 | 8 | 0.75 | Sarcoma | CR 52 |
| Unknown | D3S46 | 12 | 9 | 0.75 | Sarcoma | CR 52 |
| Unknown | Unknown | 13 | 0 | 0 | Brain | CR 50 |
| 21-qter | D3S5 | 1 | 0 | 0 | Brain | CCG 5 |
| Unknown | MOX2 | 1 | 0 | 0 | Brain | CCG 5 |
| Unknown | D3S47 | 21 | 0 | 0 | Endocrine | GCC 1 |
| Unknown | GLUT2 | 23 | 0 | 0 | Endocrine | BR 56 |
| Unknown | D3S1271 | 14 | 1 | 0.07 | Esophageal | CR 54 |
| Unknown | D3S1238 | 20 | 7 | 0.35 | Head/Neck | CR 54 |
| Unknown | D3S1-MOX2-D3S5 | 24 | 2 | 0.08 | Kidney | G 11: |
| Unknown | D3S31 | 14 | 0 | 0 | Kidney | BR 49 |
| 26.2-qTER | D3S45 | 20 | 3 | 0.15 | Kidney | CR 51 |
| all | 4 markers | 32 | 15 | 0.41 | Lung | GCC 1 |
| 12-q13 | MOX1 | 15 | 7 | 0.47 | Lung | GCC 1 |
| 12-q13 | MOX1 | 6 | 2 | 0.33 | Lung | GCC 1 |
| 12-q13 | MOX1 | 1 | 1 | 1 | Lung | GCC 1 |
| 12-q13 | MOX1 | 1 | 1 | 1 | Lung | GCC 1 |
| all | 4 markers | 46 | 8 | 0.17 | Ovary | CR 53 |
| 21-PTER | ACCE | 13 | 4 | 0.31 | Ovary | BJC 6 |
| Unknown | D3S1232-GLUT2 | 14 | 2 | 0.14 | Ovary | BJC 7 |
| Unknown | D3S31 | 13 | 0 | 0 | Prostate | G 11: |
| SUM | | 1050 | 191 | 0.18 | | |

Chromosome 4 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|---------------|-------|-------------|-----------|------------|--------------|
| 16.1 | RAF1P1 | 7 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | D4S1546 | 25 | 8 | 0.32 | Bladder | CR 55:5213 |
| Unknown | D4S124 | 16 | 0 | 0 | Brain | CR 50:5784 |
| 16 | D4S10 | 31 | 0 | 0 | Breast | GE 5:554 |
| pter-16.3 | D4S125 | 6 | 1 | 0.17 | Breast | CR 50:7184 |
| 16 | D4S95 | 33 | 4 | 0.12 | Breast | CR 53:4356 |
| pter-16.3 | D4S125 | 9 | 0 | 0 | Cervix | CR 54:4481 |
| Unknown | D4S125 | 2 | 0 | 0 | Cervix | GCC 9:119 |
| Unknown | D4S391 | 25 | 9 | 0.36 | Cervix | CR 56:197 |
| Unknown | D4S405 | 30 | 4 | 0.13 | Cervix | CR 56:197 |
| 16 | D4S10 | 11 | 0 | 0 | Colon | CCG 48:167 |
| pter-16.3 | D4S125 | 8 | 0 | 0 | Colon | CCG 48:167 |
| 11.0-15 | D4S174 | 21 | 0 | 0 | Endocrine | GCC 13:9 |
| Unknown | D4S2397 | 18 | 1 | 0.06 | Endocrine | CR 56:599 |
| Unknown | D4S124 | 21 | 2 | 0.1 | Esophageal | CR 54:2996 |
| Unknown | D4S125 | 40 | 7 | 0.17 | Esophageal | GCC 10:177 |
| pter-16.3 | D4S125 | 9 | 0 | 0 | Esophageal | CR 51:2113 |
| Unknown | D4S394 | 15 | 1 | 0.07 | Head&Neck | CR 54:4756 |
| Unknown | D4S394 | 18 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D4S404 | 21 | 8 | 0.38 | Head&Neck | CR 54:1152 |
| pter-16.3 | D4S125 | 7 | 0 | 0 | Kidney | CR 51:820 |
| Unknown | D4S431 | 28 | 2 | 0.07 | Kidney | PNAS 92:2854 |
| 16.3 | D4S10 | 5 | 1 | 0.2 | Liver | CCG 48:72 |
| 16 | D4S10 | 6 | 2 | 0.33 | Liver | CR 51:4367 |
| pter-16.3 | D4S125 | 4 | 0 | 0 | Liver | CR 51:89 |
| Unknown | D4S125 | 6 | 0 | 0 | Liver | PNAS 86:8852 |
| 16.1 | RAF1P1 | 13 | 2 | 0.15 | Liver | IJCR 81:108 |
| pter-16.3 | D4S125 | 28 | 2 | 0.07 | Lung | CR 52:2478 |
| pter-16.3 | D4S125 | 24 | 10 | 0.42 | Ovary | CR 51:5118 |
| Unknown | D4S125-D4S124 | 29 | 10 | 0.34 | Ovary | CR 53:2393 |
| 15.1-11 | D4S16 | 19 | 2 | 0.11 | Ovary | IJC 54:546 |
| 11.0-15 | D4S174 | 20 | 3 | 0.15 | Ovary | BJC 69:429 |
| 16.2-15.1 | D4S49 | 20 | 5 | 0.25 | Ovary | IJC 54:546 |
| 12.0-13 | GABRB1 | 16 | 2 | 0.12 | Ovary | BJC 69:429 |
| pter-16.3 | D4S125 | 3 | 0 | 0 | Pancreas | CR 54:2761 |
| 12.0-13 | GABRB1 | 13 | 0 | 0 | Prostate | G 11:530 |
| Unknown | D4S124 | 13 | 1 | 0.08 | Sarcoma | CR 52:2419 |
| Unknown | D4S125 | 17 | 3 | 0.18 | Testis | O 9:2245 |
| pter-16.3 | D4S125 | 9 | 0 | 0 | Testis | LI 73:606 |
| Unknown | D4S129 | 10 | 1 | 0.1 | Testis | GCC 13:249 |
| pter-16.3 | D4S125 | 2 | 0 | 0 | Uterus | GCC 9:119 |
| 11.0-15 | D4S174 | 21 | 1 | 0.05 | Uterus | CR 54:4294 |
| 16 | D4S43 | 25 | 1 | 0.04 | Uterus | CR 54:4294 |
| 12.0-13 | GABRB1 | 25 | 0 | 0 | Uterus | CR 54:4294 |
| 16.1 | RAF1P1 | 7 | 0 | 0 | Uterus | CR 51:5632 |

Chromosome 4 - p Arm

| | | | |
|-----|-----|----|------|
| SUM | 729 | 93 | 0.13 |
|-----|-----|----|------|

Chromosome 4 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------------|-------|-------------|-----------|------------|--------------|
| p11-q21 | MT2P1 | 4 | 0 | 0 | Uterus | CR 51:5632 |
| 33-35 | D4S171 | 29 | 15 | 0.52 | Bladder | CR 55:5213 |
| 25-34 | D4S243 | 29 | 15 | 0.52 | Bladder | CR 55:5213 |
| Unknown | Unknown | 20 | 2 | 0.1 | Brain | CR 50:5784 |
| Unknown | D4S125 | 34 | 2 | 0.06 | Breast | CR 50:7184 |
| 25-34 | D4S192 | 54 | 13 | 0.24 | Breast | BCRT 32:5 |
| 28 | FGA | 19 | 4 | 0.21 | Breast | GCC 2:191 |
| 28 | FGA | 18 | 0 | 0 | Breast | CR 53:4356 |
| p11-q21 | MT2P1 | 17 | 0 | 0 | Breast | JNCI 84:506 |
| 21-23 | ADH3 | 22 | 12 | 0.55 | Cervix | CR 54:4481 |
| 21-23 | ADH5 | 24 | 11 | 0.46 | Cervix | CR 54:4481 |
| Unknown | D4S163 | 41 | 12 | 0.29 | Cervix | CR 54:4481 |
| Unknown | D4S402 | 28 | 8 | 0.29 | Cervix | CR 56:197 |
| Unknown | D4S415 | 26 | 8 | 0.31 | Cervix | CR 56:197 |
| q11-q13 | ALB | 11 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D4S415 | 19 | 1 | 0.05 | Endocrine | CR 56:599 |
| Unknown | D4S163 | 21 | 2 | 0.1 | Esophageal | CR 51:2996 |
| Unknown | D4S163 | 35 | 9 | 0.26 | Esophageal | GCC 10:177 |
| Unknown | D4S402 | 16 | 3 | 0.19 | Head&Neck | CR 54:4756 |
| Unknown | D4S402 | 20 | 1 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D4S430 | 24 | 9 | 0.38 | Head&Neck | CR 54:1152 |
| Unknown | D4S163 | 23 | 2 | 0.09 | Kidney | CR 51:820 |
| Unknown | D4S426-D4S415 | 20 | 1 | 0.05 | Kidney | PNAS 92:2854 |
| Unknown | D4S426-D4S415 | 5 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D4S:408-429 | 23 | 4 | 0.17 | Leukemia | CR 55:5377 |
| Unknown | Unknown | 8 | 0 | 0 | Liver | BJC 64:1083 |
| 21-23 | ADH3 | 4 | 0 | 0 | Liver | JJCR 81:108 |
| 21-23 | ADH3 | 6 | 1 | 0.17 | Liver | CR 51:4367 |
| q11-q13 | ALB | 5 | 5 | 1 | Liver | PNAS 86:8852 |
| Unknown | D4S16 | 5 | 2 | 0.4 | Liver | JJCR 81:108 |
| Unknown | D4S163 | 20 | 3 | 0.15 | Liver | CR 51:89 |
| p11-q21 | MT2P1 | 16 | 8 | 0.5 | Liver | JJCR 81:108 |
| p11-q21 | MT2P1 | 21 | 9 | 0.43 | Liver | JJCR 84:893 |
| p11-q21 | MT2P1 | 19 | 4 | 0.21 | Liver | CR 54:281 |
| Unknown | D4S163 | 31 | 6 | 0.26 | Lung | CR 52:2478 |
| 21-23 | ADH3 | 18 | 1 | 0.06 | Ovary | IJC 54:546 |
| 11.0-15 | D4S1540 | 20 | 3 | 0.15 | Ovary | BJC 69:429 |
| 11.0-15 | D4S1607 | 20 | 3 | 0.15 | Ovary | BJC 69:429 |
| Unknown | D4S163 | 16 | 1 | 0.06 | Ovary | CR 51:5118 |
| 33-35 | D4S171 | 12 | 4 | 0.33 | Ovary | BJC 69:429 |
| 25-34 | D4S175 | 20 | 7 | 0.35 | Ovary | BJC 69:429 |
| Unknown | D4S27 | 29 | 10 | 0.34 | Ovary | CR 53:2393 |
| p11-q21 | MT2P1 | 21 | 2 | 0.1 | Ovary | IJC 54:546 |
| 35 | Unknown | 6 | 1 | 0.17 | Pancreas | CR 54:2761 |
| 28 | FGA | 9 | 0 | 0 | Prostate | G 17:530 |
| Unknown | D4S163 | 17 | 3 | 0.18 | Sarcoma | CR 52:2419 |

Chromosome 4 - q Arm

| | | | | | | |
|---------|--------|-----|-----|------|--------|------------|
| 21-23 | ADH3 | 24 | 0 | 0 | Testis | 0 9:2245 |
| 33-35 | D4S171 | 23 | 0 | 0 | Uterus | CR 54:4294 |
| p11-q21 | MT2P1 | 4 | 0 | 0 | Uterus | CR 51:5632 |
| SUM | | 952 | 209 | 0.22 | | |

Chromosome 5 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|---------|-------|-------------|-----------|------------|--------------|
| Unknown | D5S392 | 34 | 8 | 0.24 | Cervix | JNCI 87:742 |
| Unknown | D5S392 | 19 | 0 | 0 | Endocrine | CR 56:599 |
| Unknown | D5S392 | 26 | 5 | 0.19 | Head&Neck | CR 54:1152 |
| Unknown | D5S392 | 19 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D5S392 | 5 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D5S13 | 21 | 1 | 0.05 | Breast | CR 53:4356 |
| Unknown | D5S13 | 17 | 4 | 0.24 | Breast | GCC 2:191 |
| pter-p15 | D5S4 | 10 | 1 | 0.1 | Breast | GCC 2:191 |
| pter-p15 | D5S4 | 17 | 2 | 0.12 | Colon | IJC 53:382 |
| pter-p15 | D5S4 | 11 | 0 | 0 | Colon | CCG 48:167 |
| pter-p15 | D5S4 | 29 | 1 | 0.03 | Colon | CR 50:7166 |
| pter-p15 | D5S4 | 19 | 4 | 0.21 | Ovary | CR 53:2393 |
| pter-p15 | D5S4 | 3 | 0 | 0 | Testis | CCG 52:72 |
| pter-p15 | D5S4 | 1 | 0 | 0 | Testis | CCG 52:72 |
| pter-p15 | D5S4 | 1 | 0 | 0 | Testis | CCG 52:72 |
| 15.1-15.2 | D5S406 | 25 | 12 | 0.48 | Cervix | JNCI 87:742 |
| 15.2-15.1 | D5S12 | 12 | 1 | 0.08 | Brain | CR 50:5784 |
| 15.2-15.1 | D5S12 | 13 | 5 | 0.38 | Cervix | CR 54:4481 |
| 15.2-15.1 | D5S12 | 9 | 0 | 0 | Ovary | O 5:219 |
| 15.2-15.1 | D5S12 | 17 | 0 | 0 | Prostate | G 11:530 |
| 15.2-15.1 | D5S12 | 26 | 11 | 0.42 | Testis | O 9:2245 |
| 15.1-15.3 | D5S208 | 20 | 10 | 0.5 | Cervix | JNCI 87:742 |
| 15-21 | D5S630 | 5 | 2 | 0.4 | Lung | O 12:97 |
| 15-21 | D5S630 | 13 | 3 | 0.23 | Lung | O 12:97 |
| 14 | D5S432 | 29 | 8 | 0.28 | Cervix | JNCI 87:742 |
| 15.1-15.3 | D5S117 | 25 | 8 | 0.32 | Cervix | JNCI 87:742 |
| 15.1-15.3 | D5S117 | 13 | 2 | 0.15 | Ovary | BJC 69:429 |
| 15.1-15.3 | D5S117 | 22 | 1 | 0.05 | Uterus | CR 54:4294 |
| Unknown | D5S268 | 14 | 3 | 0.21 | Ovary | BJC 69:429 |
| Unknown | D5S419 | 26 | 3 | 0.12 | Cervix | CR 56:197 |
| Unknown | D5S419 | 28 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D5S419 | 16 | 3 | 0.19 | Head&Neck | CR 54:4756 |
| 14 | D5S19 | 23 | 13 | 0.57 | Cervix | CR 54:4481 |
| Unknown | D5S395 | 28 | 6 | 0.21 | Cervix | CR 56:197 |
| 13 | D5S20 | 21 | 1 | 0.05 | Ovary | IJC 54:546 |
| 11.0-13 | D5S21 | 9 | 5 | 0.56 | Cervix | CR 54:4481 |
| 11.0-13 | D5S21 | 9 | 5 | 0.56 | Cervix | CR 54:4481 |
| Unknown | Unknown | 4 | 0 | 0 | Brain | CR 49:6572 |
| Unknown | D5S1 | 5 | 1 | 0.2 | Breast | GCC 2:191 |
| Unknown | Unknown | 5 | 0 | 0 | Colon | BJC 67:1007 |
| Unknown | D5S1 | 3 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D5S1 | 28 | 7 | 0.25 | Esophageal | CR 54:2996 |
| Unknown | Unknown | 4 | 0 | 0 | Liver | BJC 67:1007 |
| Unknown | Unknown | 8 | 3 | 0.38 | Liver | BJC 64:1083 |
| Unknown | Unknown | 3 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | Unknown | 7 | 0 | 0 | Pancreas | BJC 65:809 |

Chromosome 5 - p Arm

| | | | | | | |
|---------|---------|-----|-----|------|--------|------------|
| Unknown | Unknown | 29 | 1 | 0.03 | Testis | GCC 13:249 |
| SUM | | 722 | 135 | 0.19 | | |

Chromosome 5 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|--------|-------|-------------|-----------|------------|------------|
| 15-21 | D5S491 | 1 | 0 | 0 | Lung | O 12:97 |
| 15-21 | D5S491 | 8 | 3 | 0.38 | Lung | O 12:97 |
| Unknown | D5S427 | 22 | 4 | 0.18 | Cervix | CR 56:197 |
| 11.2-13.3 | D5S6 | 30 | 1 | 0.03 | Breast | GE 5:554 |
| 11.2-13.3 | D5S6 | 4 | 2 | 0.5 | Colon | O 9:991 |
| 11.2-13.3 | D5S6 | 32 | 9 | 0.28 | Colon | CR 50:7166 |
| 11.2-13.3 | D5S6 | 17 | 1 | 0.06 | Pediatric | CR 50:3279 |
| 15-21 | D5S637 | 5 | 1 | 0.2 | Lung | O 12:97 |
| 15-21 | D5S637 | 9 | 6 | 0.67 | Lung | O 12:97 |
| 15-21 | D5S626 | 4 | 1 | 0.25 | Lung | O 12:97 |
| 15-21 | D5S626 | 17 | 9 | 0.53 | Lung | O 12:97 |
| Unknown | D5S107 | 19 | 2 | 0.11 | Leukemia | B 83:3449 |
| Unknown | D5S107 | 33 | 2 | 0.06 | Stomach | CR 56:612 |
| Unknown | D5S107 | 30 | 1 | 0.03 | Uterus | CR 54:4294 |
| Unknown | D5S428 | 20 | 7 | 0.35 | Stomach | CR 56:612 |
| Unknown | D5S37 | 2 | 0 | 0 | Colon | O 9:991 |
| Unknown | D5S37 | 11 | 6 | 0.55 | Colon | CR 50:7166 |
| Unknown | D5S37 | 28 | 7 | 0.25 | Esophageal | CR 54:2996 |
| Unknown | D5S37 | 3 | 0 | 0 | Liver | CCG 48:72 |
| Unknown | D5S37 | 12 | 5 | 0.42 | Sarcoma | CR 52:2419 |
| Unknown | D5S37 | 18 | 4 | 0.22 | Testis | GCC 13:249 |
| 15-21 | D5S644 | 9 | 3 | 0.33 | Lung | O 12:97 |
| 15-21 | D5S644 | 22 | 12 | 0.55 | Lung | O 12:97 |
| 14-21 | D5S71 | 10 | 1 | 0.1 | Colon | S 241:961 |
| 14-21 | D5S71 | 6 | 3 | 0.5 | Colon | CR 50:7166 |
| 14-21 | D5S71 | 8 | 3 | 0.38 | Colon | GCC 3:468 |
| 14-21 | D5S71 | 4 | 0 | 0 | Colon | CCG 48:167 |
| 14-21 | D5S71 | 21 | 1 | 0.05 | Ovary | IJC 54:546 |
| 14-21 | D5S71 | 1 | 1 | 1 | Pancreas | GCC 3:468 |
| 14-21 | D5S71 | 6 | 0 | 0 | Stomach | GCC 3:468 |
| 14-21 | D5S71 | 6 | 2 | 0.33 | Testis | GCC 13:249 |
| 14-21 | D5S71 | 1 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | D5S409 | 17 | 1 | 0.06 | Endocrine | CR 56:599 |
| Unknown | D5S409 | 17 | 6 | 0.35 | Stomach | CR 56:612 |
| Unknown | D5S409 | 9 | 6 | 0.67 | Stomach | CR 55:1933 |
| 14-21 | D5S82 | 15 | 4 | 0.27 | Colon | JJCR 82:10 |
| Unknown | D5S82 | 16 | 1 | 0.06 | Stomach | CR 54:41 |
| 21 | D5S421 | 25 | 5 | 0.2 | Bladder | CR 55:5213 |
| 21 | D5S421 | 20 | 5 | 0.25 | Head&Neck | CR 54:1152 |
| 21 | D5S421 | 5 | 0 | 0 | Kidney | GCC 12:76 |
| 21-22 | D5S81 | 13 | 0 | 0.23 | Cervix | BJC 67:71 |
| Unknown | D5S81 | 31 | 19 | 0.61 | Colon | CR 50:7166 |
| 21-22 | D5S81 | 5 | 4 | 0.8 | Colon | BJC 67:100 |
| 21-22 | D5S81 | 13 | 4 | 0.22 | Colon | JJCR 82:10 |
| Unknown | D5S81 | 28 | 5 | 0.18 | Kidney | CR 51:5817 |
| 21-22 | D5S81 | 13 | 3 | 0.23 | Kidney | CR 51:820 |

Chromosome 5 - q Arm

| | | | | | | |
|---------|---------|----|----|------|------------|------------|
| 21-22 | D5S81 | 6 | 1 | 0.17 | Liver | BJC 64:108 |
| 21-22 | D5S81 | 4 | 0 | 0 | Liver | BJC 67:100 |
| 21-22 | D5S81 | 5 | 1 | 0.2 | Pancreas | BJC 65:809 |
| 21-22 | D5S81 | 12 | 5 | 0.42 | Stomach | HG 92:244 |
| Unknown | D5S81 | 9 | 2 | 0.22 | Testis | GCC 13:249 |
| Unknown | L5.71 | 13 | 5 | 0.38 | Colon | JJCR 82:10 |
| Unknown | MCC | 13 | 5 | 0.38 | Colon | JJCR 82:10 |
| 21 | MCC | 4 | 1 | 0.25 | Colon | O 9:991 |
| 21 | MCC | 31 | 9 | 0.29 | Colon | CR 52:741 |
| 21 | MCC | 34 | 12 | 0.35 | Colon | EJC 30A:66 |
| 21 | MCC | 35 | 22 | 0.63 | Esophageal | CR 52:6525 |
| Unknown | L5.71 | 2 | 2 | 1 | Lung | CR 52:2478 |
| Unknown | L5.71 | 16 | 4 | 0.25 | Lung | CR 52:2478 |
| Unknown | L5.71 | 1 | 1 | 1 | Lung | CR 52:2478 |
| Unknown | L5.71 | 4 | 0 | 0 | Lung | CR 52:2478 |
| Unknown | MCC | 2 | 2 | 1 | Lung | CR 52:2478 |
| 21 | MCC | 41 | 9 | 0.22 | Lung | CR 55:220 |
| Unknown | MCC | 1 | 1 | 1 | Lung | CR 52:2478 |
| Unknown | MCC | 16 | 4 | 0.25 | Lung | CR 52:2478 |
| Unknown | MCC | 4 | 0 | 0 | Lung | CR 52:2478 |
| 21 | MCC | 7 | 7 | 1 | Stomach | JJCR 84:10 |
| 21 | MCC | 36 | 4 | 0.11 | Stomach | CL 96:169 |
| 21 | MCC | 8 | 0 | 0 | Stomach | CR 54:41 |
| 21 | MCC-APC | 25 | 7 | 0.28 | Breast | BJC 68:64 |
| 21 | MCC-APC | 6 | 0 | 0 | Cervix | GCC 9:119 |
| 21 | MCC-APC | 45 | 16 | 0.36 | Colon | GAST 104:1 |
| 21 | MCC-APC | 56 | 37 | 0.66 | Colon | O 8:1391 |
| 21 | MCC-APC | 26 | 20 | 0.77 | Esophageal | PNAS 89:33 |
| 21 | MCC-APC | 6 | 4 | 0.67 | Lung | CR 55:513 |
| 21 | MCC-APC | 5 | 2 | 0.4 | Lung | CR 52:1996 |
| 21 | MCC-APC | 7 | 0 | 0 | Uterus | GCC 9:119 |
| 21 | APC | 21 | 7 | 0.33 | Colon | CR 52:741 |
| Unknown | APC | 37 | 3 | 0.08 | Colon | EJC 30A:66 |
| Unknown | APC | 33 | 6 | 0.18 | Colon | EJC 30A:66 |
| 21 | APC | 21 | 5 | 0.24 | Esophageal | GCC 10:177 |
| 21 | APC | 36 | 24 | 0.67 | Esophageal | CR 52:6525 |
| 21 | APC | 19 | 1 | 0.05 | Liver | CR 54:281 |
| 21 | APC | 20 | 14 | 0.7 | Lung | O 12:97 |
| 21 | APC | 53 | 17 | 0.32 | Lung | CR 55:220 |
| 21 | APC | 7 | 5 | 0.71 | Lung | CR 54:1772 |
| 21 | APC | 8 | 3 | 0.38 | Lung | O 12:97 |
| Unknown | APC | 18 | 9 | 0.5 | Ovary | GO 55:245 |
| Unknown | APC | 15 | 3 | 0.2 | Prostate | JU 151:107 |
| 21 | APC | 7 | 3 | 0.43 | Prostate | BJU 73:390 |
| Unknown | APC | 13 | 4 | 0.31 | Stomach | LI 74:835 |
| Unknown | APC | 35 | 3 | 0.09 | Stomach | CL 96:169 |

Chromosome 5 - q Arm

| | | | | | | |
|---------|---------|----|----|------|-----------|------------|
| 21 | APC | 12 | 0 | 0 | Stomach | CR 54:41 |
| 21 | APC | 14 | 12 | 0.86 | Stomach | JJCR 84:10 |
| 21-22 | D5S346 | 18 | 0 | 0 | Endocrine | GCC 13:9 |
| 21-22 | D5S346 | 46 | 1 | 0.02 | Kidney | BJC 69:230 |
| 21-22 | D5S346 | 15 | 6 | 0.4 | Ovary | BJC 69:429 |
| 21-22 | D5S346 | 18 | 2 | 0.11 | Stomach | CR 56:612 |
| 21-22 | D5S346 | 22 | 1 | 0.05 | Uterus | CR 54:4294 |
| Unknown | Unknown | 19 | 3 | 0.16 | Colon | JJCR 82:10 |
| Unknown | Unknown | 10 | 2 | 0.2 | Kidney | CR 51:5817 |
| 21-22 | D5S84 | 11 | 2 | 0.18 | Breast | CR 50:7184 |
| 21-22 | D5S84 | 21 | 1 | 0.05 | Breast | CR 53:4356 |
| 21-22 | D5S84 | 3 | 1 | 0.33 | Cervix | GCC 9:119 |
| 21-22 | D5S84 | 8 | 0 | 0 | Cervix | BJC 67:71 |
| 21-22 | D5S84 | 5 | 2 | 0.4 | Kidney | CR 51:5817 |
| 21-22 | D5S84 | 5 | 2 | 0.4 | Kidney | CR 51:820 |
| 21-22 | D5S84 | 9 | 4 | 0.44 | Liver | CR 51:89 |
| 21-22 | D5S84 | 15 | 0 | 0 | Ovary | CR 51:5118 |
| 21-22 | D5S84 | 13 | 1 | 0.08 | Uterus | GCC 9:119 |
| 21-22 | D5S86 | 6 | 2 | 0.33 | Colon | GCC 3:468 |
| 21-22 | D5S86 | 4 | 1 | 0.25 | Pancreas | GCC 3:468 |
| 21-22 | D5S86 | 8 | 3 | 0.38 | Stomach | GCC 3:468 |
| 31-33 | D5S804 | 19 | 6 | 0.32 | Ovary | GO 55:245 |
| 21-22 | FBN2 | 15 | 6 | 0.4 | Ovary | BJC 69:429 |
| 21-22 | FBN2 | 15 | 4 | 0.27 | Stomach | CR 56:612 |
| 33-35 | D5S70 | 24 | 9 | 0.38 | Cervix | CR 54:4481 |
| 33-35 | D5S70 | 3 | 0 | 0 | Colon | GCC 3:468 |
| 33-35 | D5S70 | 3 | 0 | 0 | Pancreas | GCC 3:468 |
| 33-35 | D5S70 | 13 | 5 | 0.38 | Stomach | GCC 3:468 |
| 33-35 | D5S70 | 13 | 3 | 0.23 | Testis | O 9:2245 |
| 21-22 | D5S178 | 15 | 6 | 0.4 | Ovary | BJC 69:429 |
| 21-22 | D5S178 | 19 | 2 | 0.11 | Stomach | CR 56:612 |
| 31-32 | GRL | 8 | 0 | 0 | Ovary | CR 50:2724 |
| 21-22 | D5S210 | 15 | 6 | 0.4 | Ovary | BJC 69:429 |
| 21-22 | D5S210 | 19 | 5 | 0.26 | Stomach | CR 56:612 |
| 21-22 | D5S209 | 15 | 6 | 0.4 | Ovary | BJC 69:429 |
| 21-22 | D5S209 | 23 | 2 | 0.09 | Stomach | CR 56:612 |
| 34-qter | D5S22 | 18 | 0 | 0 | Prostate | G 11:530 |
| 34-qter | D5S2 | 3 | 1 | 0.33 | Cervix | CR 49:3598 |
| 34-qter | D5S2 | 2 | 0 | 0 | Colon | N 331:273 |
| 34-qter | D5S2 | 8 | 0 | 0 | Liver | JJCR 81:10 |
| 34-qter | D5S2 | 11 | 1 | 0.09 | Lung | PN 84:9252 |
| Unknown | D5S2 | 11 | 1 | 0.09 | Lung | PNAS 84:92 |
| Unknown | D5S2 | 5 | 1 | 0.2 | Stomach | CR 52:3099 |
| 34-qter | D5S2 | 2 | 0 | 0 | Stomach | CR 48:2988 |
| 34-qter | D5S2 | 1 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | D5S400 | 32 | 5 | 0.16 | Cervix | CR 56:197 |

Chromosome 5 - q Arm

| | | | | | | |
|---------|-----------|----|----|------|------------|------------|
| Unknown | D5S429 | 3 | 0 | 0 | Kidney | PNAS 92:28 |
| Unknown | D5S429 | 19 | 1 | 0.05 | Kidney | PNAS 92:28 |
| 35-qter | D5S43 | 17 | 1 | 0.06 | Colon | CR 50:7166 |
| 35-qter | D5S43 | 5 | 2 | 0.4 | Colon | BJC 67:100 |
| 35-qter | D5S43 | 31 | 9 | 0.29 | Colon | BJC 59:750 |
| 35-qter | D5S43 | 10 | 0 | 0 | Endocrine | N 328:524 |
| 35-qter | D5S43 | 10 | 3 | 0.3 | Liver | BJC 67:100 |
| 35-qter | D5S43 | 10 | 5 | 0.5 | Liver | BJC 64:108 |
| 35-qter | D5S43 | 7 | 0 | 0 | Pancreas | CR 54:2761 |
| 35-qter | D5S43 | 11 | 0 | 0 | Pancreas | BJC 65:809 |
| 35-qter | D5S43 | 10 | 1 | 0.1 | Stomach | BJC 59:750 |
| 35-qter | D5S43 | 34 | 8 | 0.24 | Stomach | CR 51:2926 |
| 35-qter | D5S43 | 25 | 5 | 0.2 | Testis | GCC 13:249 |
| 35-qter | D5S43 | 25 | 5 | 0.2 | Testis | GCC 13:249 |
| Unknown | Unknown | 12 | 2 | 0.17 | Brain | CR 50:5784 |
| 15-21 | Unknown | 6 | 0 | 0 | Cervix | BJC 67:71 |
| 21 | Unknown | 2 | 0 | 0 | Cervix | BJC 67:71 |
| Unknown | Unknown | 2 | 1 | 0.5 | Cervix | BJC 67:71 |
| Unknown | Unknown | 11 | 2 | 0.18 | Cervix | BJC 67:71 |
| Unknown | Unknown | 23 | 8 | 0.35 | Colon | JJCR 82:10 |
| Unknown | Unknown | 2 | 1 | 0.5 | Colon | JJCR 82:10 |
| Unknown | Unknown | 19 | 7 | 0.37 | Colon | JJCR 82:10 |
| Unknown | Unknown | 1 | 1 | 1 | Colon | JJCR 82:10 |
| Unknown | Unknown | 17 | 1 | 0.06 | Colon | JJCR 82:10 |
| Unknown | Unknown | 10 | 5 | 0.5 | Colon | JJCR 82:10 |
| Unknown | Unknown | 17 | 6 | 0.35 | Colon | JJCR 82:10 |
| Unknown | Unknown | 3 | 0 | 0 | Colon | JJCR 82:10 |
| 15-21 | Unknown | 1 | 1 | 1 | Colon | BJC 67:100 |
| 21 | Unknown | 4 | 3 | 0.75 | Colon | BJC 67:100 |
| 21 | C11p11 | 3 | 1 | 0.33 | Colon | N 331:273 |
| Unknown | CRI-L1265 | 16 | 1 | 0.06 | Colon | S 241:961 |
| Unknown | CRI-L45 | 21 | 2 | 0.1 | Colon | S 241:961 |
| 33 | CSF1R | 11 | 4 | 0.36 | Colon | CR 50:7166 |
| 21 | D5S141 | 3 | 2 | 0.67 | Colon | BJC 67:100 |
| Unknown | EMS | 9 | 2 | 0.22 | Colon | N 331:273 |
| 21-22 | LS5.34 | 5 | 3 | 0.6 | Colon | CR 50:7166 |
| 21 | D5S141 | 35 | 13 | 0.37 | Esophageal | GCC 10:177 |
| Unknown | D5S410 | 31 | 1 | 0.03 | Head&Neck | CR 54:4756 |
| Unknown | D5S410 | 35 | 4 | 0.11 | Head&Neck | CR 54:4756 |
| 21 | D5S133 | 6 | 1 | 0.17 | Kidney | CR 51:5817 |
| 21 | D5S140 | 16 | 3 | 0.19 | Kidney | CR 51:5817 |
| 21 | D5S141 | 26 | 8 | 0.31 | Kidney | CR 51:5817 |
| Unknown | D5S89 | 15 | 5 | 0.33 | Leukemia | B 83:199 |
| Unknown | Unknown | 10 | 1 | 0.1 | Liver | CR 51:89 |
| 21 | Unknown | 6 | 0 | 0 | Liver | BJC 67:100 |
| 15-21 | Unknown | 5 | 0 | 0 | Liver | BJC 67:100 |

Chromosome 5 - q Arm

| | | | | | | |
|---------------|-----------------|------|-----|------|----------|------------|
| 21 | D5S141 | 7 | 0 | 0 | Liver | BJC 67:100 |
| 21-21-34-qter | D5S43-D5S81 | 45 | 14 | 0.31 | Liver | JJCR 84:89 |
| 21 | ECB27 | 8 | 1 | 0.12 | Liver | BJC 64:108 |
| Unknown | FMS | 2 | 0 | 0 | Lung | PN 84:9252 |
| 13-12 | del-27 | 15 | 11 | 0.73 | Lung | O 12:97 |
| 13-12 | del-27 | 8 | 3 | 0.38 | Lung | O 12:97 |
| 13-12 | del-27 | 7 | 4 | 0.57 | Lung | CR 54:1772 |
| 21 | D5S122 | 11 | 5 | 0.45 | Ovary | GO 55:245 |
| Unknown | D5S6-D5S107-APC | 37 | 16 | 0.43 | Ovary | CR 53:2393 |
| 21-22 | IRF-1 | 15 | 6 | 0.4 | Ovary | BJC 69:429 |
| 15-21 | Unknown | 5 | 0 | 0 | Pancreas | BJC 65:809 |
| 15-21 | D5S98 | 13 | 3 | 0.23 | Stomach | HG 92:244 |
| 21-22 | IRF-1 | 22 | 6 | 0.27 | Stomach | CR 56:612 |
| 15-21 | D5S98 | 7 | 1 | 0.14 | Testis | GCC 13:249 |
| Unknown | FMS | 21 | 1 | 0.05 | Uterus | CR 54:4294 |
| SUM | | 2866 | 763 | 0.27 | | |

Chromosome 6 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|----------|---------|-------|-------------|-----------|------------|--------------|
| Unknown | D6S477 | 33 | 15 | 0.45 | Colon | CR 56:145 |
| 24-25 | F13A1 | 18 | 5 | 0.28 | Ovary | GO 55:245 |
| 24-25 | F13A1 | 18 | 4 | 0.22 | Ovary | BJC 69:429 |
| Unknown | D6S309 | 18 | 1 | 0.06 | Kidney | PNAS 92:2854 |
| Unknown | D6S309 | 4 | 1 | 0.25 | Kidney | PNAS 92:2854 |
| pter-p25 | D6F21S1 | 12 | 4 | 0.33 | Ovary | BJC 67:551 |
| Unknown | D6S89 | 14 | 1 | 0.07 | Ovary | BJC 67:551 |
| Unknown | D6S289 | 36 | 13 | 0.36 | Colon | CR 56:145 |
| Unknown | D6S260 | 32 | 14 | 0.44 | Cervix | CR 56:197 |
| 21.3-24 | D6S109 | 17 | 3 | 0.18 | Ovary | BJC 69:429 |
| 21.3-24 | D6S109 | 16 | 2 | 0.12 | Uterus | CR 54:4294 |
| Unknown | D6S276 | 20 | 10 | 0.5 | Cervix | CR 56:197 |
| Unknown | D6S299 | 21 | 1 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D6S299 | 20 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D6S299 | 26 | 2 | 0.08 | Melanoma | CR 56:589 |
| Unknown | D6S105 | 27 | 2 | 0.07 | Esophageal | IJC 69:1 |
| Unknown | D6S105 | 19 | 4 | 0.21 | Head&Neck | CR 54:1152 |
| Unknown | D6S105 | 26 | 2 | 0.08 | Uterus | CR 54:4294 |
| Unknown | D6S258 | 33 | 15 | 0.45 | Colon | CR 56:145 |
| Unknown | D6S10 | 35 | 4 | 0.11 | Breast | GCC 2:191 |
| Unknown | D6S10 | 32 | 9 | 0.28 | Cervix | CR 54:4481 |
| Unknown | D6S10 | 2 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | D6S10 | 13 | 0 | 0 | Prostate | G 11:530 |
| Unknown | D6S10 | 32 | 4 | 0.12 | Testis | O 9:2245 |
| 21.3 | HLA-DRB | 21 | 3 | 0.14 | Ovary | BJC 67:551 |
| 21.3 | HLA-DQA | 18 | 4 | 0.22 | Ovary | BJC 67:551 |
| 21.3 | HLA-DQA | 3 | 0 | 0 | Testis | CCG 52:72 |
| 21.3 | HLA-DQA | 1 | 0 | 0 | Testis | CCG 52:72 |
| 21.3 | HLA-DQA | 4 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | TNFA | 33 | 14 | 0.42 | Colon | CR 56:145 |
| Unknown | D6S291 | 12 | 1 | 0.09 | Brain | CR 55:4696 |
| Unknown | D6S291 | 12 | 1 | 0.08 | Brain | CR 55:4696 |
| Unknown | D6S29 | 17 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D6S29 | 22 | 3 | 0.14 | Kidney | CR 51:5817 |
| Unknown | D6S29 | 13 | 1 | 0.08 | Liver | CR 51:89 |
| Unknown | D6S29 | 12 | 6 | 0.5 | Ovary | CR 51:5118 |
| Unknown | D6S29 | 19 | 4 | 0.21 | Ovary | IJC 54:546 |
| Unknown | D6S29 | 9 | 0 | 0 | Ovary | CR 50:2724 |
| Unknown | D6S29 | 16 | 3 | 0.19 | Stomach | GCC 14:28 |
| Unknown | D6S271 | 44 | 17 | 0.39 | Colon | CR 56:145 |
| Unknown | D6S282 | 32 | 6 | 0.19 | Cervix | CR 56:197 |
| Unknown | D6S282 | 22 | 0 | 0 | Endocrine | CR 56:599 |
| 12.0-11 | KRAS P1 | 8 | 1 | 0.12 | Ovary | BJC 67:551 |
| 12.0-11 | KRAS P1 | 2 | 0 | 0 | Uterus | CR 51:5632 |
| 11.2 | D6S294 | 37 | 11 | 0.3 | Ovary | GCC 15:223 |
| Unknown | D6S257 | 42 | 13 | 0.31 | Colon | CR 56:145 |

Chromosome 6 - p Arm

| | | | | | | |
|---------|---------------------|------|-----|------|------------|-------------|
| Unknown | D6S257 | 42 | 13 | 0.31 | Colon | CR 56:145 |
| Unknown | Unknown | 14 | 1 | 0.07 | Brain | CR 50:5783 |
| Unknown | D6S40 | 24 | 2 | 0.08 | Brain | CR 49:6572 |
| Unknown | D6S40 | 28 | 5 | 0.18 | Breast | CR 50:7184 |
| Unknown | D6S40 | 3 | 1 | 0.33 | Cervix | GCC 9:119 |
| Unknown | D6S344 | 22 | 0 | 0 | Endocrine | CR 56:599 |
| Unknown | D6S139 | 49 | 12 | 0.24 | Esophageal | GCC 10:177 |
| Unknown | D6S40 | 23 | 7 | 0.3 | Esophageal | CR 54:2996 |
| Unknown | D6S40 | 14 | 1 | 0.07 | Esophageal | CR 51:2113 |
| Unknown | D6S265 | 19 | 8 | 0.42 | Head&Neck | CR 54:1152 |
| Unknown | TCTE | 14 | 2 | 0.14 | Head&Neck | CR 54:1152 |
| 21.3 | D6S138 | 34 | 6 | 0.18 | Kidney | CR 51:5817 |
| 21.2 | D6S160 | 23 | 5 | 0.22 | Kidney | CR 51:5817 |
| Unknown | D6S4-C2-D6S1 | 19 | 5 | 0.26 | Kidney | CR 49:5087 |
| Unknown | D6S40 | 14 | 3 | 0.21 | Kidney | CR 51:820 |
| Unknown | Unknown | 20 | 15 | 0.75 | Lung | CR 54:2322 |
| Unknown | D6S4-C2-D6S1 | 1 | 1 | 1 | Lung | CR 49:5087 |
| Unknown | D6S40 | 22 | 4 | 0.18 | Lung | CR 52:2478 |
| 21-27 | Unknown | 7 | 2 | 0.29 | Ovary | O 5:219 |
| Unknown | D6S114E | 3 | 0 | 0 | Ovary | BJC 67:551 |
| Unknown | D6S40 | 7 | 4 | 0.57 | Ovary | O 5:219 |
| Unknown | F13A1-D6S249 | 17 | 4 | 0.24 | Ovary | BJC 72:1330 |
| 12-21.3 | FTHP1 | 14 | 5 | 0.36 | Ovary | BJC 69:429 |
| 12-21.2 | FTHP1 | 10 | 2 | 0.2 | Ovary | BJC 67:551 |
| Unknown | PIM-HLA-D6S91-D6S41 | 34 | 21 | 0.62 | Ovary | CR 53:2393 |
| Unknown | D6S4-C2-D6S1 | 2 | 1 | 0.5 | Sarcoma | CR 49:5087 |
| Unknown | D6S40 | 13 | 7 | 0.54 | Sarcoma | CR 52:2419 |
| 21.3 | HLA-DXA | 2 | 0 | 0 | Testis | CCG 52:72 |
| 21.3 | HLA-DXA | 2 | 0 | 0 | Testis | CCG 52:72 |
| 21.3 | HLA-DXA | 1 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D6S40 | 5 | 0 | 0 | Uterus | GCC 9:119 |
| SUM | | 1383 | 328 | 0.24 | | |

Chromosome 6 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|--------|-------|-------------|-----------|------------|------------|
| Unknown | D6Z1 | 8 | 2 | 0.25 | Ovary | BJC 67:551 |
| Unknown | D6Z1 | 22 | 0 | 0 | Stomach | GCC 14:28 |
| 13 | D6S313 | 30 | 3 | 0.1 | Breast | BJC 71:290 |
| 13 | D6S254 | 5 | 0 | 0 | Breast | BJC 73:144 |
| 13 | D6S280 | 20 | 8 | 0.4 | Breast | BJC 71:290 |
| 14-15 | D6S284 | 26 | 5 | 0.19 | Breast | BJC 71:290 |
| 14-15 | D6S284 | 5 | 1 | 0.2 | Breast | BJC 73:144 |
| 16.3-21 | D6S286 | 27 | 8 | 0.3 | Breast | BJC 71:290 |
| 14-15 | D6S286 | 11 | 4 | 0.36 | Breast | BJC 73:144 |
| 16.3-21 | D6S286 | 17 | 1 | 0.06 | Endocrine | CR 56:599 |
| 14-15 | D6S286 | 17 | 8 | 0.47 | Ovary | GCC 15:223 |
| Unknown | EDDR1 | 14 | 4 | 0.29 | Ovary | GCC 15:223 |
| 22.3-23.1 | D6S270 | 5 | 1 | 0.2 | Breast | BJC 73:144 |
| 22.3-23.1 | D6S270 | 22 | 7 | 0.32 | Ovary | GCC 15:223 |
| Unknown | D6S310 | 23 | 7 | 0.3 | Endocrine | CR 56:599 |
| Unknown | D6S310 | 33 | 10 | 0.3 | Ovary | GCC 15:223 |
| Unknown | D6S311 | 27 | 5 | 0.19 | Cervix | CR 56:197 |
| Unknown | D6S311 | 6 | 4 | 0.67 | Endocrine | CR 56:599 |
| Unknown | D6S311 | 32 | 10 | 0.31 | Ovary | GCC 15:223 |
| Unknown | D6S194 | 4 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S194 | 16 | 5 | 0.31 | Ovary | GCC 15:223 |
| Unknown | D6S194 | 16 | 4 | 0.25 | Ovary | CR 52:5815 |
| Unknown | D6S142 | 30 | 8 | 0.27 | Kidney | CR 51:5817 |
| Unknown | D6S142 | 6 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S142 | 12 | 7 | 0.58 | Ovary | CR 52:5815 |
| Unknown | D6S142 | 6 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S161 | 27 | 6 | 0.22 | Kidney | CR 51:5817 |
| Unknown | D6S161 | 11 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S161 | 17 | 7 | 0.41 | Ovary | CR 52:5815 |
| Unknown | D6S161 | 5 | 1 | 0.2 | Ovary | CR 52:5815 |
| Unknown | D6S251 | 67 | 16 | 0.24 | Breast | BJC 73:144 |
| Unknown | D6S251 | 36 | 13 | 0.36 | Colon | CR 56:145 |
| Unknown | D6S251 | 5 | 0 | 0 | Ovary | CR 55:2169 |
| Unknown | D6S251 | 28 | 0 | 0 | Ovary | CR 55:2169 |
| 13 | D6S239 | 27 | 9 | 0.33 | Breast | BJC 71:290 |
| 13 | D6S239 | 10 | 3 | 0.3 | Ovary | CR 55:2169 |
| 13 | D6S239 | 27 | 1 | 0.04 | Ovary | CR 55:2169 |
| 14-16.2 | D6S252 | 48 | 11 | 0.23 | Breast | BJC 73:144 |
| 14-16.2 | D6S252 | 27 | 2 | 0.07 | Stomach | GCC 14:28 |
| 14 | D6S300 | 32 | 11 | 0.34 | Breast | BJC 71:290 |
| 14 | D6S300 | 17 | 3 | 0.18 | Endocrine | CR 56:599 |
| 16.3 | D6S246 | 27 | 9 | 0.33 | Breast | BJC 71:290 |
| Unknown | D6S246 | 16 | 1 | 0.06 | Ovary | CR 55:2169 |
| Unknown | D6S246 | 9 | 2 | 0.22 | Ovary | CR 55:2169 |
| 16.3-21 | D6S249 | 28 | 9 | 0.32 | Breast | BJC 73:144 |
| 16.3-21 | D6S283 | 30 | 5 | 0.17 | Breast | BJC 71:290 |

Chromosome 6 - q Arm

| | | | | | | |
|-----------|--------|----|----|------|---------------|-------------|
| 16.3-21 | D6S283 | 10 | 2 | 0.2 | Stomach | GCC 14:28 |
| Unknown | D6S268 | 4 | 1 | 0.25 | Kidney | GCC 12:76 |
| Unknown | D6S268 | 9 | 1 | 0.11 | Stomach | GCC 14:28 |
| 16.3-21 | D6S302 | 30 | 13 | 0.43 | Breast | BJC 73:144 |
| 21-23.3 | D6S261 | 34 | 7 | 0.21 | Breast | BJC 71:290 |
| 21-23 | D6S261 | 25 | 5 | 0.2 | Breast | BJC 73:144 |
| 21-23 | D6S287 | 33 | 4 | 0.12 | Breast | BJC 73:144 |
| 21-23 | D6S287 | 22 | 4 | 0.18 | Endocrine | CR 56:599 |
| Unknown | D6S267 | 18 | 5 | 0.28 | Ovary | GCC 15:223 |
| 22.3-23.1 | ARG | 12 | 2 | 0.17 | Breast | BJC 73:144 |
| 22.3-23.1 | ARG | 15 | 0 | 0 | Stomach | GCC 14:28 |
| 22.3-23.1 | D6S262 | 28 | 10 | 0.36 | Breast | BJC 73:144 |
| Unknown | D6S262 | 35 | 12 | 0.34 | Colon | CR 56:145 |
| Unknown | D6S262 | 17 | 1 | 0.06 | Head&Neck | CR 54:4756 |
| Unknown | D6S262 | 21 | 3 | 0.14 | Head&Neck | CR 54:4756 |
| Unknown | D6S32 | 18 | 9 | 0.5 | Stomach | GCC 14:28 |
| 23.1 | D6S87 | 17 | 6 | 0.35 | Ovary | BJC 69:429 |
| 23.1 | D6S87 | 18 | 3 | 0.17 | Ovary | CR 55:2169 |
| 23.1 | D6S87 | 7 | 2 | 0.29 | Ovary | CR 55:2169 |
| 23.1 | D6S87 | 20 | 1 | 0.05 | Uterus | CR 54:4294 |
| 22-23 | MYB | 10 | 0 | 0 | Cervix | CR 49:3598 |
| 22-23 | MYB | 11 | 2 | 0.18 | Colon | N 331:273 |
| 22-23 | MYB | 20 | 2 | 0.1 | Colon | IJC 53:382 |
| 22-23 | MYB | 13 | 0 | 0 | Liver | JJCR 81:108 |
| 22-23 | MYB | 18 | 3 | 0.17 | Lung | PN 84:9252 |
| 22-23 | MYB | 7 | 3 | 0.43 | Melanoma | CR 51:5449 |
| 22-23 | MYB | 5 | 0 | 0 | Neuroblastoma | CR 49:1095 |
| 22-23 | MYB | 9 | 6 | 0.67 | Ovary | BJC 67:551 |
| 22-23 | MYB | 4 | 1 | 0.25 | Ovary | GO 55:245 |
| 22-23 | MYB | 8 | 1 | 0.12 | Ovary | CR 50:2724 |
| 22-23 | MYB | 7 | 0 | 0 | Prostate | G 11:530 |
| 22-23 | MYB | 20 | 6 | 0.3 | Sarcoma | CR 52:2419 |
| 22-23 | MYB | 12 | 1 | 0.08 | Stomach | GCC 14:28 |
| 22-23 | MYB | 13 | 0 | 0 | Stomach | CR 48:2988 |
| 22-23 | MYB | 12 | 2 | 0.17 | Stomach | CR 52:3099 |
| 22-23 | MYB | 7 | 1 | 0.14 | Uterus | CR 51:5632 |
| Unknown | D6S250 | 24 | 1 | 0.04 | Ovary | CR 55:2169 |
| Unknown | D6S250 | 10 | 3 | 0.3 | Ovary | CR 55:2169 |
| Unknown | D6S136 | 16 | 2 | 0.12 | Kidney | CR 51:5817 |
| Unknown | D6S136 | 3 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S136 | 9 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S441 | 11 | 1 | 0.09 | Endocrine | CR 56:599 |
| Unknown | D6S441 | 30 | 13 | 0.43 | Ovary | GCC 15:223 |
| 24-27 | ESR | 16 | 0 | 0 | Cervix | CGC 79:74 |
| 24-27 | ESR | 8 | 3 | 0.38 | Colon | GCC 3:468 |
| 24-27 | ESR | 8 | 4 | 0.5 | Melanoma | CR 51:5449 |

Chromosome 6 - q Arm

| | | | | | | |
|---------|--------|----|----|------|-----------|--------------|
| 24-27 | ESR | 23 | 6 | 0.26 | Ovary | CR 55:2169 |
| 24-27 | ESR | 6 | 1 | 0.17 | Ovary | CR 55:2169 |
| 24-27 | ESR | 13 | 2 | 0.15 | Ovary | GO 47:137 |
| 24-27 | ESR | 14 | 9 | 0.64 | Ovary | CR 50:2724 |
| 24-27 | ESR | 22 | 1 | 0.05 | Ovary | TJC 54:546 |
| 24-27 | ESR | 15 | 10 | 0.67 | Ovary | BJC 67:551 |
| 24-27 | ESR | 18 | 10 | 0.56 | Ovary | GCC 15:223 |
| 24-27 | ESR | 1 | 1 | 1 | Pancreas | GCC 3:468 |
| 24-27 | ESR | 6 | 0 | 0 | Stomach | GCC 3:468 |
| 24-27 | ESR | 16 | 0 | 0 | Stomach | CR 51:2926 |
| 24-27 | ESR | 6 | 1 | 0.17 | Uterus | CR 51:5632 |
| Unknown | D6S415 | 22 | 9 | 0.41 | Ovary | GCC 15:223 |
| 25.2 | D6S255 | 9 | 3 | 0.33 | Breast | BJC 73:144 |
| 25.2 | D6S255 | 23 | 2 | 0.09 | Head&Neck | CR 54:1152 |
| 25.2 | D6S255 | 7 | 3 | 0.43 | Ovary | CR 55:2169 |
| 25.2 | D6S255 | 11 | 2 | 0.18 | Ovary | CR 55:2169 |
| Unknown | D6S305 | 29 | 4 | 0.14 | Cervix | CR 56:197 |
| Unknown | D6S305 | 40 | 16 | 0.4 | Colon | CR 56:145 |
| Unknown | D6S305 | 15 | 2 | 0.13 | Endocrine | CR 56:599 |
| Unknown | D6S305 | 29 | 9 | 0.31 | Melanoma | CR 56:589 |
| Unknown | D6S305 | 35 | 13 | 0.37 | Ovary | GCC 15:223 |
| Unknown | IGF2R | 16 | 11 | 0.69 | Liver | O 10:1725 |
| Unknown | IGF2R | 2 | 0 | 0 | Ovary | CR 55:2169 |
| Unknown | IGF2R | 4 | 1 | 0.25 | Ovary | CR 55:2169 |
| Unknown | IGF2R | 18 | 5 | 0.28 | Ovary | GCC 15:223 |
| Unknown | IGF2R | 11 | 3 | 0.27 | Ovary | CR 55:2169 |
| Unknown | IGF2R | 7 | 0 | 0 | Ovary | CR 55:2169 |
| Unknown | IGF2R | 18 | 2 | 0.11 | Stomach | GCC 14:28 |
| Unknown | IGF2R | 10 | 2 | 0.2 | Uterus | CR 54:4294 |
| 26-27 | PLG | 2 | 0 | 0 | Liver | PNAS 86:8852 |
| Unknown | D6S195 | 14 | 5 | 0.36 | Ovary | CR 52:5815 |
| Unknown | D6S195 | 2 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S195 | 5 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S191 | 16 | 3 | 0.19 | Ovary | CR 52:5815 |
| Unknown | D6S191 | 5 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | D6S191 | 8 | 0 | 0 | Ovary | CR 52:5815 |
| 26 | D6S186 | 25 | 5 | 0.2 | Breast | BJC 71:290 |
| 26 | D6S186 | 34 | 7 | 0.21 | Kidney | CR 51:5817 |
| 26 | D6S186 | 19 | 8 | 0.42 | Ovary | CR 52:5815 |
| 26 | D6S186 | 19 | 8 | 0.42 | Ovary | GCC 15:223 |
| 26 | D6S186 | 6 | 1 | 0.17 | Ovary | CR 52:5815 |
| 26 | D6S186 | 5 | 0 | 0 | Ovary | CR 52:5815 |
| Unknown | SOD2 | 11 | 3 | 0.27 | Melanoma | CR 51:5449 |
| Unknown | SOD2 | 8 | 4 | 0.5 | Ovary | BJC 67:551 |
| Unknown | SOD2 | 23 | 5 | 0.22 | Stomach | GCC 14:28 |
| Unknown | D6S264 | 32 | 13 | 0.41 | Colon | CR 56:145 |

Chromosome 6 - q Arm

| | | | | | | |
|---------|--------|----|----|------|------------|------------|
| Unknown | D6S264 | 12 | 5 | 0.42 | Endocrine | CR 56:599 |
| Unknown | D6S264 | 15 | 5 | 0.33 | Head&Neck | CR 54:1152 |
| Unknown | D6S264 | 3 | 1 | 0.33 | Kidney | GCC 12:76 |
| Unknown | D6S264 | 34 | 12 | 0.35 | Ovary | GCC 15:223 |
| Unknown | D6S503 | 34 | 14 | 0.41 | Colon | CR 56:145 |
| 21-qter | D6S2 | 8 | 3 | 0.38 | Colon | GCC 3:468 |
| 21-qter | D6S2 | 19 | 4 | 0.21 | Ovary | IJC 52:575 |
| 21-qter | D6S2 | 5 | 3 | 0.6 | Ovary | O 5:219 |
| 21-qter | D6S2 | 21 | 1 | 0.05 | Ovary | IJC 54:546 |
| 21-qter | D6S2 | 1 | 1 | 1 | Pancreas | GCC 3:468 |
| 21-qter | D6S2 | 6 | 0 | 0 | Stomach | GCC 3:468 |
| Unknown | D6S133 | 22 | 14 | 0.64 | Ovary | BJC 67:551 |
| Unknown | D6S193 | 56 | 9 | 0.16 | Esophageal | GCC 10:177 |
| Unknown | D6S193 | 38 | 23 | 0.61 | Ovary | GCC 15:223 |
| 27 | D6S297 | 19 | 4 | 0.21 | Breast | BJC 71:290 |
| Unknown | D6S297 | 27 | 14 | 0.52 | Ovary | GCC 15:223 |
| Unknown | TCPI0 | 17 | 12 | 0.71 | Ovary | BJC 67:551 |
| 27 | D6S44 | 56 | 4 | 0.07 | Breast | CR 53:4356 |
| 27 | D6S44 | 12 | 4 | 0.33 | Breast | GCC 2:191 |
| 27 | D6S44 | 29 | 4 | 0.14 | Ovary | IJC 54:546 |
| 27 | D6S44 | 18 | 0 | 0 | Testis | NI 73:606 |
| Unknown | D6S149 | 19 | 6 | 0.32 | Ovary | GCC 15:223 |
| Unknown | D6S149 | 8 | 2 | 0.25 | Ovary | CR 52:5815 |
| Unknown | D6S149 | 9 | 1 | 0.11 | Ovary | CR 52:5815 |
| Unknown | D6S149 | 22 | 10 | 0.45 | Ovary | CR 52:5815 |
| Unknown | D6S37 | 4 | 1 | 0.25 | Breast | CR 53:3804 |
| Unknown | D6S37 | 23 | 2 | 0.09 | Breast | CR 50:7184 |
| Unknown | D6S37 | 20 | 4 | 0.2 | Cervix | CR 54:4481 |
| Unknown | D6S37 | 5 | 2 | 0.4 | Cervix | GCC 9:119 |
| Unknown | D6S37 | 5 | 4 | 0.8 | Endocrine | CR 56:599 |
| Unknown | D6S37 | 13 | 2 | 0.15 | Esophageal | CR 54:2996 |
| Unknown | D6S37 | 13 | 4 | 0.31 | Kidney | CR 51:820 |
| Unknown | D6S37 | 25 | 9 | 0.36 | Kidney | CR 51:5817 |
| Unknown | D6S37 | 29 | 1 | 0.03 | Lung | CR 52:2478 |
| Unknown | D6S37 | 10 | 4 | 0.4 | Melanoma | CR 51:5449 |
| Unknown | D6S37 | 13 | 8 | 0.62 | Ovary | BJC 67:551 |
| Unknown | D6S37 | 29 | 5 | 0.17 | Ovary | CR 51:5118 |
| Unknown | D6S37 | 14 | 3 | 0.21 | Sarcoma | CR 52:2419 |
| Unknown | D6S37 | 30 | 11 | 0.37 | Stomach | GCC 14:28 |
| Unknown | D6S37 | 29 | 2 | 0.07 | Testis | O 9:2245 |
| Unknown | D6S37 | 11 | 1 | 0.09 | Uterus | GCC 9:119 |
| 27 | D6S446 | 24 | 11 | 0.46 | Ovary | GCC 15:223 |
| Unknown | D6S132 | 15 | 11 | 0.73 | Ovary | BJC 67:551 |
| 27 | D6S281 | 27 | 5 | 0.19 | Breast | BJC 71:290 |
| 27 | D6S281 | 39 | 13 | 0.33 | Ovary | GCC 15:223 |
| 27 | D6S281 | 39 | 13 | 0.33 | Ovary | GCC 15:223 |

Chromosome 6 - q Arm

| | | | | | | |
|-----------|----------------------|------|-----|------|----------|--------------|
| Unknown | Unknown | 22 | 2 | 0.09 | Brain | CR 50:5784 |
| 27 | D6S193 | 29 | 8 | 0.28 | Breast | BJC 71:290 |
| 25.2-27 | D6S220 | 19 | 5 | 0.26 | Breast | BJC 71:290 |
| 14-15 | D6S330 | 12 | 6 | 0.5 | Breast | BJC 71:290 |
| 23.3-25.2 | D6S355 | 24 | 4 | 0.17 | Breast | BJC 71:290 |
| 21-23.3 | D6S357 | 20 | 2 | 0.1 | Breast | BJC 71:290 |
| 21-23.3 | D6S359 | 37 | 8 | 0.22 | Breast | BJC 71:290 |
| 14-16 | D6S39 | 1 | 1 | 1 | Breast | CR 53:3804 |
| 16-21 | D6S48 | 3 | 1 | 0.33 | Breast | CR 53:3804 |
| 25.1 | ER | 47 | 9 | 0.19 | Breast | BJC 71:448 |
| 24 | D6S135 | 9 | 5 | 0.56 | Kidney | CR 51:5817 |
| 21 | D6S154 | 15 | 3 | 0.2 | Kidney | CR 51:5817 |
| 27 | D6S156 | 27 | 7 | 0.26 | Kidney | CR 51:5817 |
| 23 | D6S164 | 11 | 1 | 0.09 | Kidney | CR 51:5817 |
| Unknown | D6S281-D6S311-D6S278 | 22 | 4 | 0.18 | Kidney | PNAS 92:2854 |
| Unknown | D6S281-D6S311-D6S278 | 6 | 1 | 0.17 | Kidney | PNAS 92:2854 |
| Unknown | Unknown | 20 | 15 | 0.75 | Lung | CR 54:2322 |
| 12.0-21 | CGA | 13 | 3 | 0.23 | Melanoma | CR 51:5449 |
| Unknown | D6S29 | 4 | 0 | 0 | Melanoma | CR 51:5449 |
| 27 | Unknown | 130 | 4 | 0.03 | Ovary | IJC 52:575 |
| Unknown | Unknown | 23 | 1 | 0.04 | Ovary | IJC 52:575 |
| 13 | ACTBP2 | 21 | 7 | 0.33 | Ovary | GO 55:245 |
| Unknown | D6S125 | 17 | 4 | 0.24 | Ovary | BJC 67:551 |
| 27 | D6S193 | 10 | 1 | 0.1 | Ovary | CR 52:5815 |
| 27 | D6S193 | 11 | 1 | 0.09 | Ovary | CR 52:5815 |
| 27 | D6S193 | 23 | 11 | 0.48 | Ovary | CR 52:5815 |
| Unknown | D6S225 | 26 | 0 | 0 | Ovary | CR 55:2169 |
| Unknown | D6S225 | 13 | 2 | 0.15 | Ovary | CR 55:2169 |
| 23.3-25.2 | D6S355 | 6 | 0 | 0 | Ovary | CR 55:2169 |
| Unknown | D6S366 | 14 | 2 | 0.14 | Ovary | CR 55:2169 |
| Unknown | D6S366 | 19 | 1 | 0.05 | Ovary | CR 55:2169 |
| Unknown | D6S86 | 22 | 13 | 0.59 | Ovary | BJC 67:551 |
| Unknown | HCG-A | 8 | 4 | 0.5 | Ovary | BJC 67:551 |
| Unknown | IGF2R-D6S:251-249 | 17 | 3 | 0.18 | Ovary | BJC 72:1330 |
| Unknown | MYB-DMDL-SOD2-D6S44 | 37 | 21 | 0.57 | Ovary | CR 53:2393 |
| 27 | Unknown | 3 | 0 | 0 | Pancreas | CR 54:2761 |
| 21.3 | TNFB | 13 | 2 | 0.15 | Uterus | CR 54:4294 |
| SUM | | 3960 | 978 | 0.25 | | |

Chromosome 7 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|----------|---------|-------|-------------|-----------|------------|--------------|
| 22 | D7S21 | 36 | 5 | 0.14 | Stomach | CR 51:2926 |
| 22 | D7S21 | 19 | 1 | 0.05 | Stomach | HG 92:244 |
| 22 | D7S21 | 26 | 1 | 0.04 | Testis | GCC 13:249 |
| Unknown | D7S517 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D7S517 | 21 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D7S370 | 18 | 3 | 0.17 | Brain | CR 50:5784 |
| Unknown | D7S370 | 8 | 1 | 0.12 | Breast | CR 50:7184 |
| Unknown | D7S370 | 24 | 2 | 0.08 | Cervix | CR 54:4481 |
| Unknown | D7S370 | 24 | 5 | 0.21 | Esophageal | CR 54:2996 |
| Unknown | D7S370 | 10 | 2 | 0.2 | Kidney | CR 51:820 |
| Unknown | D7S370 | 10 | 0 | 0 | Liver | CR 51:89 |
| Unknown | D7S370 | 18 | 5 | 0.28 | Lung | CR 52:2478 |
| Unknown | D7S370 | 26 | 4 | 0.15 | Ovary | IJC 54:546 |
| Unknown | D7S370 | 2 | 2 | 1 | Pancreas | CR 54:2761 |
| Unknown | D7S370 | 23 | 1 | 0.04 | Testis | O 9:2245 |
| Unknown | D7S370 | 20 | 2 | 0.1 | Esophageal | GCC 10:177 |
| Unknown | D7S370 | 10 | 1 | 0.1 | Esophageal | CR 51:2113 |
| Unknown | D7S370 | 7 | 3 | 0.43 | Ovary | CR 51:5118 |
| Unknown | D7S370 | 17 | 2 | 0.12 | Sarcoma | CR 52:2419 |
| Unknown | D7S371 | 21 | 1 | 0.05 | Breast | CR 53:4356 |
| Unknown | D7S371 | 2 | 0 | 0 | Ovary | CR 51:5118 |
| 13.0-12 | EGFR | 8 | 1 | 0.12 | Cervix | CR 49:3598 |
| 13.0-12 | EGFR | 4 | 0 | 0 | Liver | PNAS 86:8852 |
| 11.2-12 | EGFR | 18 | 3 | 0.17 | Ovary | BJC 69:429 |
| 11.2-12 | EGFR | 14 | 0 | 0 | Ovary | CR 49:1220 |
| 13.0-12 | EGFR | 5 | 1 | 0.2 | Ovary | CR 50:2724 |
| Unknown | EGFR | 11 | 0 | 0 | Ovary | CR 50:2724 |
| 13.0-12 | EGFR | 13 | 1 | 0.08 | Prostate | G 11:530 |
| Unknown | EGFR | 10 | 0 | 0 | Uterus | CR 51:5632 |
| 13.0-12 | EGFR | 16 | 2 | 0.12 | Uterus | CR 54:4294 |
| 13.0-12 | EGFR | 16 | 2 | 0.12 | Uterus | CR 54:4294 |
| Unknown | D7S372 | 12 | 0 | 0 | Brain | CR 49:6572 |
| Unknown | D7S493 | 32 | 2 | 0.06 | Cervix | CR 56:197 |
| Unknown | D7S507 | 25 | 1 | 0.04 | Cervix | CR 56:197 |
| 2.2-ter | Unknown | 35 | 1 | 0.03 | Colon | BJC 59:750 |
| Unknown | D7S481 | 22 | 16 | 0.73 | Colon | CR 56:145 |
| Unknown | D7S507 | 20 | 1 | 0.05 | Endocrine | CR 56:599 |
| Unknown | D7S481 | 21 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D7S481 | 22 | 1 | 0.18 | Head&Neck | CR 54:4756 |
| Unknown | D7S507 | 26 | 6 | 0.23 | Head&Neck | CR 54:1152 |
| pter-q22 | Unknown | 11 | 1 | 0.09 | Liver | BJC 64:1083 |
| pter-q22 | Unknown | 13 | 1 | 0.08 | Liver | BJC 67:1007 |
| Unknown | D7S481 | 30 | 1 | 0.03 | Melanoma | CR 56:589 |
| Unknown | D7S135 | 11 | 4 | 0.36 | Ovary | CR 53:2393 |
| pter-q22 | Unknown | 10 | 0 | 0 | Pancreas | BJC 65:809 |
| 2.2-ter | Unknown | 10 | 0 | 0 | Stomach | BJC 59:750 |

Chromosome 7 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|----------|-------|-------------|-----------|-------------------|---------------|
| 21.3-22.1 | COL1A2 | 29 | 1 | 0.03 | Breast | GCC 2:191 |
| 21.3-22.1 | COL1A2 | 6 | 0 | 0 | Cervix | CR 49:3598 |
| 21.3-22.1 | COL1A2 | 12 | 0 | 0 | Colon | N 331:273 |
| 21.3-22.1 | COL1A2 | 15 | 1 | 0.07 | Liver | JJCR 81:108 |
| 21.3-22.1 | COL1A2 | 11 | 0 | 0 | Liver | CCG 48:72 |
| 21.3-22.1 | COL1A2 | 5 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| 21.3-22.1 | COL1A2 | 10 | 2 | 0.2 | Stomach | CR 52:3099 |
| 21.3-22.1 | COL1A2 | 6 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | D7S527 | 21 | 4 | 0.19 | Breast | PNAS 91:12155 |
| Unknown | D7S527 | 8 | 1 | 0.12 | Colon | CR 55:1347 |
| Unknown | D7S527 | 9 | 2 | 0.22 | Head&Neck | CR 55:1347 |
| Unknown | D7S527 | 8 | 1 | 0.12 | Prostate | CR 54:6370 |
| Unknown | D7S479 | 12 | 1 | 0.08 | Breast | PNAS 91:12155 |
| Unknown | D7S479 | 17 | 0 | 0 | Endocrine | CR 56:599 |
| Unknown | D7S518 | 27 | 6 | 0.22 | Breast | PNAS 91:12155 |
| Unknown | D7S518 | 8 | 0 | 0 | Colon | CR 55:1347 |
| Unknown | D7S518 | 13 | 2 | 0.15 | Head&Neck | CR 55:1347 |
| Unknown | D7S518 | 11 | 3 | 0.27 | Prostate | CR 54:6370 |
| Unknown | D7S515 | 13 | 3 | 0.23 | Breast | PNAS 91:12155 |
| Unknown | D7S496 | 17 | 8 | 0.47 | Breast | PNAS 91:12155 |
| Unknown | D7S496 | 13 | 4 | 0.31 | Colon | CR 55:1347 |
| Unknown | D7S496 | 10 | 1 | 0.1 | Head&Neck | CR 55:1347 |
| Unknown | D7S496 | 8 | 3 | 0.38 | Prostate | CR 54:6370 |
| 22.3-31.2 | D7S13 | 21 | 4 | 0.19 | Breast | PNAS 91:12155 |
| Unknown | D7S523 | 22 | 12 | 0.55 | Breast | PNAS 91:12155 |
| Unknown | D7S523 | 9 | 4 | 0.44 | Colon | CR 55:1347 |
| Unknown | D7S523 | 13 | 5 | 0.38 | Head&Neck | CR 55:1347 |
| Unknown | D7S523 | 7 | 2 | 0.29 | Prostate | CR 54:6370 |
| Unknown | D7S18 | 7 | 3 | 0.43 | Breast | PNAS 91:12155 |
| Unknown | D7S486 | 15 | 5 | 0.33 | Breast | PNAS 91:12155 |
| Unknown | D7S486 | 18 | 9 | 0.5 | Colon | CR 55:1347 |
| Unknown | D7S486 | 10 | 3 | 0.3 | Head&Neck | CR 55:1347 |
| Unknown | D7S486 | 6 | 2 | 0.33 | Prostate | CR 54:6370 |
| Unknown | D7S23 | 18 | 7 | 0.39 | Breast | PNAS 91:12155 |
| Unknown | D7S23 | 11 | 1 | 0.09 | Ovary | BJC 69:429 |
| Unknown | D7S23 | 15 | 2 | 0.13 | Ovary | CR 53:2393 |
| Unknown | D7S23 | 20 | 3 | 0.15 | Uterus | CR 54:4294 |
| 31 | MET | 31 | 1 | 0.03 | Breast | CR 53:4356 |
| 31 | MET | 121 | 49 | 0.4 | Breast | L 339:140 |
| 31 | MET | 221 | 84 | 0.38 | Breast | GCC 12:304 |
| 31 | MET | 18 | 8 | 0.44 | Breast | PNAS 91:12155 |
| 31 | MET | 24 | 2 | 0.08 | Breast | GCC 2:191 |
| 31 | MET | 15 | 0 | 0 | Colon | CCG 48:167 |
| 31 | MDR1-MET | 12 | 0 | 0 | Prostate | G 11:530 |
| 31 | MET | 9 | 3 | 0.33 | Prostate | GCC 11:179 |

Chromosome 7 - q Arm

| | | | | | | |
|---------|--------|----|---|------|-----------|---------------|
| 31 | MET | 14 | 1 | 0.07 | Sarcoma | CR 52:2419 |
| 31 | MET | 35 | 7 | 0.2 | Stomach | IJC 59:597 |
| 31 | MET | 1 | 0 | 0 | Testis | CCG 52:72 |
| 31 | MET | 1 | 0 | 0 | Testis | CCG 52:72 |
| 31 | MET | 1 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D7S633 | 7 | 4 | 0.57 | Colon | CR 55:1347 |
| Unknown | D7S633 | 6 | 2 | 0.33 | Head&Neck | CR 55:1347 |
| Unknown | D7S633 | 7 | 3 | 0.43 | Prostate | CR 54:6370 |
| Unknown | D7S677 | 9 | 6 | 0.67 | Colon | CR 55:1347 |
| Unknown | D7S677 | 10 | 4 | 0.4 | Head&Neck | CR 55:1347 |
| Unknown | D7S677 | 8 | 5 | 0.62 | Prostate | CR 54:6370 |
| Unknown | D7S655 | 8 | 4 | 0.5 | Colon | CR 55:1347 |
| Unknown | D7S655 | 7 | 3 | 0.43 | Head&Neck | CR 55:1347 |
| Unknown | D7S655 | 14 | 6 | 0.43 | Prostate | CR 54:6370 |
| Unknown | D7S522 | 11 | 9 | 0.82 | Breast | PNAS 91:12155 |
| Unknown | D7S522 | 10 | 8 | 0.8 | Colon | CR 55:1347 |
| Unknown | D7S522 | 15 | 8 | 0.53 | Head&Neck | CR 55:1347 |
| Unknown | D7S522 | 6 | 5 | 0.83 | Prostate | CR 54:6370 |
| Unknown | D7S480 | 21 | 9 | 0.43 | Breast | PNAS 91:12155 |
| Unknown | D7S480 | 27 | 4 | 0.15 | Cervix | CR 56:197 |
| Unknown | D7S480 | 16 | 7 | 0.44 | Colon | CR 55:1347 |
| Unknown | D7S480 | 10 | 4 | 0.4 | Head&Neck | CR 55:1347 |
| Unknown | D7S480 | 11 | 3 | 0.27 | Prostate | CR 54:6370 |
| Unknown | D7S487 | 15 | 4 | 0.27 | Breast | PNAS 91:12155 |
| Unknown | D7S487 | 8 | 2 | 0.25 | Colon | CR 55:1347 |
| Unknown | D7S487 | 10 | 0 | 0 | Head&Neck | CR 55:1347 |
| Unknown | D7S487 | 19 | 1 | 0.05 | Leukemia | CR 55:5377 |
| Unknown | D7S487 | 8 | 1 | 0.12 | Prostate | CR 54:6370 |
| 31 | CFTR | 9 | 2 | 0.22 | Ovary | BJC 69:429 |
| Unknown | D7S490 | 14 | 5 | 0.36 | Breast | PNAS 91:12155 |
| Unknown | D7S490 | 10 | 4 | 0.4 | Colon | CR 55:1347 |
| Unknown | D7S490 | 12 | 4 | 0.33 | Head&Neck | CR 55:1347 |
| Unknown | D7S490 | 6 | 1 | 0.17 | Prostate | CR 54:6370 |
| 31-32 | D7S125 | 12 | 5 | 0.42 | Breast | PNAS 91:12155 |
| 31-32 | D7S125 | 15 | 2 | 0.13 | Ovary | IJC 54:546 |
| Unknown | D7S504 | 22 | 6 | 0.27 | Breast | PNAS 91:12155 |
| Unknown | D7S514 | 10 | 1 | 0.1 | Breast | PNAS 91:12155 |
| Unknown | D7S500 | 19 | 3 | 0.16 | Breast | PNAS 91:12155 |
| Unknown | D7S500 | 31 | 9 | 0.29 | Cervix | CR 56:197 |
| Unknown | D7S495 | 18 | 0 | 0 | Breast | PNAS 91:12155 |
| Unknown | D7S495 | 17 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D7S495 | 20 | 1 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D7S495 | 24 | 7 | 0.29 | Head&Neck | CR 54:1152 |
| Unknown | D7S495 | 26 | 1 | 0.04 | Melanoma | CR 56:589 |
| Unknown | D7S498 | 18 | 2 | 0.11 | Breast | PNAS 91:12155 |
| Unknown | D7S498 | 9 | 2 | 0.22 | Colon | CR 55:1347 |

Chromosome 7 - q Arm

| | | | | | | |
|-----------|---------|------|-----|------|------------|----------------|
| Unknown | D7S498 | 8 | 0 | 0 | Head&Neck | CR 55:1347 |
| Unknown | D7S498 | 4 | 0 | 0 | Prostate | CR 54:6370 |
| Unknown | D7S483 | 19 | 1 | 0.05 | Breast | PNAS 91:12155 |
| Unknown | D7S505 | 11 | 0 | 0 | Breast | PNAS 91:12155 |
| Unknown | D7S396 | 5 | 0 | 0 | Brain | CR 49:6572 |
| Unknown | D7S396 | 22 | 6 | 0.27 | Breast | PNAS 91:12155 |
| Unknown | D7S396 | 20 | 3 | 0.15 | Breast | CR 50:7184 |
| Unknown | D7S396 | 17 | 1 | 0.06 | Esophageal | CR 54:2996 |
| Unknown | D7S396 | 44 | 5 | 0.11 | Esophageal | GCC 10:177 |
| Unknown | D7S396 | 23 | 6 | 0.26 | Kidney | CR 51:820 |
| Unknown | D7S396 | 28 | 3 | 0.11 | Liver | CR 51:89 |
| Unknown | D7S396 | 34 | 5 | 0.15 | Lung | CR 52:2478 |
| Unknown | D7S396 | 19 | 4 | 0.21 | Ovary | CR 51:5118 |
| Unknown | D7S396 | 18 | 0 | 0 | Sarcoma | CR 52:2419 |
| 36 | D7S550 | 6 | 0 | 0 | Colon | CR 55:1347 |
| 36 | D7S550 | 28 | 3 | 0.11 | Esophageal | IJC 69:1 |
| 36 | D7S550 | 6 | 0 | 0 | Head&Neck | CR 55:1347 |
| 36 | D7S550 | 8 | 1 | 0.12 | Prostate | CR 54:6370 |
| 36 | D7S550 | 8 | 1 | 0.12 | Prostate | CR 54:6370 |
| Unknown | Unknown | 31 | 0 | 0 | Brain | CR 50:5784 |
| Unknown | ABP1 | 6 | 2 | 0.33 | Breast | PNAS 91:12155 |
| 32-qter | D7S228 | 18 | 2 | 0.11 | Cervix | CR 54:4481 |
| Unknown | D7S96 | 10 | 3 | 0.3 | Cervix | GCC 9:119 |
| 3.3-ter | Unknown | 32 | 0 | 0 | Colon | BJC 59:750 |
| Unknown | D7S368 | 21 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D7S22 | 11 | 0 | 0 | Endocrine | N 328:524 |
| Unknown | Unknown | 10 | 0 | 0 | Liver | BJC 64:1083 |
| 36 | Unknown | 12 | 0 | 0 | Liver | BJC 67:1007 |
| 31.3-qter | Unknown | 7 | 1 | 0.14 | Pancreas | BJC 65:809 |
| 36 | Unknown | 4 | 0 | 0 | Pancreas | CR 54:2761 |
| 31.3-qter | Unknown | 19 | 2 | 0.11 | Prostate | CSurveys 11:15 |
| Unknown | Unknown | 19 | 2 | 0.11 | Prostate | PNAS 87:8731 |
| 3.3-ter | Unknown | 9 | 0 | 0 | Stomach | BJC 59:750 |
| Unknown | D7S22 | 47 | 11 | 0.23 | Stomach | IJC 59:597 |
| Unknown | D7S22 | 41 | 10 | 0.24 | Stomach | CR 51:2926 |
| Unknown | D7S63 | 35 | 9 | 0.23 | Stomach | IJC 59:597 |
| Unknown | D7S64 | 16 | 0 | 0 | Stomach | IJC 59:597 |
| Unknown | D7S95 | 30 | 13 | 0.43 | Stomach | IJC 59:597 |
| Unknown | D7S22 | 22 | 2 | 0.09 | Testis | GCC 13:249 |
| 32-qter | D7S228 | 23 | 2 | 0.09 | Testis | O 9:2245 |
| Unknown | TCBR | 3 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | TCBR | 3 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | TCBR | 2 | 0 | 0 | Testis | CCG 52:72 |
| 11.23 | D7S440 | 19 | 1 | 0.05 | Uterus | CR 54:4294 |
| Unknown | D7S96 | 16 | 3 | 0.19 | Uterus | GCC 9:119 |
| SUM | | 2325 | 517 | 0.22 | | |

Chromosome 7 - p Arm

| | | | |
|-----|-----|----|------|
| SUM | 747 | 87 | 0.12 |
|-----|-----|----|------|

Chromosome 8 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|----------|---------|-------|-------------|-----------|------------|------------|
| 21 | D8S17 | 21 | 7 | 0.33 | Breast | CR 53:4356 |
| 21 | D8S17 | 3 | 1 | 0.33 | Breast | CR 53:3804 |
| 21 | D8S17 | 9 | 1 | 0.11 | Ovary | IJC 54:546 |
| Unknown | D8S264 | 30 | 6 | 0.2 | Cervix | CR 56:197 |
| Unknown | D8S262 | 5 | 2 | 0.4 | Kidney | GCC 12:76 |
| Unknown | D8S262 | 15 | 2 | 0.13 | Leukemia | CR 55:5377 |
| Unknown | D8S262 | 18 | 9 | 0.5 | Prostate | CR 54:6061 |
| 23 | D8S201 | 9 | 5 | 0.56 | Colon | AJP 144:1 |
| 23 | D8S201 | 28 | 6 | 0.21 | Prostate | O 11:2121 |
| 23 | D8S201 | 15 | 8 | 0.53 | Prostate | AJP 144:1 |
| 23 | D8S201 | 22 | 3 | 0.14 | Prostate | CR 53:3869 |
| 23 | D8S201 | 3 | 1 | 0.33 | Sarcoma | AJP 144:1 |
| 23 | D8S7 | 11 | 5 | 0.45 | Colon | GCC 10:1 |
| 23 | D8S7 | 18 | 6 | 0.33 | Esophageal | CR 54:2996 |
| 23 | D8S7 | 10 | 4 | 0.4 | Ovary | CR 53:2393 |
| 23 | D8S7 | 8 | 3 | 0.38 | Prostate | GCC 3:215 |
| 23 | D8S7 | 6 | 3 | 0.5 | Prostate | G 11:530 |
| 23 | D8S7 | 10 | 1 | 0.1 | Sarcoma | CR 52:2419 |
| Unknown | D8S277 | 18 | 0 | 0 | Endocrine | CR 56:599 |
| Unknown | D8S277 | 26 | 11 | 0.42 | Prostate | CR 54:6061 |
| 23.1-.2 | D8S337 | 18 | 5 | 0.28 | Colon | CR 53:1172 |
| 23.1-.2 | D8S337 | 15 | 7 | 0.47 | Liver | GCC 7:152 |
| 23.1-.2 | D8S337 | 3 | 0 | 0 | Lung | GCC 8:75 |
| 23.1-.2 | D8S337 | 14 | 6 | 0.43 | Prostate | GCC 13:168 |
| 23.1-.2 | D8S336 | 39 | 10 | 0.26 | Colon | CR 53:1172 |
| 23.1-.2 | D8S336 | 48 | 18 | 0.38 | Liver | GCC 7:152 |
| 23.1-.2 | D8S336 | 7 | 3 | 0.43 | Lung | GCC 8:75 |
| 21.3-22 | D8S335 | 53 | 18 | 0.34 | Colon | CR 53:1172 |
| 21.3-22 | D8S335 | 30 | 15 | 0.5 | Colon | GCC 10:7 |
| 21.3-22 | D8S335 | 46 | 17 | 0.37 | Liver | GCC 7:152 |
| 21.3-22 | D8S335 | 18 | 4 | 0.22 | Liver | GCC 10:7 |
| 21.3-22 | D8S335 | 27 | 12 | 0.44 | Lung | GCC 10:7 |
| 21.3-22 | D8S335 | 5 | 1 | 0.2 | Lung | GCC 7:85 |
| Unknown | D8S265 | 22 | 5 | 0.23 | Cervix | CR 56:197 |
| Unknown | D8S265 | 22 | 11 | 0.5 | Prostate | CR 54:6061 |
| 22 | CTSB | 33 | 14 | 0.42 | Colon | CR 53:1172 |
| 22 | CTSB | 23 | 7 | 0.3 | Liver | GCC 7:152 |
| 11.21-.2 | Unknown | 33 | 10 | 0.3 | Colon | CR 52:5368 |
| 11.21-.2 | Unknown | 34 | 8 | 0.24 | Colon | CR 53:1172 |
| 11.21-.2 | Unknown | 34 | 0 | 0 | Liver | GCC 7:152 |
| 11.21-.2 | Unknown | 12 | 0 | 0 | Lung | GCC 7:85 |
| Unknown | D8S254 | 13 | 4 | 0.31 | Breast | CR 55:4995 |
| Unknown | D8S261 | 16 | 1 | 0.06 | Head&Neck | CR 54:4756 |
| Unknown | D8S261 | 18 | 1 | 0.06 | Head&Neck | CR 54:4756 |
| Unknown | D8S261 | 20 | 8 | 0.4 | Head&Neck | CR 54:1152 |
| Unknown | D8S261 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |

Chromosome 8 - p Arm

| | | | | | | |
|---------|----------|----|----|------|----------|-------------|
| Unknown | D8S261 | 24 | 3 | 0.12 | Melanoma | CR 56:589 |
| Unknown | D8S261 | 31 | 17 | 0.55 | Prostate | CR 54:6061 |
| 22-pter | D8S163 | 44 | 19 | 0.43 | Colon | CR 53:1172 |
| 22-pter | D8S163 | 31 | 14 | 0.45 | Liver | GCC 7:152 |
| 22-pter | D8S163 | 14 | 3 | 0.21 | Lung | GCC 8:75 |
| 22-pter | D8S163 | 1 | 0 | 0 | Pancreas | CR 54:2761 |
| 22-pter | D8S163 | 23 | 14 | 0.61 | Prostate | CR 53:3669 |
| 22-pter | D8S163 | 18 | 9 | 0.5 | Prostate | GCC 13:168 |
| 21.3-22 | CI8-1344 | 71 | 25 | 0.35 | Colon | GCC 10:7 |
| 21.3-22 | CI8-1344 | 40 | 10 | 0.25 | Liver | GCC 10:7 |
| 21.3-22 | CI8-1344 | 30 | 8 | 0.27 | Lung | GCC 10:7 |
| 21.3-22 | CI8-2195 | 35 | 15 | 0.43 | Colon | GCC 10:7 |
| 21.3-22 | CI8-2195 | 32 | 7 | 0.22 | Liver | GCC 10:7 |
| 21.3-22 | CI8-2195 | 20 | 6 | 0.3 | Lung | GCC 10:7 |
| 21.3-22 | CI8-2014 | 24 | 7 | 0.29 | Colon | GCC 10:7 |
| 21.3-22 | CI8-2014 | 6 | 2 | 0.33 | Liver | GCC 10:7 |
| 21.3-22 | CI8-2014 | 17 | 7 | 0.41 | Lung | GCC 10:7 |
| 21.3-22 | CI8-2014 | 8 | 3 | 0.38 | Prostate | GCC 13:168 |
| 21.3-22 | D8S233 | 21 | 10 | 0.48 | Colon | GCC 10:7 |
| 21.3-22 | D8S233 | 24 | 11 | 0.46 | Colon | CR 53:1172 |
| 21.3-22 | D8S233 | 28 | 12 | 0.43 | Liver | GCC 7:152 |
| 21.3-22 | D8S233 | 14 | 5 | 0.36 | Liver | GCC 10:7 |
| 21.3-22 | D8S233 | 9 | 2 | 0.22 | Lung | GCC 8:75 |
| 21.3-22 | D8S233 | 7 | 3 | 0.43 | Lung | GCC 10:7 |
| Unknown | MSR | 56 | 5 | 0.09 | Breast | CR 52:5368 |
| 21.3-22 | MSR | 74 | 27 | 0.36 | Colon | GCC 10:7 |
| Unknown | MSR | 26 | 12 | 0.46 | Colon | CR 52:5368 |
| 22 | MSR | 74 | 28 | 0.38 | Colon | CR 53:1172 |
| Unknown | MSR | 27 | 2 | 0.07 | Kidney | CR 52:5368 |
| Unknown | MSR | 33 | 14 | 0.42 | Liver | JJCR 84:893 |
| 22 | MSR | 87 | 37 | 0.43 | Liver | GCC 7:152 |
| 21.3-22 | MSR | 54 | 10 | 0.19 | Liver | GCC 10:7 |
| Unknown | MSR | 35 | 14 | 0.4 | Lung | CR 52:5368 |
| Unknown | MSR | 21 | 9 | 0.43 | Lung | GCC 8:75 |
| 21.3-22 | MSR | 38 | 16 | 0.42 | Lung | GCC 10:7 |
| Unknown | MSR | 12 | 4 | 0.33 | Ovary | CR 52:5368 |
| 21.3-22 | MSR | 29 | 18 | 0.62 | Prostate | GCC 13:168 |
| 22 | MSR | 29 | 20 | 0.69 | Prostate | CR 53:3669 |
| Unknown | MSR | 18 | 4 | 0.22 | Stomach | CR 52:5368 |
| 21.3-22 | Unknown | 33 | 16 | 0.48 | Colon | GCC 10:7 |
| 21.3-22 | Unknown | 9 | 3 | 0.33 | Liver | GCC 10:7 |
| 21.3-22 | Unknown | 20 | 12 | 0.6 | Lung | GCC 10:7 |
| 21.3-22 | Unknown | 18 | 11 | 0.61 | Prostate | GCC 13:168 |
| 21.3-22 | Unknown | 21 | 9 | 0.43 | Colon | GCC 10:7 |
| 21.3-22 | Unknown | 6 | 2 | 0.33 | Liver | GCC 10:7 |
| 21.3-22 | Unknown | 22 | 15 | 0.68 | Lung | GCC 10:7 |

Chromosome 8 - p Arm

| | | | | | | |
|---------|-------------|----|----|------|----------|------------|
| 21.3-22 | Unknown | 12 | 19 | 0.45 | Colon | GCC 10:7 |
| 21.3-22 | Unknown | 33 | 10 | 0.3 | Liver | GCC 10:7 |
| 21.3-22 | Unknown | 21 | 10 | 0.48 | Lung | GCC 10:7 |
| 21.3-22 | Unknown | 15 | 8 | 0.53 | Prostate | GCC 13:168 |
| 21.3-22 | Unknown | 48 | 14 | 0.29 | Colon | GCC 10:7 |
| 21.3-22 | Unknown | 39 | 9 | 0.23 | Liver | GCC 10:7 |
| 21.3-22 | Unknown | 22 | 7 | 0.32 | Lung | GCC 10:7 |
| 21.3-22 | Unknown | 15 | 8 | 0.53 | Prostate | GCC 13:168 |
| 21.3-22 | Unknown | 49 | 22 | 0.45 | Colon | GCC 10:7 |
| 21.3-22 | Unknown | 40 | 9 | 0.23 | Liver | GCC 10:7 |
| 21.3-22 | Unknown | 23 | 7 | 0.3 | Lung | GCC 10:7 |
| 21.3-22 | Unknown | 15 | 8 | 0.53 | Prostate | GCC 13:168 |
| 21.3-22 | Unknown | 51 | 31 | 0.61 | Colon | GCC 10:7 |
| 21.3-22 | Unknown | 54 | 16 | 0.3 | Liver | GCC 10:7 |
| 21.3-22 | Unknown | 24 | 5 | 0.21 | Lung | GCC 10:7 |
| 21.3-22 | Unknown | 20 | 8 | 0.4 | Colon | GCC 10:7 |
| 21.3-22 | Unknown | 25 | 7 | 0.28 | Liver | GCC 10:7 |
| 21.3-22 | Unknown | 17 | 4 | 0.24 | Lung | GCC 10:7 |
| 21 | Unknown | 1 | 0 | 0 | Pancreas | CR 54:2761 |
| 22 | LPL | 10 | 4 | 0.4 | Colon | GCC 11:195 |
| 22 | LPL | 13 | 2 | 0.15 | Colon | AJP 144:1 |
| 22 | LPL | 32 | 4 | 0.12 | Colon | GCC 10:1 |
| 22 | LPL | 21 | 3 | 0.14 | Colon | CR 53:1172 |
| 22 | LPL | 47 | 10 | 0.21 | Colon | BJC 70:18 |
| 22 | LPL | 17 | 4 | 0.24 | Leukemia | B 83:3449 |
| 22 | LPL | 38 | 19 | 0.5 | Liver | GCC 7:152 |
| 22 | LPL | 6 | 4 | 0.67 | Lung | CR 55:28 |
| 22 | LPL | 7 | 3 | 0.43 | Lung | GCC 8:75 |
| 22 | LPL | 19 | 8 | 0.42 | Prostate | AJP 144:1 |
| 22 | LPL | 13 | 5 | 0.38 | Prostate | GCC 13:278 |
| 22 | LPL | 7 | 6 | 0.86 | Prostate | GCC 3:215 |
| 22 | LPL | 32 | 15 | 0.47 | Prostate | CR 53:3869 |
| 22 | LPL | 24 | 11 | 0.46 | Prostate | O 11:2121 |
| p22 | LPL-G214-15 | 29 | 14 | 0.48 | Prostate | CR 54:6061 |
| 22 | LPL | 2 | 0 | 0 | Sarcoma | AJP 144:1 |
| 22 | LPL | 19 | 2 | 0.11 | Uterus | CR 54:4294 |
| Unknown | D8S258 | 16 | 3 | 0.19 | Breast | CR 55:4995 |
| Unknown | D8S282 | 27 | 13 | 0.48 | Prostate | CR 54:6061 |
| Unknown | D8S298 | 30 | 18 | 0.6 | Prostate | CR 54:6061 |
| 21.3 | D8S232 | 59 | 17 | 0.29 | Colon | CR 53:1172 |
| 21.3 | D8S232 | 40 | 13 | 0.33 | Liver | GCC 7:152 |
| 21.3 | D8S232 | 19 | 7 | 0.37 | Lung | GCC 7:85 |
| 21.3 | D8S334 | 47 | 16 | 0.34 | Colon | CR 53:1172 |
| 21.3-22 | D8S334 | 49 | 18 | 0.37 | Colon | GCC 10:7 |
| 21.3-22 | D8S334 | 37 | 8 | 0.22 | Liver | GCC 10:7 |
| 21.3 | D8S334 | 39 | 15 | 0.38 | Liver | GCC 7:152 |

Chromosome 8 - p Arm

| | | | | | | |
|---------|---------|----|----|------|----------|------------|
| 21.3-22 | D8S334 | 19 | 8 | 0.42 | Lung | GCC 10:7 |
| 21.3 | D8S334 | 6 | 2 | 0.33 | Lung | GCC 7:85 |
| 21.3 | D8S334 | 16 | 9 | 0.56 | Prostate | GCC 13:168 |
| 21-23 | EGR3 | 28 | 14 | 0.5 | Colon | CR 53:1172 |
| 21-23 | EGR3 | 33 | 12 | 0.36 | Liver | GCC 7:152 |
| 21.2-.3 | CI8-586 | 25 | 7 | 0.28 | Colon | CR 53:1172 |
| 21.2-.3 | CI8-586 | 20 | 9 | 0.45 | Liver | GCC 7:152 |
| 21 | D8S133 | 10 | 5 | 0.5 | Prostate | GCC 11:119 |
| 21 | D8S133 | 27 | 7 | 0.26 | Prostate | O 11:2121 |
| 21 | D8S133 | 29 | 16 | 0.55 | Prostate | CR 54:6061 |
| 21.2-.3 | D8S220 | 50 | 18 | 0.36 | Colon | CR 53:1172 |
| 21.2-.3 | D8S220 | 35 | 13 | 0.37 | Colon | CR 52:5368 |
| 21.2-.3 | D8S220 | 43 | 16 | 0.37 | Liver | CR 52:5368 |
| 21.2-.3 | D8S220 | 50 | 17 | 0.34 | Liver | GCC 7:152 |
| 21.2-.3 | D8S220 | 17 | 4 | 0.24 | Lung | GCC 7:85 |
| 21.2-.3 | D8S220 | 18 | 6 | 0.33 | Prostate | GCC 13:168 |
| 21.2-.3 | D8S220 | 27 | 16 | 0.59 | Prostate | CR 53:3869 |
| Unknown | SFTP2 | 40 | 11 | 0.28 | Colon | GCC 10:1 |
| Unknown | D8S136 | 20 | 7 | 0.35 | Breast | CR 55:4995 |
| Unknown | D8S136 | 11 | 6 | 0.55 | Colon | GCC 11:195 |
| Unknown | D8S136 | 1 | 1 | 1 | Prostate | AJP 144:1 |
| Unknown | D8S136 | 28 | 16 | 0.57 | Prostate | CR 54:6061 |
| 21.1-.2 | D8S221 | 53 | 14 | 0.26 | Colon | CR 53:1172 |
| 21.1-.2 | D8S221 | 41 | 10 | 0.24 | Liver | GCC 7:152 |
| 21.1-.2 | D8S221 | 10 | 0 | 0 | Lung | GCC 7:85 |
| 21 | NEFL | 15 | 1 | 0.07 | Brain | CR 50:5784 |
| 21 | NEFL | 2 | 1 | 0.5 | Breast | CR 53:3804 |
| 21 | NEFL | 22 | 3 | 0.14 | Cervix | CR 54:4481 |
| 21 | NEFL | 35 | 11 | 0.31 | Colon | GCC 10:1 |
| 21 | NEFL | 8 | 4 | 0.5 | Colon | GCC 11:195 |
| 21 | NEFL | 50 | 22 | 0.44 | Colon | CR 53:1172 |
| 21 | NEFL | 47 | 19 | 0.4 | Liver | GCC 7:152 |
| 21 | NEFL | 14 | 5 | 0.36 | Lung | GCC 7:85 |
| 21 | NEFL | 6 | 2 | 0.33 | Prostate | CR 53:3869 |
| 21 | NEFL | 8 | 7 | 0.88 | Prostate | GCC 3:215 |
| 21 | NEFL | 19 | 8 | 0.42 | Prostate | GCC 13:168 |
| 21 | NEFL | 21 | 9 | 0.43 | Prostate | O 11:2121 |
| 21 | NEFL | 19 | 3 | 0.16 | Testis | O 9:2245 |
| Unknown | D8S137 | 16 | 10 | 0.62 | Breast | CR 55:4995 |
| Unknown | D8S137 | 85 | 29 | 0.34 | Colon | BJC 70:18 |
| Unknown | D8S137 | 1 | 1 | 1 | Prostate | AJP 144:1 |
| Unknown | D8S137 | 23 | 16 | 0.7 | Prostate | CR 54:6061 |
| Unknown | D8S137 | 2 | 2 | 1 | Sarcoma | AJP 144:1 |
| Unknown | D8S283 | 28 | 11 | 0.39 | Prostate | CR 54:6061 |
| p12 | D8S87 | 14 | 2 | 0.14 | Colon | AJP 144:1 |
| p12 | D8S87 | 24 | 9 | 0.38 | Prostate | CR 54:6061 |

Chromosome 8 - p Arm

| | | | | | | |
|-----------|----------------------|------|------|------|----------|--------------|
| p12 | D8S87 | 20 | 5 | 0.25 | Prostate | O 11:2121 |
| p12 | D8S87 | 18 | 4 | 0.22 | Prostate | AJP 144:1 |
| p12 | D8S87 | 4 | 4 | 1 | Sarcoma | AJP 144:1 |
| p12 | D8S87 | 25 | 5 | 0.2 | Uterus | CR 54:4294 |
| Unknown | D8S255 | 28 | 10 | 0.36 | Prostate | CR 54:6061 |
| Unknown | D8S255 | 10 | 1 | 0.1 | Testis | LI 73:606 |
| 11.2 | ANK1 | 78 | 18 | 0.23 | Colon | BJC 70:18 |
| 11.2 | ANK1 | 7 | 4 | 0.57 | Prostate | AJP 144:1 |
| 11.2 | ANK1 | 1 | 0 | 0 | Sarcoma | AJP 144:1 |
| 11.21-.22 | D8S194 | 40 | 6 | 0.15 | Colon | CR 52:5368 |
| 11.21-.22 | D8S194 | 40 | 5 | 0.12 | Colon | CR 53:1172 |
| 11.21-.22 | D8S194 | 45 | 5 | 0.11 | Liver | CR 52:5368 |
| 11.21-.22 | D8S194 | 45 | 5 | 0.11 | Liver | GCC 7:152 |
| 11.21-.22 | D8S194 | 26 | 3 | 0.12 | Prostate | CR 53:3869 |
| 11.22-.23 | D8S234 | 58 | 13 | 0.22 | Colon | CR 53:1172 |
| 11.22-.23 | D8S234 | 57 | 14 | 0.25 | Liver | GCC 7:152 |
| 11.22-.23 | D8S234 | 13 | 3 | 0.23 | Lung | GCC 7:85 |
| 11.22-.23 | D8S234 | 15 | 2 | 0.13 | Prostate | GCC 13:168 |
| 23.2-.3 | D8S140 | 33 | 6 | 0.18 | Colon | CR 52:5368 |
| 23.2-.3 | D8S140 | 29 | 8 | 0.28 | Colon | CR 53:1172 |
| 23.2-.3 | D8S140 | 39 | 7 | 0.18 | Liver | GCC 7:152 |
| 23.2-.3 | D8S140 | 39 | 7 | 0.18 | Liver | CR 52:5368 |
| 23.2-.3 | D8S140 | 38 | 4 | 0.11 | Prostate | CR 53:3869 |
| 11.0-12 | POLB | 15 | 0 | 0 | Colon | GCC 10:1 |
| 12-11.2 | PLAT | 7 | 2 | 0.29 | Prostate | GCC 3:215 |
| 12-11.2 | PLAT | 18 | 0 | 0 | Prostate | O 11:2121 |
| 11.23 | D8S223 | 24 | 0 | 0 | Colon | CR 53:1172 |
| 11.23 | D8S223 | 37 | 0 | 0 | Liver | GCC 7:152 |
| 11.23 | D8S223 | 37 | 0 | 0 | Liver | GCC 7:152 |
| Unknown | D8S262-261 | 26 | 17 | 0.65 | Bladder | CR 55:5213 |
| Unknown | D8S2 | 5 | 2 | 0.4 | Breast | CR 53:3804 |
| Unknown | D8S26 | 27 | 1 | 0.04 | Breast | CR 53:4356 |
| Unknown | D8S349 | 18 | 10 | 0.56 | Breast | CR 55:4995 |
| Unknown | D8S264-D8S265-D8S560 | 22 | 4 | 0.18 | Kidney | PNAS 92:2854 |
| Unknown | D8S264-D8S265-D8S560 | 6 | 1 | 0.17 | Kidney | PNAS 92:2854 |
| Unknown | D8S238 | 37 | 7 | 0.19 | Liver | CR 52:5368 |
| 21 | ARDRA3 | 19 | 5 | 0.26 | Ovary | IJC 54:546 |
| Unknown | D8S339 | 28 | 10 | 0.36 | Prostate | CR 54:6061 |
| 22-21.3 | D8S360 | 11 | 5 | 0.45 | Prostate | O 11:2121 |
| Unknown | D8S18 | 18 | 0 | 0 | Testis | G 5:134 |
| SUM | | 5603 | 1838 | 0.33 | | |

Chromosome 8 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------------|-------|-------------|-----------|-------------------|--------------|
| Unknown | D8S260 | 28 | 7 | 0.25 | Prostate | CR 54:6061 |
| q22 | D8S167 | 35 | 4 | 0.11 | Prostate | CR 54:6061 |
| Unknown | D8S257 | 16 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D8S257 | 20 | 8 | 0.4 | Head&Neck | CR 54:1152 |
| Unknown | D8S257 | 14 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D8S257 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | D8S257 | 26 | 2 | 0.08 | Melanoma | CR 56:589 |
| Unknown | D8S257 | 31 | 17 | 0.55 | Prostate | CR 54:6061 |
| Unknown | D8S273 | 30 | 6 | 0.2 | Cervix | CR 56:197 |
| Unknown | D8S273 | 19 | 3 | 0.16 | Head&Neck | CR 54:1152 |
| Unknown | D8S284 | 21 | 5 | 0.24 | Cervix | CR 56:197 |
| 24 | TG | 2 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| 24 | TG | 14 | 4 | 0.29 | Ovary | CR 53:2393 |
| 24 | TG | 9 | 0 | 0 | Prostate | G 11:530 |
| 24 | TG | 8 | 0 | 0 | Prostate | GCC 3:215 |
| 24 | D8S39 | 14 | 1 | 0.07 | Breast | CR 50:7184 |
| 24 | D8S39 | 14 | 0 | 0 | Cervix | CR 54:4481 |
| 24 | D8S39 | 5 | 0 | 0 | Cervix | GCC 9:119 |
| 24 | D8S39 | 9 | 0 | 0 | Esophageal | CR 51:2113 |
| 24 | D8S39 | 22 | 0 | 0 | Esophageal | CR 54:2996 |
| 24 | D8S39 | 12 | 1 | 0.08 | Kidney | CR 51:820 |
| 24 | D8S39 | 20 | 4 | 0.2 | Liver | CR 51:89 |
| 24 | D8S39 | 1 | 1 | 1 | Lung | CR 52:2478 |
| 24 | D8S39 | 3 | 1 | 0.33 | Lung | CR 52:2478 |
| 24 | D8S39 | 8 | 1 | 0.12 | Lung | CR 52:2478 |
| 24 | D8S39 | 1 | 1 | 1 | Lung | CR 52:2478 |
| 24 | D8S39 | 16 | 5 | 0.31 | Ovary | CR 51:5118 |
| 24 | D8S39 | 7 | 0 | 0 | Prostate | GCC 3:215 |
| 24 | D8S39 | 17 | 2 | 0.12 | Prostate | CR 53:3869 |
| 24 | D8S39 | 14 | 1 | 0.07 | Sarcoma | CR 52:2419 |
| 24 | D8S39 | 18 | 4 | 0.22 | Testis | O 9:2245 |
| 24 | D8S39 | 8 | 0 | 0 | Uterus | GCC 9:119 |
| 24 | D8S39 | 8 | 0 | 0 | Uterus | GCC 9:119 |
| Unknown | Unknown | 25 | 0 | 0 | Brain | CR 50:5784 |
| 22-23 | Unknown | 2 | 0 | 0 | Cervix | BJC 67:71 |
| Unknown | D8S272 | 15 | 0 | 0 | Endocrine | CR 56:599 |
| Unknown | D8S177 | 42 | 4 | 0.1 | Esophageal | GCC 10:177 |
| Unknown | D8S272-D8S284 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D8S272-D8S284 | 21 | 1 | 0.05 | Kidney | PNAS 92:2854 |
| Unknown | D8S:272-281 | 21 | 2 | 0.1 | Leukemia | CR 55:5377 |
| 22-QTER | D8S161 | 19 | 5 | 0.26 | Ovary | BJC 69:429 |
| Unknown | D8S198 | 22 | 1 | 0.05 | Uterus | CR 54:4294 |
| Unknown | D8S84 | 20 | 0 | 0 | Uterus | CR 54:4294 |
| SUM | | 661 | 94 | 0.14 | | |

Chromosome 9 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|--------|-------|-------------|-----------|------------|-------------|
| Unknown | D9S143 | 33 | 17 | 0.52 | Ovary | BJC 73:420 |
| Unknown | D9S129 | 33 | 18 | 0.55 | Ovary | BJC 73:420 |
| 22-24 | D9S54 | 61 | 11 | 0.18 | Bladder | CR 54:2848 |
| 22-PTER | D9S54 | 10 | 3 | 0.3 | Ovary | BJC 69:429 |
| Unknown | D9S132 | 5 | 1 | 0.2 | Ovary | O 11:1249 |
| Unknown | D9S132 | 3 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | D9S199 | 21 | 15 | 0.71 | Head&Neck | CR 54:1152 |
| Unknown | D9S199 | 10 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | D9S199 | 12 | 2 | 0.17 | Ovary | O 11:1249 |
| Unknown | D9S199 | 33 | 17 | 0.52 | Ovary | BJC 73:420 |
| Unknown | D9S324 | 23 | 2 | 0.09 | Ovary | CR 55:2150 |
| Unknown | D9S144 | 12 | 1 | 0.08 | Ovary | O 11:1249 |
| Unknown | D9S144 | 8 | 3 | 0.38 | Ovary | O 11:1249 |
| 22 | IFNA | 40 | 26 | 0.65 | Bladder | CR 54:2848 |
| 22 | IFNA | 12 | 1 | 0.08 | Brain | CR 54:1397 |
| 22 | IFNA | 19 | 4 | 0.21 | Brain | CR 54:1397 |
| 22 | IFNA | 89 | 21 | 0.24 | Breast | IJC 64:378 |
| Unknown | IFNA | 13 | 4 | 0.31 | Esophageal | CL 97:129 |
| 22 | IFNA | 2 | 0 | 0 | Kidney | GCC 12:76 |
| Unknown | IFNA | 40 | 8 | 0.2 | Kidney | JJCR 86:795 |
| Unknown | IFNA | 6 | 5 | 0.83 | Lung | CR 55:28 |
| Unknown | IFNA | 15 | 8 | 0.53 | Ovary | GO 55:245 |
| Unknown | IFNA | 28 | 3 | 0.11 | Ovary | CR 55:2150 |
| Unknown | IFNA | 33 | 19 | 0.58 | Ovary | BJC 73:420 |
| 22 | IFNA | 58 | 20 | 0.34 | Ovary | AJHG 55:143 |
| Unknown | IFNA | 7 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | IFNA | 3 | 0 | 0 | Ovary | O 11:1249 |
| 22 | IFNA | 19 | 5 | 0.26 | Stomach | CR 55:1933 |
| Unknown | IFNB | 252 | 153 | 0.61 | Bladder | CR 53:1230 |
| 22 | IFNB1 | 252 | 153 | 0.61 | Bladder | CR 53:1230 |
| Unknown | IFNB | 6 | 0 | 0 | Breast | CR 53:4356 |
| 22 | IFNB1 | 1 | 0 | 0 | Breast | GCC 2:191 |
| 22 | IFNB1 | 12 | 1 | 0.08 | Cervix | CR 54:4481 |
| 22 | IFNB1 | 42 | 5 | 0.12 | Leukemia | AHEM 68:171 |
| 22 | IFNB1 | 44 | 0 | 0 | Leukemia | AHEM 68:171 |
| 22 | IFNB1 | 6 | 0 | 0 | Prostate | G 11:530 |
| 22 | IFNB1 | 7 | 5 | 0.71 | Testis | O 9:2245 |
| Unknown | D9S156 | 126 | 30 | 0.24 | Breast | IJC 64:378 |
| Unknown | D9S156 | 11 | 4 | 0.36 | Esophageal | CL 97:129 |
| Unknown | D9S156 | 18 | 13 | 0.72 | Head&Neck | CR 54:1152 |
| Unknown | D9S156 | 3 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | D9S156 | 13 | 4 | 0.31 | Ovary | O 11:1249 |
| 21 | D9S157 | 133 | 30 | 0.23 | Breast | IJC 64:378 |
| 21 | D9S157 | 30 | 5 | 0.17 | Cervix | CR 56:197 |
| 21 | D9S157 | 13 | 6 | 0.46 | Esophageal | CL 97:129 |
| 21 | D9S157 | 65 | 25 | 0.38 | Esophageal | IJC 69:1 |

Chromosome 9 - p Arm

| | | | | | | |
|---------|---------------|-----|-----|------|------------|--------------|
| 21 | D9S157 | 5 | 1 | 0.2 | Kidney | GCC 12:76 |
| Unknown | D9S168 | 120 | 17 | 0.14 | Breast | IJC 64:378 |
| Unknown | D9S168 | 33 | 15 | 0.45 | Ovary | BJC 73:420 |
| 21 | CDKN2 | 109 | 20 | 0.18 | Bladder | JNCI 87:1524 |
| 21 | p15-p16 | 50 | 28 | 0.56 | Esophageal | HMG 4:1883 |
| 21 | CDKN2 | 55 | 1 | 0.02 | Kidney | JJCR 86:795 |
| 21 | CDKN2 | 34 | 7 | 0.21 | Lung | GCC 14:164 |
| 21 | CDKN2 | 50 | 24 | 0.48 | Ovary | IJC 63:222 |
| 21 | p15-p16 | 56 | 3 | 0.05 | Sarcoma | CGC 86:136 |
| 21 | MTS2 | 100 | 18 | 0.18 | Bladder | JNCI 87:1524 |
| 21 | D9S162 | 90 | 10 | 0.11 | Breast | IJC 64:378 |
| 21 | D9S162 | 9 | 3 | 0.33 | Esophageal | CL 97:129 |
| 21 | D9S162 | 33 | 4 | 0.12 | Head&Neck | CR 54:4756 |
| 21 | D9S162 | 41 | 13 | 0.32 | Head&Neck | CR 54:4756 |
| 21 | D9S162 | 4 | 0 | 0 | Kidney | GCC 12:76 |
| 21 | D9S162 | 33 | 17 | 0.52 | Ovary | BJC 73:420 |
| 21 | D9S162 | 12 | 1 | 0.08 | Ovary | O 11:1249 |
| 21 | D9S162 | 15 | 3 | 0.2 | Ovary | O 11:1249 |
| 21 | D9S171 | 139 | 28 | 0.2 | Breast | IJC 64:378 |
| 21 | D9S171 | 60 | 19 | 0.32 | Esophageal | IJC 69:1 |
| 21 | D9S171 | 11 | 4 | 0.36 | Esophageal | CL 97:129 |
| 21 | D9S171 | 3 | 0 | 0 | Kidney | GCC 12:76 |
| 21 | D9S171 | 12 | 3 | 0.25 | Kidney | JJCR 86:795 |
| Unknown | D9S:162-171 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| 21 | D9S171 | 24 | 4 | 0.17 | Lung | GCC 14:164 |
| 21 | D9S171 | 8 | 5 | 0.62 | Lung | CR 54:2307 |
| Unknown | D9S:162-171 | 35 | 16 | 0.46 | Melanoma | CR 56:589 |
| 21 | D9S171 | 9 | 3 | 0.33 | Ovary | O 11:1249 |
| 21 | D9S171 | 33 | 16 | 0.48 | Ovary | BJC 73:420 |
| 21 | D9S171 | 15 | 1 | 0.07 | Ovary | O 11:1249 |
| Unknown | D9S126 | 252 | 152 | 0.6 | Bladder | CR 53:1230 |
| Unknown | D9S126 | 252 | 152 | 0.6 | Bladder | CR 53:1230 |
| Unknown | D9S126 | 80 | 15 | 0.19 | Breast | IJC 64:378 |
| Unknown | D9S126 | 16 | 3 | 0.19 | Endocrine | CR 56:599 |
| Unknown | IFN2a- D9S126 | 5 | 5 | 1 | Lung | CR 55:513 |
| Unknown | D9S126 | 9 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | D9S126 | 11 | 1 | 0.09 | Ovary | O 11:1249 |
| Unknown | D9S126 | 51 | 17 | 0.33 | Ovary | AJHG 55:143 |
| Unknown | D9S126 | 30 | 3 | 0.1 | Ovary | CR 55:2150 |
| Unknown | D9S126 | 33 | 17 | 0.52 | Ovary | BJC 73:420 |
| Unknown | D9S736 | 33 | 18 | 0.55 | Ovary | BJC 73:420 |
| Unknown | D9S3 | 252 | 154 | 0.61 | Bladder | CR 53:1230 |
| 21 | D9S3 | 16 | 3 | 0.19 | Bladder | CR 54:2848 |
| 21 | D9S3 | 4 | 1 | 0.25 | Breast | CR 53:3804 |
| 21 | D9S169 | 22 | 4 | 0.18 | Cervix | CR 56:197 |
| 21 | D9S169 | 8 | 6 | 0.75 | Lung | CR 54:2307 |

Chromosome 9 - p Arm

| | | | | | | |
|---------|--|------|------|------|------------|---------------|
| 21 | S161 | 15 | 5 | 0.33 | Esophageal | CL 97:129 |
| 21 | S161 | 5 | 1 | 0.2 | Kidney | GCC 12:76 |
| 21 | S161 | 10 | 2 | 0.2 | Ovary | O 11:1249 |
| 21 | S161 | 14 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | D9S104 | 117 | 20 | 0.17 | Breast | IJC 64:378 |
| Unknown | D9S104 | 63 | 27 | 0.43 | Esophageal | IJC 69:1 |
| Unknown | D9S104 | 33 | 15 | 0.45 | Ovary | BJC 73:420 |
| Unknown | D9S104 | 19 | 4 | 0.21 | Uterus | CR 54:4294 |
| 21-qter | D9S52 | 12 | 5 | 0.42 | Ovary | GO 55:245 |
| Unknown | D9S165 | 4 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | D9S165 | 8 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | D9S200 | 11 | 2 | 0.18 | Esophageal | CL 97:129 |
| Unknown | D9S200 | 25 | 13 | 0.52 | Head&Neck | CR 54:1152 |
| Unknown | D9S200 | 33 | 13 | 0.39 | Ovary | BJC 73:420 |
| Unknown | D9S200 | 13 | 1 | 0.08 | Ovary | O 11:1249 |
| Unknown | D9S200 | 13 | 4 | 0.31 | Ovary | O 11:1249 |
| 12 | D9S55 | 14 | 1 | 0.07 | Brain | CR 54:1397 |
| 12 | D9S55 | 18 | 2 | 0.11 | Brain | CR 54:1397 |
| 12 | D9S55 | 18 | 2 | 0.11 | Brain | CR 54:1397 |
| Unknown | D9S47 | 252 | 152 | 0.6 | Bladder | CR 53:1230 |
| Unknown | IFNa- D9S1751- 736-1747-1748- 1752-171 | 31 | 19 | 0.61 | Bladder | CR 55:5213 |
| Unknown | Unknown | 12 | 0 | 0 | Brain | CR 50:5784 |
| Unknown | D9S18 | 30 | 17 | 0.57 | Esophageal | GCC 10:177 |
| Unknown | MTS1 | 5 | 5 | 1 | Esophageal | O 9:3737 |
| Unknown | D9S168-D9S166 | 5 | 2 | 0.4 | Kidney | PNAS 92:2854 |
| Unknown | D9S168-D9S166 | 19 | 3 | 0.16 | Kidney | PNAS 92:2854 |
| Unknown | D9S168-171 | 50 | 20 | 0.4 | Leukemia | CR 55:5377 |
| Unknown | Unknown | 33 | 17 | 0.52 | Lung | CR 54:2322 |
| Unknown | D9S171-D9S126- D9S169 | 29 | 17 | 0.59 | Lung | JCRCO 121:291 |
| Unknown | D9S171-D9S126- D9S169 | 6 | 0 | 0 | Lung | JCRCO 121:291 |
| Unknown | D9S171-D9S126- D9S169 | 47 | 10 | 0.21 | Lung | JCRCO 121:291 |
| Unknown | OVC | 15 | 5 | 0.33 | Ovary | CR 53:2393 |
| SUM | | 4921 | 1868 | 0.38 | | |

Chromosome 9 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|----------|--------|-------|-------------|-----------|---------------|-------------|
| Unknown | D9S15 | 70 | 37 | 0.53 | Bladder | O 11:1671 |
| Unknown | D9S15 | 11 | 1 | 0.09 | Breast | CR 50:7184 |
| 13-21.1 | D9S15 | 6 | 3 | 0.5 | Cervix | GCC 9:119 |
| 13-21.1 | D9S15 | 14 | 1 | 0.07 | Esophageal | CR 54:2996 |
| Unknown | D9S15 | 22 | 9 | 0.41 | Esophageal | GCC 10:177 |
| Unknown | D9S15 | 12 | 2 | 0.17 | Kidney | CR 51:820 |
| 13-21.1 | D9S15 | 6 | 1 | 0.17 | Kidney | GCC 12:76 |
| Unknown | D9S15 | 8 | 1 | 0.12 | Lung | CR 52:2478 |
| 13-21.1 | D9S15 | 14 | 5 | 0.36 | Ovary | BJC 69:429 |
| Unknown | D9S15 | 4 | 0 | 0 | Ovary | CR 51:5118 |
| Unknown | D9S15 | 16 | 2 | 0.12 | Ovary | CR 55:2150 |
| Unknown | D9S15 | 33 | 15 | 0.45 | Ovary | BJC 73:420 |
| Unknown | D9S15 | 10 | 3 | 0.3 | Sarcoma | CR 52:2419 |
| 13-21.1 | D9S15 | 10 | 2 | 0.2 | Uterus | GCC 9:119 |
| Unknown | D9S18 | 252 | 151 | 0.6 | Bladder | CR 53:1230 |
| Unknown | D9S18 | 7 | 0 | 0 | Cervix | GCC 5:119 |
| Unknown | D9S18 | 28 | 10 | 0.36 | Esophageal | CR 54:2996 |
| Unknown | D9S18 | 13 | 4 | 0.31 | Ovary | IJC 54:546 |
| Unknown | D9S18 | 16 | 1 | 0.06 | Uterus | GCC 9:119 |
| Unknown | D9S27 | 8 | 2 | 0.25 | Testis | O 9:2245 |
| Unknown | D9S103 | 70 | 36 | 0.51 | Bladder | O 11:1671 |
| Unknown | D9S103 | 33 | 16 | 0.48 | Ovary | BJC 73:420 |
| Unknown | D9S166 | 8 | 2 | 0.25 | Ovary | O 11:1249 |
| Unknown | D9S166 | 3 | 0 | 0 | Ovary | O 11:1249 |
| Unknown | ASSP3 | 252 | 155 | 0.62 | Bladder | CR 53:1230 |
| Unknown | ASSP3 | 8 | 0 | 0 | Liver | CCG 48:72 |
| 11-22.0 | ASSP3 | 19 | 7 | 0.37 | Ovary | BJC 69:429 |
| 11-22.0 | ASSP3 | 8 | 0 | 0 | Stomach | CR 48:2988 |
| Unknown | S153 | 70 | 37 | 0.53 | Bladder | O 11:1671 |
| pter-q11 | D9S1 | 2 | 0 | 0 | Cervix | CR 49:3598 |
| pter-q11 | D9S1 | 13 | 1 | 0.08 | Colon | IJC 53:382 |
| pter-q11 | D9S1 | 7 | 0 | 0 | Liver | JJCR 81:108 |
| pter-q11 | D9S1 | 5 | 0 | 0 | Neuroblastoma | CR 49:1095 |
| pter-q11 | D9S1 | 1 | 0 | 0 | Pancreas | CR 54:2761 |
| pter-q11 | D9S1 | 14 | 1 | 0.07 | Stomach | CR 52:3099 |
| pter-q11 | D9S1 | 6 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | D9S167 | 70 | 38 | 0.54 | Bladder | O 11:1671 |
| Unknown | D9S201 | 70 | 36 | 0.51 | Bladder | O 11:1671 |
| Unknown | D9S201 | 26 | 7 | 0.27 | Ovary | CR 55:2150 |
| Unknown | D9S201 | 33 | 13 | 0.39 | Ovary | BJC 73:420 |
| Unknown | D9S283 | 70 | 37 | 0.53 | Bladder | O 11:1671 |
| Unknown | D9S283 | 33 | 13 | 0.39 | Ovary | BJC 73:420 |
| Unknown | D9S12 | 70 | 36 | 0.51 | Bladder | O 11:1671 |
| Unknown | D9S12 | 9 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D9S12 | 33 | 12 | 0.36 | Ovary | BJC 73:420 |

Chromosome 9 - q Arm

| | | | | | | |
|---------|--------|-----|-----|------|-----------|------------|
| Unknown | D9S12 | 13 | 6 | 0.46 | Ovary | CR 55:2150 |
| Unknown | D9S119 | 70 | 38 | 0.54 | Bladder | O 11:1671 |
| Unknown | D9S197 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | D9S197 | 26 | 5 | 0.19 | Melanoma | CR 56:589 |
| Unknown | D9S22 | 252 | 154 | 0.61 | Bladder | CR 53:1230 |
| Unknown | D9S176 | 70 | 38 | 0.54 | Bladder | O 11:1671 |
| Unknown | D9S176 | 6 | 1 | 0.17 | Kidney | GCC 12:76 |
| Unknown | D9S29 | 4 | 1 | 0.25 | Head&Neck | CL 79:67 |
| Unknown | D9S29 | 19 | 11 | 0.58 | Ovary | CR 55:2150 |
| Unknown | D9S109 | 70 | 37 | 0.53 | Bladder | O 11:1671 |
| Unknown | D9S109 | 5 | 1 | 0.2 | Kidney | GCC 12:76 |
| Unknown | D9S109 | 29 | 6 | 0.21 | Ovary | CR 55:2150 |
| Unknown | D9S127 | 70 | 36 | 0.51 | Bladder | O 11:1671 |
| Unknown | D9S127 | 24 | 7 | 0.29 | Ovary | CR 55:2150 |
| Unknown | D9S127 | 33 | 18 | 0.55 | Ovary | BJC 73:420 |
| Unknown | D9S53 | 70 | 38 | 0.54 | Bladder | O 11:1671 |
| Unknown | D9S53 | 19 | 3 | 0.16 | Head&Neck | CR 54:1152 |
| Unknown | D9S53 | 35 | 12 | 0.34 | Ovary | CR 55:2150 |
| Unknown | D9S53 | 33 | 19 | 0.58 | Ovary | BJC 73:420 |
| Unknown | D9S53 | 24 | 1 | 0.04 | Uterus | CR 54:4294 |
| Unknown | D9S58 | 70 | 37 | 0.53 | Bladder | O 11:1671 |
| Unknown | D9S58 | 27 | 7 | 0.26 | Ovary | CR 55:2150 |
| Unknown | D9S105 | 70 | 37 | 0.53 | Bladder | O 11:1671 |
| Unknown | HXB | 70 | 39 | 0.56 | Bladder | O 11:1671 |
| Unknown | HXB | 33 | 17 | 0.52 | Ovary | BJC 73:420 |
| Unknown | HXB | 24 | 10 | 0.42 | Ovary | CR 55:2150 |
| Unknown | HXB | 19 | 1 | 0.05 | Uterus | CR 54:4294 |
| Unknown | D9S155 | 33 | 15 | 0.45 | Ovary | BJC 73:420 |
| Unknown | D9S16 | 12 | 6 | 0.5 | Ovary | CR 55:2150 |
| Unknown | D9S59 | 70 | 37 | 0.53 | Bladder | O 11:1671 |
| Unknown | D9S59 | 33 | 18 | 0.55 | Ovary | BJC 73:420 |
| Unknown | D9S59 | 30 | 10 | 0.33 | Ovary | CR 55:2150 |
| Unknown | D9S154 | 70 | 38 | 0.54 | Bladder | O 11:1671 |
| Unknown | D9S154 | 34 | 5 | 0.15 | Cervix | CR 56:197 |
| Unknown | D9S302 | 36 | 4 | 0.11 | Brain | CR 55:4696 |
| Unknown | D9S302 | 36 | 4 | 0.11 | Brain | CR 55:4696 |
| Unknown | D9S258 | 70 | 35 | 0.5 | Bladder | O 11:1671 |
| 33 | GSN | 70 | 39 | 0.56 | Bladder | O 11:1671 |
| 33 | GSN | 17 | 3 | 0.18 | Head&Neck | CR 54:1152 |
| 33 | GSN | 5 | 0 | 0 | Kidney | GCC 12:76 |
| 33 | GSN | 18 | 8 | 0.44 | Ovary | BJC 69:429 |
| Unknown | GSN | 33 | 16 | 0.48 | Ovary | BJC 73:420 |
| 33 | GSN | 15 | 7 | 0.47 | Ovary | CR 55:2150 |
| Unknown | D9S49 | 252 | 154 | 0.61 | Bladder | CR 53:1230 |
| 31-34 | D9S28 | 39 | 5 | 0.13 | Bladder | CR 54:2848 |
| 31-34 | D9S28 | 1 | 1 | 1 | Head&Neck | CL 79:67 |

Chromosome 9 - q Arm

| | | | | | | |
|---------|--------|-----|-----|------|------------|--------------|
| Unknown | D9S60 | 70 | 36 | 0.51 | Bladder | O 11:1671 |
| Unknown | D9S61 | 70 | 38 | 0.54 | Bladder | O 11:1671 |
| 34-QTER | D9S64 | 17 | 8 | 0.47 | Ovary | BJC 69:429 |
| Unknown | D9S64 | 18 | 10 | 0.56 | Ovary | CR 55:2150 |
| 34.1 | ABL | 65 | 13 | 0.2 | Bladder | CR 54:2848 |
| 34.1 | ABL | 70 | 37 | 0.53 | Bladder | O 11:1671 |
| 34.1 | ABL | 33 | 15 | 0.45 | Ovary | BJC 73:420 |
| 34.1 | ABL | 25 | 10 | 0.4 | Ovary | CR 55:2150 |
| 34-qter | ASS | 20 | 5 | 0.25 | Bladder | CR 54:2848 |
| 34-qter | ASS | 17 | 0 | 0 | Brain | CR 54:1397 |
| 34-qter | ASS | 12 | 0 | 0 | Brain | CR 54:1397 |
| 34-qter | ASS | 14 | 2 | 0.14 | Lung | PN 84:9252 |
| 34-qter | ASS | 34 | 13 | 0.38 | Ovary | CR 55:2150 |
| Unknown | D9S164 | 6 | 1 | 0.17 | Kidney | PNAS 92:2854 |
| Unknown | D9S164 | 20 | 3 | 0.15 | Kidney | PNAS 92:2854 |
| Unknown | D9S10 | 252 | 154 | 0.61 | Bladder | CR 53:1230 |
| 34.3 | D9S10 | 41 | 13 | 0.32 | Bladder | CR 54:2848 |
| 34.3 | D9S10 | 15 | 8 | 0.53 | Ovary | CR 55:2150 |
| Unknown | D9S66 | 70 | 38 | 0.54 | Bladder | O 11:1671 |
| Unknown | D9S14 | 252 | 151 | 0.6 | Bladder | CR 53:1230 |
| Unknown | D9S67 | 70 | 36 | 0.51 | Bladder | O 11:1671 |
| Unknown | D9S13 | 252 | 151 | 0.6 | Bladder | CR 53:1230 |
| 34 | D9S17 | 35 | 6 | 0.17 | Breast | CR 50:7184 |
| 34 | D9S17 | 21 | 16 | 0.16 | Esophageal | GCC 10:177 |
| 34 | D9S17 | 31 | 8 | 0.26 | Lung | CR 52:2478 |
| 34 | D9S17 | 20 | 2 | 0.1 | Ovary | CR 51:5118 |
| Unknown | D9S7 | 252 | 155 | 0.62 | Bladder | CR 53:1230 |
| 34 | D9S7 | 65 | 13 | 0.2 | Bladder | CR 54:2848 |
| 34 | D9S7 | 7 | 0 | 0 | Brain | CR 49:6572 |
| 34 | D9S7 | 21 | 2 | 0.1 | Breast | GCC 2:191 |
| Unknown | D9S7 | 44 | 6 | 0.14 | Breast | CR 53:4356 |
| 34 | D9S7 | 5 | 1 | 0.2 | Breast | CR 53:3804 |
| 34 | D9S7 | 3 | 2 | 0.67 | Cervix | GCC 9:119 |
| 34 | D9S7 | 33 | 5 | 0.15 | Cervix | CR 54:4481 |
| 34 | D9S7 | 20 | 1 | 0.05 | Endocrine | GCC 13:9 |
| Unknown | D9S7 | 9 | 0 | 0 | Esophageal | CR 51:2113 |
| 34 | D9S7 | 24 | 7 | 0.29 | Esophageal | CR 54:2996 |
| 34 | D9S7 | 10 | 1 | 0.1 | Kidney | CR 51:820 |
| 34 | D9S7 | 9 | 0 | 0 | Liver | CR 51:89 |
| 34 | D9S7 | 6 | 1 | 0.17 | Liver | BJC 64:1083 |
| 34 | D9S7 | 11 | 1 | 0.09 | Liver | BJC 67:1007 |
| Unknown | D9S7 | 32 | 6 | 0.19 | Ovary | IJC 54:546 |
| 34 | D9S7 | 6 | 1 | 0.17 | Ovary | CR 55:2150 |
| 34 | D9S7 | 2 | 0 | 0 | Pancreas | CR 54:2761 |
| 34 | D9S7 | 13 | 1 | 0.08 | Pancreas | BJC 65:809 |
| 34 | D9S7 | 12 | 0 | 0 | Prostate | G 11:530 |

Chromosome 9 - q Arm

| | | | | | | |
|-----------|------------------|------|------|------|-----------|----------------|
| 34 | D9S7 | 13 | 2 | 0.15 | Prostate | CSurveys 11:15 |
| 34 | D9S7 | 11 | 2 | 0.18 | Sarcoma | CR 52:2419 |
| Unknown | D9S7 | 19 | 1 | 0.05 | Testis | GCC 13:249 |
| Unknown | D9S7 | 33 | 16 | 0.48 | Testis | O 9:2245 |
| 34 | D9S7 | 5 | 1 | 0.2 | Uterus | GCC 9:119 |
| Unknown | D9S11 | 252 | 153 | 0.61 | Bladder | CR 53:1230 |
| 34 | D9S7-D9S11-D9S13 | 252 | 149 | 0.59 | Bladder | O 8:1083 |
| 34 | D9S7-D9S11-D9S13 | 252 | 149 | 0.59 | Bladder | O 8:1083 |
| Unknown | GSN-D9S:15-12 | 28 | 17 | 0.61 | Bladder | CR 55:5213 |
| Unknown | Unknown | 20 | 1 | 0.05 | Brain | CR 50:5784 |
| 21.1-22.2 | Unknown | 14 | 1 | 0.07 | Brain | CR 54:1397 |
| 21.1-22.2 | Unknown | 19 | 0 | 0 | Brain | CR 54:1397 |
| Unknown | D9S6 | 13 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D9S146 | 9 | 1 | 0.11 | Endocrine | CR 56:599 |
| Unknown | D9S160-180 | 44 | 26 | 0.59 | Head&Neck | CR 54:4756 |
| Unknown | D9S160-180 | 39 | 2 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D9S:154-164-180 | 52 | 10 | 0.19 | Leukemia | CR 55:5377 |
| Unknown | Unknown | 33 | 16 | 0.48 | Lung | CR 54:2322 |
| Unknown | D9S15-10 | 26 | 14 | 0.54 | Ovary | CR 53:2393 |
| Unknown | Unknown | 19 | 2 | 0.11 | Prostate | PNAS 87:8751 |
| SUM | | 6593 | 3076 | 0.47 | | |

Chromosome 10 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|------------|-----------------|-------|-------------|-----------|------------|-------------|
| pter-p11.2 | D10S89 | 17 | 0 | 0 | Uterus | CR 54:4294 |
| Unknown | Unknown | 38 | 15 | 0.39 | Brain | CR 50:5784 |
| Unknown | D10S109 | 7 | 0 | 0 | Brain | CR 53:2386 |
| Unknown | D10S109 | 6 | 2 | 0.33 | Brain | CR 53:2386 |
| 11.2 | D10S111 | 9 | 0 | 0 | Brain | CR 53:2386 |
| 11.2 | D10S111 | 6 | 0 | 0 | Brain | CR 53:2386 |
| pter-p11.2 | D10S89 | 8 | 0 | 0 | Brain | CR 53:2386 |
| pter-p11.2 | D10S89 | 16 | 1 | 0.06 | Brain | CR 54:1397 |
| pter-p11.2 | D10S89 | 6 | 1 | 0.17 | Brain | CR 53:2386 |
| pter-p11.2 | D10S89 | 13 | 0 | 0 | Brain | CR 54:1397 |
| Unknown | FNRB-- D10S28 | 72 | 31 | 0.43 | Brain | CR 56:164 |
| pter-q13 | D10 S28 | 32 | 4 | 0.12 | Breast | CR 50:7184 |
| Unknown | D10S15 | 15 | 0 | 0 | Breast | GCC 2:191 |
| pter-q13 | D10 S28 | 42 | 9 | 0.21 | Cervix | CR 54:4481 |
| Unknown | D10S191 | 32 | 1 | 0.03 | Cervix | CR 56:1974 |
| 13-12.2 | D10S24 | 4 | 0 | 0 | Cervix | CR 54:4481 |
| Unknown | D10S28 | 7 | 1 | 0.14 | Cervix | GCC 9:119 |
| Unknown | D10S249 | 14 | 1 | 0.07 | Endocrine | CR 56:599 |
| pter-p11.2 | D10S89 | 20 | 1 | 0.05 | Endocrine | GCC 13:9 |
| pter-q13 | D10S17 | 33 | 11 | 0.33 | Esophageal | GCC 10:177 |
| pter-q13 | D10S17 | 14 | 2 | 0.14 | Esophageal | CR 54:2996 |
| Unknown | D10S226 | 11 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D10S226 | 12 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D10S249 | 22 | 5 | 0.23 | Head&Neck | CR 54:1152 |
| pter-q13 | D10 S28 | 31 | 3 | 0.1 | Kidney | CR 51:5817 |
| pter-q13 | D10 S28 | 34 | 3 | 0.09 | Kidney | CR 51:820 |
| pter-q13 | D10S17 | 11 | 1 | 0.09 | Kidney | CR 51:5817 |
| Unknown | D10S226 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | D10S249-D10S191 | 21 | 0 | 0 | Kidney | PNAS 92:285 |
| Unknown | D10S249-D10S191 | 5 | 0 | 0 | Kidney | PNAS 92:285 |
| pter-q13 | D10 S28 | 39 | 0 | 0 | Liver | CR 51:89 |
| pter-q13 | D10 S28 | 35 | 5 | 0.14 | Lung | CR 52:2478 |
| 11-23.0 | D10S14 | 8 | 4 | 0.5 | Melanoma | GCC 8:178 |
| Unknown | D10S15 | 5 | 3 | 0.6 | Melanoma | GCC 8:178 |
| Unknown | D10S226 | 23 | 4 | 0.17 | Melanoma | CR 56:589 |
| Unknown | D10S28 | 14 | 5 | 0.36 | Melanoma | GCC 8:178 |
| Unknown | D10S33 | 3 | 0 | 0 | Melanoma | GCC 8:178 |
| pter-p11.2 | D10S89 | 10 | 4 | 0.4 | Melanoma | GCC 8:178 |
| pter-q13 | D10 S28 | 27 | 3 | 0.11 | Ovary | CR 51:5118 |
| pter-q13 | D10 S28 | 35 | 5 | 0.14 | Ovary | IJC 54:546 |
| Unknown | D10S13-28 | 33 | 4 | 0.12 | Ovary | CR 53:2393 |
| pter-q13 | D10 S28 | 7 | 3 | 0.43 | Pancreas | CR 54:2761 |
| pter-q13 | D10 S28 | 19 | 4 | 0.21 | Prostate | BJU 73:390 |
| 11-23.0 | D10S14 | 11 | 3 | 0.27 | Prostate | GCC 3:215 |
| 13-pter | D10S17 | 18 | 0 | 0 | Prostate | CSurveys 11 |

Chromosome 10 - p Arm

| | | | | | | |
|------------|---------|-----|-----|------|----------|-------------|
| pTER-p13 | D10S17 | 11 | 6 | 0.55 | Prostate | G 11:530 |
| pTER-p12 | D10S17 | 11 | 6 | 0.55 | Prostate | GCC 3:215 |
| pTER-p13 | D10S17 | 18 | 0 | 0 | Prostate | PNAS 87:875 |
| 13-12.2 | D10S24 | 14 | 4 | 0.29 | Prostate | GCC 3:215 |
| pTER-p12 | D10S17 | 14 | 5 | 0.36 | Sarcoma | CR 52:2419 |
| pTER-q13 | D10 S28 | 47 | 5 | 0.11 | Testis | O 9:2245 |
| Unknown | D10S28 | 14 | 4 | 0.29 | Uterus | GCC 9:119 |
| pTER-p11.2 | D10S89 | 17 | 0 | 0 | Uterus | CR 54:4294 |
| SUM | | 980 | 172 | 0.18 | | |

Chromosome 10 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|-----------------|-------|-------------|-----------|------------|--------------|
| 24-TER | PLAU | 5 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | Unknown | 37 | 14 | 0.38 | Brain | CR 50:5784 |
| 12-qter | Unknown | 12 | 0 | 0 | Brain | CR 54:1397 |
| 11.2 | Unknown | 12 | 0 | 0 | Brain | CR 54:1397 |
| 11.2 | Unknown | 17 | 2 | 0.12 | Brain | CR 54:1397 |
| 12-qter | Unknown | 15 | 1 | 0.07 | Brain | CR 54:1397 |
| Unknown | D10S25:22-1 | 64 | 21 | 0.33 | Brain | CR 56:164 |
| 22-23 | D10S1 | 5 | 0 | 0 | Brain | CR 48:5546 |
| 22-23 | D10S1 | 4 | 0 | 0 | Brain | CR 48:5546 |
| 22-23 | D10S1 | 10 | 10 | 1 | Brain | CR 48:5546 |
| Unknown | D10S169 | 7 | 0 | 0 | Brain | CR 53:2386 |
| Unknown | D10S169 | 5 | 2 | 0.4 | Brain | CR 53:2386 |
| 22-23 | D10S4 | 21 | 20 | 0.95 | Brain | CR 48:5546 |
| 22-23 | D10S4 | 6 | 0 | 0 | Brain | CR 48:5546 |
| 22-23 | D10S4 | 11 | 0 | 0 | Brain | CR 48:5546 |
| 24-TER | PLAU | 10 | 0 | 0 | Brain | CR 48:5546 |
| 24-TER | PLAU | 5 | 0 | 0 | Brain | CR 48:5546 |
| 24-TER | PLAU | 14 | 14 | 1 | Brain | CR 48:5546 |
| 22-23 | D10S1 | 18 | 2 | 0.11 | Breast | CR 53:4356 |
| 26 | D10S25 | 6 | 2 | 0.33 | Breast | CR 53:3804 |
| 26 | D10S25 | 23 | 2 | 0.09 | Breast | CR 50:7184 |
| 26 | D10S25 | 30 | 5 | 0.17 | Breast | GCC 2:191 |
| 22-23 | D10S4 | 18 | 4 | 0.22 | Breast | GCC 2:191 |
| Unknown | D10S205 | 32 | 4 | 0.12 | Cervix | CR 56:197 |
| 26 | D10S25 | 32 | 9 | 0.28 | Cervix | CR 54:4481 |
| 26 | D10S25 | 8 | 2 | 0.25 | Cervix | GCC 9:119 |
| 11 | D10S30 | 8 | 2 | 0.25 | Cervix | GCC 9:119 |
| 21.1 | D10S5 | 17 | 1 | 0.06 | Cervix | CR 54:4481 |
| 24-TER | PLAU | 4 | 1 | 0.25 | Cervix | CR 49:3598 |
| 24-TER | PLAU | 6 | 0 | 0 | Colon | IJC 53:382 |
| Unknown | D10S187 | 22 | 2 | 0.09 | Endocrine | CR 56:599 |
| 26 | D10S25 | 25 | 4 | 0.16 | Esophageal | CR 54:2996 |
| 26 | D10S25 | 36 | 6 | 0.17 | Esophageal | GCC 10:177 |
| 26 | D10S25 | 17 | 0 | 0 | Esophageal | CR 51:2113 |
| Unknown | D10S185 | 12 | 3 | 0.25 | Head&Neck | CR 54:4756 |
| Unknown | D10S185 | 21 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D10S221 | 24 | 5 | 0.21 | Head&Neck | CR 54:1152 |
| 22-25 | D10S13 | 32 | 9 | 0.28 | Kidney | CR 51:5817 |
| 21 | D10S14 | 17 | 5 | 0.29 | Kidney | CR 51:5817 |
| Unknown | D10S185 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| 21-TER | D10S20 | 25 | 8 | 0.32 | Kidney | CR 51:5817 |
| Unknown | D10S212-D10S190 | 19 | 1 | 0.05 | Kidney | PNAS 92:2854 |
| Unknown | D10S212-D10S190 | 5 | 0 | 0 | Kidney | PNAS 92:2854 |
| 21 | D10S22 | 10 | 3 | 0.3 | Kidney | CR 51:5817 |
| 21 | D10S23 | 15 | 3 | 0.2 | Kidney | CR 51:5817 |
| 26 | D10S25 | 30 | 10 | 0.33 | Kidney | CR 51:5817 |

Chromosome 10 - q Arm

| | | | | | | |
|---------|---------------|----|---|------|-------------------|----------------|
| 26 | D10S25 | 21 | 6 | 0.29 | Kidney | CR 51:820 |
| 22-25 | D10S27 | 26 | 3 | 0.12 | Kidney | CR 51:5817 |
| 11 | D10S30 | 13 | 2 | 0.15 | Kidney | CR 51:5817 |
| 26 | D10S36 | 27 | 5 | 0.19 | Kidney | CR 51:5817 |
| Unknown | D10S201 | 19 | 1 | 0.05 | Leukemia | CR 55:5377 |
| Unknown | Unknown | 16 | 0 | 0 | Liver | CR 51:89 |
| 22-23 | D10S1 | 3 | 1 | 0.33 | Liver | CCG 48:72 |
| 26 | D10S25 | 24 | 6 | 0.25 | Liver | CR 51:89 |
| Unknown | D10S26 | 24 | 6 | 0.25 | Liver | CR 51:89 |
| 24-TER | PLAU | 20 | 0 | 0 | Liver | JJCR 81:108 |
| 26 | D10S25 | 25 | 5 | 0.2 | Lung | CR 52:2475 |
| Unknown | ATC | 9 | 4 | 0.44 | Melanoma | CR 54:3111 |
| Unknown | CHDC, GGA2F11 | 14 | 6 | 0.43 | Melanoma | CR 54:3111 |
| Unknown | D10S108 | 5 | 1 | 0.2 | Melanoma | CR 54:3111 |
| Unknown | D10S110 | 4 | 2 | 0.5 | Melanoma | CR 54:3111 |
| Unknown | D10S168 | 8 | 5 | 0.62 | Melanoma | CR 54:3111 |
| Unknown | D10S169 | 8 | 1 | 0.12 | Melanoma | CR 54:3111 |
| Unknown | D10S185 | 29 | 9 | 0.31 | Melanoma | CR 56:589 |
| Unknown | D10S187 | 12 | 3 | 0.25 | Melanoma | CR 54:3111 |
| 21-22 | D10S19 | 8 | 3 | 0.38 | Melanoma | GCC 8:178 |
| 21-TER | D10S20 | 4 | 3 | 0.75 | Melanoma | GCC 8:178 |
| Unknown | D10S221 | 12 | 4 | 0.33 | Melanoma | CR 54:3111 |
| 26 | D10S36 | 9 | 4 | 0.44 | Melanoma | GCC 8:178 |
| Unknown | D10S610 | 9 | 4 | 0.44 | Melanoma | CR 54:3111 |
| Unknown | D10S88 | 6 | 3 | 0.5 | Melanoma | CR 54:3111 |
| 24-TER | PLAU | 5 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| Unknown | D10S1-20 | 19 | 2 | 0.11 | Ovary | CR 53:2393 |
| Unknown | D10S173 | 16 | 3 | 0.19 | Ovary | BJC 69:429 |
| 26 | D10S25 | 34 | 4 | 0.12 | Ovary | IJC 54:546 |
| 26 | D10S25 | 24 | 5 | 0.21 | Ovary | CR 51:5118 |
| 26 | D10S25 | 4 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | Unknown | 24 | 7 | 0.29 | Prostate | CSurveys 11:15 |
| 22-23 | D10S1 | 2 | 0 | 0 | Prostate | GCC 3:215 |
| 21-22 | D10S19 | 8 | 1 | 0.12 | Prostate | GCC 3:215 |
| 21-22 | D10S19 | 7 | 0 | 0 | Prostate | GCC 11:119 |
| 21-TER | D10S20 | 8 | 2 | 0.25 | Prostate | GCC 3:215 |
| 26 | D10S25 | 8 | 3 | 0.38 | Prostate | GCC 11:119 |
| 26 | D10S25 | 13 | 4 | 0.31 | Prostate | G 11:530 |
| 26 | D10S25 | 13 | 4 | 0.31 | Prostate | GCC 3:215 |
| Unknown | D10S26 | 9 | 2 | 0.22 | Prostate | GCC 3:215 |
| 22-23 | D10S4 | 10 | 1 | 0.1 | Prostate | GCC 3:215 |
| 26 | D10S90 | 19 | 8 | 0.42 | Prostate | BJU 73:390 |
| 26 | GAT | 25 | 7 | 0.28 | Prostate | PNAS 87:8751 |
| 24-TER | PLAU | 9 | 2 | 0.22 | Prostate | GCC 3:215 |
| 26 | D10S25 | 17 | 9 | 0.53 | Sarcoma | CR 52:2419 |
| Unknown | Unknown | 2 | 0 | 0 | Stomach | CR 48:2988 |

Chromosome 10 - q Arm

| | | | | | | |
|---------|---------|------|-----|------|---------|------------|
| Unknown | D10S26 | 20 | 0 | 0 | Stomach | CR 51:2926 |
| 26 | D10S25 | 34 | 9 | 0.26 | Testis | O 9:2245 |
| 11.2 | PTC | 1 | 0 | 0 | Testis | CCG 52:72 |
| 11.2 | PTC | 2 | 1 | 0.5 | Testis | CCG 52:72 |
| 11.2 | PTC | 1 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D10S173 | 16 | 1 | 0.06 | Uterus | CR 54:4294 |
| 26 | D10S25 | 14 | 6 | 0.43 | Uterus | GCC 9:119 |
| 11 | D10S30 | 12 | 3 | 0.25 | Uterus | GCC 9:119 |
| 24-TER | PLAU | 5 | 0 | 0 | Uterus | CR 51:5632 |
| SUM | | 1509 | 351 | 0.23 | | |

Chromosome 11 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|--------------|-------|-------------|-----------|-------------------|------------|
| Unknown | HRAS1-D11S12 | 17 | 7 | 0.41 | Bladder | CR 51:5405 |
| 15.5 | HRAS | 7 | 2 | 0.29 | Brain | CR 49:6572 |
| 15.5 | HRAS | 30 | 3 | 0.1 | Breast | GCC 1:113 |
| 15.5 | HRAS | 24 | 3 | 0.12 | Breast | CR 53:4486 |
| 15.5 | HRAS | 5 | 0 | 0 | Breast | GCC 2:191 |
| 15.5 | HRAS | 68 | 21 | 0.31 | Breast | GCC 12:304 |
| 15.5 | HRAS | 30 | 8 | 0.27 | Breast | IJC 53:11 |
| 15.5 | HRAS | 29 | 5 | 0.17 | Breast | JJCR 84:11 |
| 15.5 | HRAS | 7 | 1 | 0.14 | Breast | CR 53:3804 |
| 15.5 | HRAS | 33 | 1 | 0.03 | Breast | CR 53:4356 |
| 15.5 | HRAS | 37 | 7 | 0.19 | Breast | GP 5:554 |
| 15.5 | HRAS | 6 | 0 | 0 | Cervix | CR 49:3598 |
| 15.5 | HRAS | 18 | 6 | 0.33 | Cervix | PNAS 91:69 |
| 15.5 | HRAS | 15 | 1 | 0.07 | Cervix | BJC 67:71 |
| 15.5 | HRAS | 10 | 0 | 0 | Colon | N 331:273 |
| 15.5 | HRAS | 16 | 0 | 0 | Colon | CCG 48:167 |
| 15.5 | HRAS | 9 | 0 | 0 | Colon | N 331:273 |
| 15.5 | HRAS | 9 | 1 | 0.11 | Esophageal | CR 51:2113 |
| 15.5 | HRAS | 21 | 4 | 0.19 | Esophageal | GCC 10:177 |
| 15.5 | HRAS | 20 | 8 | 0.4 | Esophageal | CR 54:2996 |
| 15.5 | HRAS | 12 | 1 | 0.08 | Head&Neck | CR 52:1494 |
| 15.5 | HRAS | 3 | 0 | 0 | Kidney | CMB 38:59 |
| 15.5 | HRAS | 14 | 1 | 0.07 | Kidney | CR 51:1071 |
| 15.5 | HRAS | 5 | 0 | 0 | Kidney | CMB 38:59 |
| 15.5 | HRAS | 13 | 4 | 0.31 | Leukemia | B 75:819 |
| 15.5 | HRAS | 5 | 0 | 0 | Liver | JJCR 81:10 |
| 15.5 | HRAS | 3 | 0 | 0 | Liver | BJC 67:100 |
| 15.5 | HRAS | 13 | 0 | 0 | Liver | GCC 1:312 |
| 15.5 | HRAS | 4 | 0 | 0 | Liver | PNAS 86:88 |
| 15.5 | HRAS | 10 | 5 | 0.5 | Liver | CCG 48:72 |
| 15.5 | HRAS | 5 | 0 | 0 | Liver | BJC 64:108 |
| 15.5 | HRAS | 47 | 7 | 0.15 | Lung | GCC 10:183 |
| 15.5 | HRAS | 39 | 7 | 0.18 | Lung | CR 54:1145 |
| 15.5 | HRAS | 13 | 5 | 0.38 | Lung | PN 86:5099 |
| 15.5 | HRAS | 13 | 6 | 0.46 | Lung | PN 91:5513 |
| 15.5 | HRAS | 2 | 1 | 0.5 | Lung | PN 91:5513 |
| 15.5 | HRAS | 12 | 6 | 0.5 | Lung | PN 86:5099 |
| 15.5 | HRAS | 7 | 1 | 0.14 | Lung | NEJ 317:11 |
| 15.5 | HRAS | 5 | 2 | 0.4 | Lung | PN 86:5099 |
| 15.5 | HRAS | 13 | 3 | 0.23 | Lung | PN 84:9252 |
| 15.5 | HRAS | 6 | 2 | 0.33 | Lung | PN 91:5513 |
| 15.5 | HRAS | 4 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| 15.5 | HRAS | 25 | 10 | 0.4 | Ovary | GO 47:137 |
| 15.5 | HRAS | 15 | 4 | 0.27 | Ovary | GO 55:245 |
| 15.5 | HRAS | 11 | 5 | 0.45 | Ovary | CR 50:2724 |

Chromosome 11 - p Arm

| | | | | | | |
|---------|----------|----|----|------|-----------|------------|
| 15.5 | HRAS | 11 | 2 | 0.18 | Ovary | IJC 54:546 |
| 15.5 | HRAS | 27 | 12 | 0.44 | Ovary | C 72:2423 |
| 15.5 | HRAS | 10 | 5 | 0.5 | Ovary | CR 49:1220 |
| 15.5 | HRAS | 13 | 2 | 0.15 | Ovary | BJC 67:268 |
| 15.5 | HRAS | 19 | 9 | 0.47 | Ovary | BRJ 66:103 |
| 15.5 | HRAS | 5 | 2 | 0.4 | Pancreas | BJC 65:809 |
| 15.5 | HRAS | 20 | 7 | 0.35 | Pediatric | CR 50:3279 |
| 15.5 | HRAS | 15 | 5 | 0.33 | Pediatric | BG 97:163 |
| 15.5 | HRAS | 9 | 0 | 0 | Prostate | GCC 11:119 |
| 15.5 | HRAS | 11 | 5 | 0.45 | Sarcoma | CR 52:2419 |
| 15.5 | HRAS | 11 | 5 | 0.45 | Sarcoma | CR 52:2419 |
| 15.5 | HRAS | 9 | 0 | 0 | Stomach | CR 48:2988 |
| 15.5 | HRAS | 28 | 1 | 0.04 | Stomach | CR 51:2926 |
| 15.5 | HRAS | 19 | 7 | 0.37 | Stomach | HG 92:244 |
| 15.5 | HRAS | 6 | 0 | 0 | Stomach | HG 89:445 |
| 15.5 | HRAS | 15 | 7 | 0.47 | Testis | GCC 9:153 |
| 15.5 | HRAS | 5 | 2 | 0.4 | Testis | CCG 52:72 |
| 15.5 | HRAS | 12 | 3 | 0.25 | Testis | GCC 9:153 |
| 15.5 | HRAS | 13 | 5 | 0.38 | Testis | G 5:134 |
| 15.5 | HRAS | 17 | 3 | 0.16 | Testis | JU 153:168 |
| 15.5 | HRAS | 15 | 0 | 0 | Testis | GCC 13:249 |
| 15.5 | HRAS | 13 | 5 | 0.33 | Testis | GCC 7:85 |
| 15.5 | HRAS | 3 | 1 | 0.33 | Testis | CCG 52:72 |
| 15.5 | HRAS | 3 | 1 | 0.33 | Testis | CCG 52:72 |
| 15.5 | HRAS | 9 | 1 | 0.11 | Uterus | CR 51:5632 |
| 15.5 | IGF2 | 7 | 2 | 0.29 | Bladder | HG 91:455 |
| 15.5 | IGF2 | 15 | 1 | 0.07 | Breast | GE 5:554 |
| 15.5 | IGF2 | 13 | 3 | 0.23 | Cervix | O 12:423 |
| 15.5 | IGF2 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | IGF2 | 7 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | IGF2 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | IGF2 | 14 | 6 | 0.43 | Ovary | BRJ 66:103 |
| 15.5 | IGF2 | 9 | 6 | 0.67 | Testis | JU 153:168 |
| 15.5 | MUC2 | 17 | 2 | 0.12 | Testis | GCC 13:249 |
| 15.5 | H19 | 14 | 2 | 0.14 | Cervix | O 12:423 |
| Unknown | D11S922 | 46 | 8 | 0.17 | Head&Neck | CR 54:4756 |
| Unknown | D11S922 | 40 | 1 | 0.03 | Head&Neck | CR 54:4756 |
| Unknown | D11S922 | 6 | 1 | 0.17 | Kidney | PNAS 92:28 |
| Unknown | D11S922 | 19 | 1 | 0.05 | Kidney | PNAS 92:28 |
| Unknown | D11S922 | 8 | 4 | 0.5 | Pediatric | HG 97:163 |
| Unknown | D11S922 | 49 | 16 | 0.33 | Stomach | CR 56:268 |
| Unknown | D11S1318 | 16 | 7 | 0.44 | Pediatric | HG 97:163 |
| Unknown | D11S1318 | 15 | 9 | 0.6 | Stomach | CR 56:268 |
| 15.5 | INS | 31 | 3 | 0.1 | Breast | CR 50:7184 |
| 15.5 | INS | 23 | 4 | 0.17 | Breast | GCC 2:191 |
| 15.5 | INS | 31 | 3 | 0.1 | Breast | CR 50:7184 |

Chromosome 11 - p Arm

| | | | | | | |
|------|-----|----|----|------|--------------|------------|
| 15.5 | INS | 3 | 0 | 0 | Cervix | CR 49:3598 |
| 15.5 | INS | 3 | 0 | 0 | Cervix | CR 49:3598 |
| 15.5 | INS | 15 | 3 | 0.2 | Colon | IJC 53:382 |
| 15.5 | INS | 15 | 3 | 0.2 | Colon | IJC 53:382 |
| 15.5 | INS | 8 | 2 | 0.25 | Endocrine | CR 51:1154 |
| 15.5 | INS | 22 | 5 | 0.23 | Kidney | CR 51:820 |
| 15.5 | INS | 7 | 0 | 0 | Kidney | CMB 38:59 |
| 15.5 | INS | 21 | 3 | 0.14 | Kidney | CR 51:1031 |
| 15.5 | INS | 7 | 0 | 0 | Kidney | CMB 38:59 |
| 15.5 | INS | 22 | 5 | 0.23 | Kidney | CR 51:820 |
| 15.5 | INS | 6 | 0 | 0 | Liver | GCC 1:312 |
| 15.5 | INS | 6 | 1 | 0.17 | Liver | CR 51:456 |
| 15.5 | INS | 9 | 0 | 0 | Liver | JJCR 81:10 |
| 15.5 | INS | 11 | 3 | 0.27 | Liver | CR 51:898 |
| 15.5 | INS | 10 | 2 | 0.2 | Liver | CCG 48:72 |
| 15.5 | INS | 10 | 3 | 0.3 | Lung | PN 86:5099 |
| 15.5 | INS | 5 | 1 | 0.2 | Lung | PN 86:5099 |
| 15.5 | INS | 14 | 7 | 0.5 | Lung | PN 86:5099 |
| 15.5 | INS | 33 | 12 | 0.36 | Lung | GCC 10:183 |
| 15.5 | INS | 8 | 1 | 0.12 | Lung | PN 91:5513 |
| 15.5 | INS | 2 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | INS | 8 | 1 | 0.12 | Lung | PN 91:5513 |
| 15.5 | INS | 12 | 3 | 0.25 | Lung | PN 84:9252 |
| 15.5 | INS | 6 | 0 | 0 | Neuroblastom | CR 49:1095 |
| 15.5 | INS | 5 | 0 | 0 | Ovary | CR 50:2724 |
| 15.5 | INS | 13 | 7 | 0.54 | Ovary | GO 55:245 |
| 15.5 | INS | 32 | 12 | 0.38 | Ovary | C 72:2423 |
| 15.5 | INS | 27 | 7 | 0.26 | Ovary | CR 51:5116 |
| 15.5 | INS | 20 | 7 | 0.35 | Ovary | BRJ 66:103 |
| 15.5 | INS | 23 | 10 | 0.43 | Pediatric | CR 50:3279 |
| 15.5 | INS | 9 | 0 | 0 | Stomach | CR 48:2988 |
| 15.5 | INS | 2 | 0 | 0 | Stomach | CR 52:3099 |
| 15.5 | INS | 15 | 4 | 0.27 | Testis | GCC 7:96 |
| 15.5 | INS | 5 | 1 | 0.2 | Testis | CCG 52:72 |
| 15.5 | INS | 2 | 0 | 0 | Testis | CCG 52:72 |
| 15.5 | INS | 5 | 2 | 0.4 | Testis | CCG 52:72 |
| 15.5 | INS | 15 | 3 | 0.2 | Testis | G 5:134 |
| 15.5 | INS | 18 | 3 | 0.17 | Testis | GCC 13:249 |
| 15.5 | INS | 3 | 0 | 0 | Uterus | CR 51:5632 |
| 15.5 | TH | 15 | 1 | 0.07 | Brain | CR 54:1397 |
| 15.5 | TH | 21 | 3 | 0.14 | Brain | CR 54:1397 |
| 15.5 | TH | 16 | 4 | 0.25 | Breast | HMG 4:1889 |
| 15.5 | TH | 14 | 4 | 0.29 | Breast | CR 54:6270 |
| 15.5 | TH | 41 | 11 | 0.27 | Breast | CR 53:4486 |
| 15.5 | TH | 14 | 1 | 0.07 | Cervix | BJC 67:71 |
| 15.5 | TH | 20 | 8 | 0.4 | Cervix | PNAS 91:69 |

Chromosome 11 - p Arm

| | | | | | | |
|-----------|---------|----|----|------|------------|------------|
| 15.5 | TH | 10 | 0 | 0 | Kidney | CMB 38:59 |
| 15.5 | TH | 8 | 0 | 0 | Kidney | CMB 38:59 |
| 15.5 | TH | 8 | 1 | 0.12 | Lung | PN 91:5513 |
| 15.5 | TH | 10 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | TH | 2 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | TH | 20 | 7 | 0.35 | Ovary | GC 49:163 |
| 15.5 | TH | 23 | 9 | 0.39 | Pediatric | HG 97:163 |
| 15.5 | DRD4 | 7 | 1 | 0.14 | Lung | PN 91:5513 |
| 15.5 | DRD4 | 3 | 0 | 0 | Lung | PN 91:5513 |
| Unknown | D11S454 | 13 | 6 | 0.46 | Liver | CR 51:499 |
| Unknown | D11S454 | 18 | 4 | 0.22 | Lung | CR 52:2478 |
| Unknown | D11S454 | 11 | 0 | 0 | Ovary | CR 51:499 |
| 15.5 | D11S988 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S988 | 2 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S988 | 17 | 6 | 0.35 | Pediatric | HG 97:163 |
| 15.5 | D11S988 | 17 | 12 | 0.71 | Stomach | CR 56:252 |
| 15.5 | D11S12 | 32 | 5 | 0.16 | Breast | GE 5:554 |
| 15.5 | D11S12 | 9 | 1 | 0.33 | Breast | GCC 27:91 |
| 15.5 | D11S12 | 0 | 0 | 0 | Cervix | CR 49:3598 |
| 15.5 | D11S12 | 12 | 5 | 0.42 | Cervix | CR 54:4481 |
| 15.5 | D11S12 | 33 | 6 | 0.18 | Esophageal | CR 54:2996 |
| 15.5 | D11S12 | 15 | 3 | 0.2 | Kidney | CR 51:1071 |
| 15.5 | D11S12 | 11 | 8 | 0.73 | Lung | PN 91:5513 |
| 15.5 | D11S12 | 1 | 1 | 1 | Lung | PN 91:5513 |
| 15.5 | D11S12 | 4 | 2 | 0.5 | Lung | PN 91:5513 |
| 15.5 | D11S12 | 4 | 2 | 0.5 | Ovary | BRJ 66:103 |
| 15.5 | D11S12 | 3 | 1 | 0.33 | Stomach | HG 89:445 |
| 15.5 | D11S12 | 1 | 1 | 1 | Testis | CCG 52:72 |
| 15.5 | D11S12 | 20 | 6 | 0.3 | Testis | O 9:2245 |
| 15.5 | D11S12 | 1 | 0 | 0 | Testis | CCG 52:72 |
| 15.5 | D11S12 | 8 | 3 | 0.38 | Testis | JU 153:168 |
| 15.5 | D11S12 | 5 | 1 | 0.2 | Uterus | CR 51:5632 |
| 15.5-15.4 | RRM1 | 42 | 7 | 0.17 | Lung | GCC 10:183 |
| 15.5 | HBB | 27 | 9 | 0.33 | Breast | CR 53:4486 |
| 15 | HBB | 6 | 0 | 0 | Liver | PNAS 86:88 |
| 15.5 | HBB | 2 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | HBB | 4 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | HBB | 6 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | HBB2 | 2 | 0 | 0 | Lung | PN 86:5099 |
| 15.5 | HBB2 | 8 | 4 | 0.5 | Lung | PN 86:5099 |
| 15.5 | HBB2 | 5 | 4 | 0.8 | Lung | PN 86:5099 |
| 15.5 | HBB | 21 | 7 | 0.33 | Pediatric | HG 97:163 |
| 15 | GLOBIN | 30 | 4 | 0.13 | Breast | GE 5:554 |
| 15 | GLOBIN | 16 | 4 | 0.25 | Ovary | BRJ 66:103 |
| Unknown | GLOBIN | 14 | 5 | 0.36 | Ovary | BRJ 66:103 |
| Unknown | GLOBIN | 13 | 2 | 0.15 | Ovary | BRJ 66:103 |

Chromosome 11 - p Arm

| | | | | | | |
|-----------|---------|----|----|------|-----------|------------|
| 15.5 | D11S932 | 5 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S932 | 9 | 1 | 0.11 | Lung | PN 91:5513 |
| 15.5 | D11S932 | 1 | 0 | 0 | Lung | PN 91:5513 |
| Unknown | D11S569 | 27 | 13 | 0.48 | Stomach | CR 56:268 |
| Unknown | D11S569 | 24 | 3 | 0.12 | Uterus | CR 54:4294 |
| pter-15.4 | PTH | 11 | 1 | 0.09 | Bladder | HG 91:455 |
| pter-15.4 | PTH | 15 | 1 | 0.07 | Kidney | CR 51:1071 |
| pter-15.4 | PTH | 7 | 0 | 0 | Liver | GCC 1:312 |
| pter-15.4 | PTH | 8 | 1 | 0.12 | Liver | CCG 48:72 |
| pter-15.4 | PTH | 7 | 1 | 0.14 | Lung | PN 91:5513 |
| pter-15.4 | PTH | 5 | 1 | 0.2 | Lung | PN 91:5513 |
| pter-15.4 | PTH | 29 | 9 | 0.31 | Ovary | C 72:2423 |
| pter-15.4 | PTH | 7 | 0 | 0 | Testis | GCC 7:96 |
| pter-15.4 | PTH | 3 | 2 | 0.67 | Testis | CCG 52:72 |
| pter-15.4 | PTH | 1 | 0 | 0 | Testis | CCG 52:72 |
| pter-15.4 | PTH | 1 | 0 | 0 | Testis | CCG 52:72 |
| pter-15.4 | PTH | 15 | 6 | 0.4 | Testis | JU 153:168 |
| 13-15.1 | D11S419 | 14 | 6 | 0.43 | Ovary | BJC 69:429 |
| Unknown | D11S902 | 28 | 8 | 0.29 | Cervix | PNAS 91:69 |
| 14-qter | D11S899 | 23 | 4 | 0.17 | Head&Neck | CR 54:1152 |
| 14-qter | D11S899 | 6 | 0 | 0 | Kidney | GCC 12:76 |
| 15.5 | D11S861 | 21 | 5 | 0.24 | Endocrine | CR 56:599 |
| 15.5 | D11S861 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S861 | 9 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S861 | 7 | 0 | 0 | Lung | PN 91:5513 |
| Unknown | D11S860 | 27 | 9 | 0.33 | Breast | CR 53:4486 |
| 15.5 | D11S860 | 36 | 10 | 0.28 | Breast | Unknown |
| 15.5 | D11S860 | 36 | 10 | 0.28 | Breast | CR 54:6270 |
| 15.5 | D11S860 | 7 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S860 | 7 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S860 | 2 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S860 | 5 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S860 | 5 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S860 | 2 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | D11S860 | 16 | 6 | 0.38 | Pediatric | HG 97:163 |
| 15.5 | D11S860 | 44 | 16 | 0.36 | Stomach | CR 56:268 |
| 15.4 | CALCA | 6 | 0 | 0 | Bladder | HG 91:455 |
| 15.4 | CALCA | 17 | 1 | 0.06 | Breast | GCC 2:191 |
| 15.4 | CALCA | 22 | 0 | 0 | Breast | GE 5:554 |
| 15.4 | CALCA | 10 | 3 | 0.3 | Cervix | BJC 67:71 |
| 15.4 | CALCA | 5 | 0 | 0 | Kidney | CMB 38:59 |
| 15.4 | CALCA | 4 | 0 | 0 | Kidney | CMB 38:59 |
| 15.4 | CALCA | 7 | 0 | 0 | Liver | CCG 48:72 |
| 15.4 | CALCA | 10 | 1 | 0.1 | Liver | CR 51:4367 |
| 15.4 | CALCA | 3 | 0 | 0 | Liver | GCC 1:312 |
| 15.4 | CALCA | 6 | 0 | 0 | Lung | PN 86:5099 |

Chromosome 11 - p Arm

| | | | | | | |
|---------|---------|----|----|------|-----------|------------|
| 15.4 | CALCA | 6 | 1 | 0.17 | Lung | PN 91:5513 |
| 15.4 | CALCA | 6 | 2 | 0.33 | Lung | PN 86:5099 |
| 15.4 | CALCA | 2 | 0 | 0 | Lung | PN 86:5099 |
| 15.4 | CALCA | 3 | 1 | 0.33 | Lung | PN 91:5513 |
| 15.4 | CALCA | 10 | 3 | 0.3 | Ovary | C 72:2423 |
| 15.4 | CALCA | 15 | 6 | 0.4 | Ovary | BRJ 66:103 |
| 15.4 | CALCA | 7 | 0 | 0 | Stomach | HG 89:445 |
| 15.4 | CALCA | 6 | 3 | 0.5 | Testis | GCC 7:96 |
| Unknown | D11S929 | 33 | 3 | 0.09 | Cervix | CR 56:197 |
| Unknown | D11S929 | 17 | 4 | 0.24 | Pediatric | HG 97:163 |
| 13 | D11S323 | 3 | 1 | 0.33 | Lung | PN 91:5513 |
| 13 | D11S323 | 3 | 1 | 0.33 | Lung | PN 91:5513 |
| 13 | D11S907 | 16 | 3 | 0.19 | Endocrine | CR 56:599 |
| 13 | D11S907 | 14 | 1 | 0.07 | Head&Neck | CR 54:1152 |
| 13 | D11S907 | 1 | 0 | 0 | Kidney | GCC 12:76 |
| 13 | D11S16 | 17 | 4 | 0.24 | Cervix | PNAS 91:69 |
| 13 | D11S16 | 30 | 4 | 0.13 | Colon | IJC 53:382 |
| 13 | D11S16 | 5 | 0 | 0 | Kidney | CMB 38:59 |
| 13 | D11S16 | 4 | 0 | 0 | Kidney | CMB 38:59 |
| 13 | D11S16 | 6 | 0 | 0 | Liver | GCC 1:312 |
| 13 | D11S16 | 7 | 2 | 0.29 | Lung | PN 91:5513 |
| 13 | D11S16 | 1 | 1 | 1 | Lung | PN 91:5513 |
| 13 | D11S16 | 10 | 7 | 0.7 | Lung | PN 91:5513 |
| 13 | D11S16 | 25 | 2 | 0.08 | Ovary | IJC 54:546 |
| 13 | D11S16 | 23 | 6 | 0.26 | Ovary | BRJ 66:103 |
| 13 | D11S16 | 7 | 4 | 0.57 | Testis | JU 153:168 |
| 13 | D11S16 | 12 | 3 | 0.25 | Testis | GCC 9:153 |
| 13 | D11S16 | 12 | 5 | 0.42 | Testis | GCC 7:96 |
| 13 | D11S16 | 5 | 2 | 0.4 | Testis | GCC 9:153 |
| 13 | D11S16 | 13 | 1 | 0.08 | Uterus | CR 51:5632 |
| 13 | D11S151 | 4 | 0 | 0 | Lung | PN 91:5513 |
| 13 | D11S151 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 13 | D11S151 | 3 | 0 | 0 | Lung | PN 91:5513 |
| 13 | D11S151 | 11 | 3 | 0.27 | Pediatric | CR 50:3279 |
| 13 | D11S151 | 1 | 0 | 0 | Testis | GCC 9:153 |
| 13 | D11S151 | 4 | 0 | 0 | Testis | GCC 9:153 |
| 13 | CAT | 18 | 13 | 0.72 | Bladder | HG 91:455 |
| 13 | CAT | 1 | 0 | 0 | Kidney | CMB 38:59 |
| 13 | CAT | 16 | 2 | 0.12 | Kidney | CR 51:1071 |
| 13 | CAT | 6 | 1 | 0.17 | Kidney | CMB 38:59 |
| 13 | CAT | 7 | 0 | 0 | Liver | CCG 48:72 |
| 13 | CAT | 9 | 0 | 0 | Liver | GCC 1:312 |
| 13 | CAT | 8 | 3 | 0.38 | Lung | PN 86:5099 |
| 13 | CAT | 2 | 0 | 0 | Lung | PN 86:5099 |
| 13 | CAT | 40 | 6 | 0.15 | Lung | GCC 10:183 |
| 13 | CAT | 7 | 1 | 0.14 | Lung | PN 86:5099 |

Chromosome 11 - p Arm

| | | | | | | |
|---------|--------------|----|----|------|------------|------------|
| 13 | CAT | 2 | 1 | 0.5 | Lung | PN 91:5513 |
| 13 | CAT | 7 | 0 | 0 | Lung | PN 91:5513 |
| 13 | CAT | 10 | 0 | 0 | Ovary | IJC 54:546 |
| 13 | CAT | 24 | 6 | 0.25 | Ovary | BRJ 66:103 |
| 13 | CAT | 14 | 2 | 0.14 | Pediatric | CR 50:3279 |
| 13 | CAT | 4 | 1 | 0.25 | Stomach | HG 89:445 |
| 13 | CAT | 12 | 5 | 0.42 | Testis | JU 153:168 |
| 13 | CAT | 1 | 0 | 0 | Testis | CCG 52:72 |
| 13 | CAT | 3 | 1 | 0.33 | Testis | CCG 52:72 |
| 13 | CAT | 1 | 0 | 0 | Testis | CCG 52:72 |
| 13 | D11S325 | 3 | 0 | 0 | Lung | PN 91:5513 |
| 13 | D11S325 | 5 | 0 | 0 | Lung | PN 91:5513 |
| 13 | D11S325 | 6 | 2 | 0.33 | Testis | GCC 9:153 |
| 13 | D11S325 | 6 | 1 | 0.17 | Testis | GCC 9:153 |
| 13 | D11S325 | 16 | 2 | 0.12 | Testis | GCC 7:96 |
| 13 | D4S414 | 15 | 5 | 0.33 | Bladder | HG 91:455 |
| 13 | D4S414 | 2 | 1 | 0.5 | Lung | CR 54:5643 |
| 13 | D4S414 | 4 | 1 | 0.25 | Lung | CR 54:5643 |
| 13 | D4S414 | 21 | 4 | 0.19 | Lung | CR 54:5643 |
| 13 | B-FSH | 16 | 6 | 0.38 | Bladder | HG 91:455 |
| 13 | B-FSH | 4 | 0 | 0 | Cervix | BJC 67:71 |
| 13 | B-FSH | 46 | 9 | 0.2 | Lung | GCC 10:183 |
| 13 | B-FSH | 24 | 7 | 0.29 | Ovary | BRJ 66:103 |
| 13 | B-FSH | 14 | 5 | 0.36 | Pediatric | CR 50:3279 |
| 13 | B-FSH | 7 | 1 | 0.14 | Stomach | HG 89:445 |
| 13 | D11S905 | 25 | 0 | 0 | Esophageal | IJC 69:1 |
| 13 | D11S905 | 18 | 4 | 0.22 | Pediatric | HG 97:163 |
| 11.2-12 | D11S149 | 3 | 0 | 0 | Endocrine | CR 51:1154 |
| 11.2-12 | D11S149 | 7 | 1 | 0.14 | Lung | PN 91:5513 |
| 11.2-12 | D11S149 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 11.2-12 | D11S149 | 5 | 0 | 0 | Lung | PN 91:5513 |
| 12 | D11S288 | 10 | 2 | 0.2 | Cervix | PNAS 91:69 |
| 12 | D11S1313 | 48 | 12 | 0.25 | Lung | GCC 13:40 |
| 12 | D11S1313 | 48 | 12 | 0.25 | Lung | GCC 13:40 |
| Unknown | D11S:907-929 | 28 | 15 | 0.54 | Bladder | CR 55:5213 |
| Unknown | Unknown | 14 | 3 | 0.21 | Brain | CR 50:5784 |
| 15 | Unknown | 35 | 2 | 0.06 | Breast | JNCI 84:50 |
| Unknown | D11SS1318 | 18 | 6 | 0.33 | Breast | HMG 4:1889 |
| Unknown | D11SS1323 | 9 | 5 | 0.56 | Breast | HMG 4:1889 |
| Unknown | D11SS1338 | 9 | 5 | 0.56 | Breast | HMG 4:1889 |
| Unknown | D11SS1760 | 7 | 2 | 0.29 | Breast | HMG 4:1889 |
| 11 | D11S554 | 22 | 5 | 0.23 | Cervix | BJC 11:814 |
| Unknown | D11S740 | 5 | 0 | 0 | Cervix | GCC 9:119 |
| 11 | D11S554 | 22 | 6 | 0.27 | Endocrine | CR 56:599 |
| 15.5 | D11S576 | 25 | 0 | 0 | Kidney | BJC 69:230 |
| Unknown | D11S:922-904 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |

Chromosome 11 - p Arm

| | | | | | | |
|-----------|---------------------|----|----|------|-----------|------------|
| 15.5 | JW1-51 | 16 | 4 | 0.25 | Kidney | CR 51:1071 |
| pter-p13 | D11S17 | 6 | 0 | 0 | Liver | CCG 48:72 |
| 13 | D11S18 | 11 | 1 | 0.09 | Liver | CCG 48:72 |
| 13 | D11S21 | 5 | 0 | 0 | Liver | CCG 48:72 |
| 15 | HBBC | 8 | 1 | 0.12 | Liver | CCG 48:72 |
| 15.3-15.4 | D11S1243 | 57 | 14 | 0.25 | Lung | GCC 13:40 |
| 14 | D11S1246 | 57 | 17 | 0.3 | Lung | GCC 13:40 |
| 15.2-15.3 | D11S1250 | 50 | 17 | 0.34 | Lung | GCC 13:40 |
| 15.4-15.5 | D11S1251 | 66 | 21 | 0.32 | Lung | GCC 13:40 |
| 11.2-12 | D11S1252 | 54 | 13 | 0.24 | Lung | GCC 13:40 |
| 15.4-15.5 | D11S1254 | 39 | 12 | 0.31 | Lung | GCC 13:40 |
| Unknown | HRAS-INS-HBG | 1 | 1 | 1 | Lung | CR 50:2303 |
| Unknown | HRAS-INS-HBG | 27 | 4 | 0.15 | Lung | CR 50:2303 |
| Unknown | HRAS-INS-HBG | 1 | 0 | 0 | Lung | CR 50:2303 |
| Unknown | HRAS-INS-HBG | 13 | 4 | 0.31 | Lung | CR 50:2303 |
| Unknown | HRAS-INS-HBG | 3 | 0 | 0 | Lung | CR 50:2303 |
| 15.5 | ST5 | 4 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | ST5 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 15.5 | ST5 | 9 | 0 | 0 | Lung | PN 91:5513 |
| Unknown | D11S:922-904 | 32 | 4 | 0.12 | Melanoma | CR 56:589 |
| Unknown | Unknown | 11 | 2 | 0.18 | Ovary | IJC 52:575 |
| 15 | Unknown | 5 | 1 | 0.2 | Ovary | O 5:219 |
| 15 | Unknown | 9 | 4 | 0.44 | Ovary | O 5:219 |
| Unknown | CALCA-HRAS1-INS-PTH | 17 | 9 | 0.53 | Ovary | GO 55:198 |
| pter-p13 | D11S17 | 17 | 6 | 0.35 | Ovary | BRJ 66:103 |
| Unknown | D11S:554-875-971 | 18 | 6 | 0.33 | Ovary | BJC 72:193 |
| Unknown | RAS-CAT-D11S16 | 34 | 12 | 0.35 | Ovary | CR 53:2393 |
| 15.5 | Unknown | 3 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | D11S1323 | 7 | 2 | 0.29 | Pediatric | HG 97:163 |
| Unknown | D11S1338 | 14 | 3 | 0.21 | Pediatric | HG 97:163 |
| Unknown | D11S937 | 10 | 1 | 0.1 | Pediatric | HG 97:163 |
| 13 | WT1 | 16 | 8 | 0.5 | Pediatric | HG 97:163 |
| Unknown | Unknown | 11 | 0 | 0 | Prostate | CSurveys 1 |
| Unknown | Unknown | 10 | 0 | 0 | Prostate | PNAS 87:87 |
| Unknown | CALCA-HRAS1-HBG2 | 15 | 0 | 0 | Prostate | G 11:530 |
| Unknown | D11S2351 | 40 | 16 | 0.4 | Stomach | CR 56:268 |
| Unknown | D11S324 | 8 | 3 | 0.38 | Testis | GCC 9:153 |
| Unknown | D11S324 | 7 | 3 | 0.43 | Testis | GCC 9:153 |
| Unknown | D11S417 | 11 | 3 | 0.27 | Testis | GCC 9:153 |
| Unknown | D11S417 | 5 | 3 | 0.6 | Testis | GCC 9:153 |
| Unknown | FSHB | 4 | 0 | 0 | Testis | GCC 9:153 |
| Unknown | FSHB | 8 | 3 | 0.38 | Testis | GCC 9:153 |
| Unknown | FSHB | 7 | 2 | 0.29 | Testis | GCC 7:96 |
| 13 | WT1 | 10 | 5 | 0.5 | Testis | GCC 7:96 |
| Unknown | D11S740 | 8 | 1 | 0.12 | Uterus | GCC 9:119 |
| 13 | WT1 | 24 | 0 | 0 | Uterus | CR 54:4294 |

Chromosome 11 - p Arm

| | | | |
|-----|------|------|------|
| SUM | 4917 | 1151 | 0.23 |
|-----|------|------|------|

Chromosome 11 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|-----------|-------|-------------|-----------|------------|--------------|
| 12-13.2 | PYGM | 12 | 5 | 0.42 | Breast | CR 54:4586 |
| 12-13.3 | PYGM-INT2 | 36 | 24 | 0.67 | Breast | CR 55:467 |
| 12-13.2 | PYGM | 30 | 5 | 0.17 | Cervix | PNAS 91:6953 |
| 12-13.2 | PYGM | 3 | 2 | 0.67 | Endocrine | GCC 12:73 |
| 12-13.2 | PYGM | 16 | 6 | 0.38 | Endocrine | CR 56:599 |
| 12-13.2 | PYGM | 4 | 2 | 0.5 | Endocrine | CR 51:1154 |
| 12-13.2 | PYGM | 42 | 5 | 0.12 | Esophageal | GCC 10:177 |
| 12-13.2 | PYGM | 15 | 2 | 0.13 | Kidney | CR 51:5817 |
| 12-13.2 | PYGM | 13 | 0 | 0 | Prostate | G 11:530 |
| 12-13.2 | PYGM | 7 | 2 | 0.29 | Stomach | HG 89:445 |
| 12 | CD20 | 12 | 3 | 0.25 | Ovary | BJC 67:268 |
| Unknown | PGA | 11 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | PGA | 6 | 1 | 0.17 | Endocrine | CR 51:1154 |
| Unknown | PGA | 15 | 2 | 0.13 | Testis | GCC 7:96 |
| Unknown | PGA | 15 | 2 | 0.13 | Testis | LI 73:606 |
| 13 | FGF3 | 40 | 4 | 0.1 | Breast | CR 54:6270 |
| 13 | FGF3 | 16 | 3 | 0.19 | Ovary | BJC 67:268 |
| 13 | D11S913 | 36 | 0 | 0 | Esophageal | IJC 69:1 |
| 13.1 | D11S97 | 25 | 7 | 0.28 | Cervix | PNAS 91:6953 |
| 13.1 | D11S97 | 23 | 4 | 0.17 | Testis | GCC 13:249 |
| 12-13.2 | D11S146 | 6 | 2 | 0.33 | Endocrine | CR 51:1154 |
| 12-13.2 | D11S146 | 15 | 1 | 0.07 | Kidney | CR 51:5817 |
| 12-13.2 | D11S146 | 23 | 3 | 0.13 | Liver | CR 51:89 |
| 12-13.2 | D11S146 | 10 | 1 | 0.1 | Ovary | BJC 67:268 |
| 13 | WT-1 | 14 | 7 | 0.5 | Bladder | HG 91:455 |
| 13 | WT-1 | 13 | 4 | 0.31 | Breast | CR 54:6270 |
| 13 | WT-1 | 20 | 6 | 0.3 | Cervix | PNAS 91:6953 |
| 13 | WT-1 | 52 | 5 | 0.1 | Lung | GCC 10:183 |
| 13 | WT-1 | 21 | 4 | 0.19 | Lung | CR 54:5643 |
| 13 | WT-1 | 2 | 1 | 0.5 | Lung | CR 54:5643 |
| 13 | WT-1 | 4 | 0 | 0 | Lung | PN 91:5513 |
| 13 | WT-1 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 13 | WT-1 | 6 | 0 | 0 | Lung | PN 91:5513 |
| 13 | WT-1 | 4 | 1 | 0.25 | Lung | CR 54:5643 |
| 13 | INT2 | 22 | 8 | 0.36 | Bladder | CR 55:5213 |
| 13 | INT2 | 3 | 0 | 0 | Breast | CR 53:3804 |
| 13 | INT2 | 12 | 0 | 0 | Breast | CR 50:7184 |
| 13 | INT2 | 34 | 5 | 0.15 | Breast | CR 53:4356 |
| 13 | INT2 | 9 | 1 | 0.11 | Cervix | GCC 9:119 |
| 13 | INT2 | 22 | 1 | 0.05 | Cervix | CR 54:4481 |
| 13 | INT2 | 3 | 1 | 0.33 | Cervix | CR 54:4481 |
| 13 | INT2 | 15 | 0 | 0 | Cervix | CR 49:3598 |
| 13 | INT2 | 22 | 8 | 0.36 | Cervix | PNAS 91:6953 |
| 13 | INT2 | 22 | 7 | 0.32 | Colon | GCC 6:45 |
| 13 | INT2 | 5 | 2 | 0.4 | Endocrine | GCC 12:73 |
| 13 | INT2 | 11 | 3 | 0.27 | Endocrine | CR 51:1154 |

Chromosome 11 - q Arm

| | | | | | | |
|---------|---------|----|----|------|------------|--------------|
| 13 | INT2 | 9 | 0 | 0 | Esophageal | CR 51:2113 |
| 13 | INT2 | 13 | 6 | 0.46 | Head&Neck | CR 54:1152 |
| 13 | INT2 | 9 | 3 | 0.33 | Kidney | CR 51:820 |
| 13 | INT2 | 9 | 3 | 0.33 | Kidney | CR 51:5817 |
| 13 | INT2 | 4 | 1 | 0.25 | Kidney | CR 51:1071 |
| 13 | INT2 | 7 | 1 | 0.14 | Liver | CR 51:4367 |
| 13 | INT2 | 11 | 3 | 0.27 | Lung | PNAS 86:5099 |
| 13 | INT2 | 3 | 1 | 0.33 | Lung | PNAS 86:5099 |
| 13 | INT2 | 11 | 2 | 0.18 | Lung | PNAS 86:5099 |
| 13 | INT2 | 24 | 3 | 0.12 | Lung | CR 52:2478 |
| 13 | INT2 | 6 | 0 | 0 | Ovary | CR 50:2724 |
| 13 | INT2 | 21 | 0 | 0 | Ovary | IJC 54:546 |
| 13 | INT2 | 19 | 1 | 0.05 | Ovary | CR 51:5118 |
| 13 | INT2 | 8 | 2 | 0.25 | Stomach | HG 89:445 |
| 13 | INT2 | 18 | 0 | 0 | Stomach | CR 51:2926 |
| 13 | INT2 | 11 | 1 | 0.09 | Stomach | CR 48:2988 |
| 13 | INT2 | 27 | 4 | 0.15 | Testis | O 9:2245 |
| 13 | INT2 | 4 | 2 | 0.5 | Testis | O 9:2245 |
| 13 | INT2 | 3 | 1 | 0.33 | Testis | CCG 52:72 |
| 13 | INT2 | 4 | 1 | 0.25 | Testis | CCG 52:72 |
| 13 | INT2 | 11 | 2 | 0.18 | Uterus | GCC 9:119 |
| 13 | INT2 | 5 | 1 | 0.2 | Uterus | CR 51:5632 |
| 13.2-22 | D11S141 | 4 | 0 | 0 | Stomach | HG 89:445 |
| 13 | D11S534 | 23 | 6 | 0.26 | Cervix | BJC 71:814 |
| 13 | D11S534 | 13 | 4 | 0.31 | Ovary | Unknown |
| Unknown | D11S533 | 38 | 12 | 0.32 | Cervix | PNAS 91:6953 |
| Unknown | D11S533 | 21 | 5 | 0.24 | Endocrine | GCC 13:9 |
| Unknown | D11S533 | 16 | 4 | 0.25 | Ovary | GO 55:245 |
| Unknown | D11S911 | 23 | 3 | 0.13 | Cervix | CR 56:197 |
| 23.3 | D11S901 | 39 | 13 | 0.33 | Breast | CR 54:4586 |
| 23.3 | D11S901 | 33 | 11 | 0.33 | Cervix | PNAS 91:6953 |
| 23.3 | D11S901 | 21 | 6 | 0.29 | Stomach | CR 56:268 |
| 14-21 | TYR | 2 | 0 | 0 | Lung | PN 91:5513 |
| 14-21 | TYR | 7 | 0 | 0 | Lung | PN 91:5513 |
| 14-21 | TYR | 7 | 1 | 0.14 | Lung | PN 91:5513 |
| 14-21 | TYR | 16 | 3 | 0.19 | Ovary | BJC 67:268 |
| 14-21 | TYR | 3 | 2 | 0.67 | Stomach | HG 89:445 |
| 22-23 | D11S923 | 36 | 2 | 0.06 | Esophageal | IJC 69:1 |
| 22 | D11S35 | 28 | 7 | 0.25 | Breast | CR 54:6270 |
| 22 | D11S35 | 34 | 12 | 0.35 | Breast | CR 54:4586 |
| 22 | D11S35 | 21 | 12 | 0.57 | Cervix | PNAS 91:6953 |
| 22 | D11S35 | 34 | 10 | 0.29 | Stomach | CR 56:268 |
| 22 | D11S35 | 33 | 4 | 0.12 | Uterus | CR 54:4294 |
| 22 | STMY1 | 12 | 6 | 0.5 | Colon | GCC 6:45 |
| 22 | STMY1 | 11 | 6 | 0.55 | Ovary | BJC 67:268 |
| 22 | STMY1 | 7 | 2 | 0.29 | Stomach | HG 89:445 |

Chromosome 11 - q Arm

| | | | | | | |
|-----------|----------|----|----|------|------------|--------------|
| 22-23 | DRD2 | 68 | 23 | 0.34 | Colon | BJC 70:395 |
| Unknown | D11S1341 | 8 | 3 | 0.38 | Stomach | CR 56:268 |
| 22.3-23.3 | D11S144 | 6 | 1 | 0.17 | Brain | CR 49:6572 |
| 22.3-23.3 | D11S144 | 19 | 13 | 0.68 | Cervix | PNAS 91:6953 |
| 22.3-23.3 | D11S144 | 15 | 3 | 0.2 | Esophageal | CR 54:2996 |
| 22.3-23.3 | D11S144 | 17 | 5 | 0.29 | Ovary | BJC 67:268 |
| 22.3-23.3 | D11S144 | 4 | 2 | 0.5 | Pancreas | CR 54:2761 |
| 22.3-23.3 | D11S144 | 21 | 4 | 0.19 | Sarcoma | CR 52:2419 |
| 22.3-23.3 | D11S144 | 4 | 0 | 0 | Stomach | HG 89:445 |
| 23.3 | D11S29 | 47 | 15 | 0.32 | Breast | CR 54:6270 |
| 23.3 | D11S29 | 1 | 0 | 0 | Breast | CR 53:3804 |
| 23.3 | D11S29 | 25 | 25 | 1 | Cervix | BJC 71:814 |
| 23.3 | D11S29 | 2 | 1 | 0.5 | Colon | GCC 6:45 |
| 23.3 | D11S29 | 12 | 7 | 0.58 | Melanoma | GCC 7:169 |
| 23.3 | D11S29 | 15 | 7 | 0.47 | Ovary | BJC 67:268 |
| 23.3 | D11S29 | 10 | 6 | 0.6 | Stomach | CR 56:268 |
| 23 | CD3 | 7 | 4 | 0.57 | Colon | GCC 6:45 |
| 23.3 | CD3 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 23.3 | CD3 | 9 | 0 | 0 | Lung | PN 91:5513 |
| 23.3 | CD3 | 3 | 0 | 0 | Lung | PN 91:5513 |
| 23.3 | CD3 | 16 | 7 | 0.44 | Ovary | BJC 67:268 |
| 23 | CD3 | 4 | 2 | 0.5 | Stomach | HG 89:445 |
| 23.3 | CD3 | 36 | 8 | 0.22 | Stomach | CR 56:268 |
| 23 | D11S528 | 42 | 16 | 0.38 | Breast | CR 54:6270 |
| 23 | D11S528 | 44 | 7 | 0.16 | Stomach | CR 56:268 |
| 22.3-23 | THY1 | 33 | 14 | 0.42 | Breast | CR 54:4591 |
| 22.3-23 | THY1 | 6 | 1 | 0.17 | Stomach | HG 89:445 |
| 23.3-qter | D11S147 | 12 | 8 | 0.67 | Ovary | BJC 67:268 |
| 22-23.3 | APOC3 | 35 | 12 | 0.34 | Breast | CR 54:4586 |
| 22-23.3 | APOC3 | 30 | 19 | 0.63 | Cervix | PNAS 91:6953 |
| 22-23.3 | APOC3 | 22 | 0 | 0 | Pediatric | HG 97:163 |
| Unknown | D11S836 | 17 | 6 | 0.35 | Ovary | Unknown |
| Unknown | D11S934 | 30 | 5 | 0.17 | Cervix | CR 56:197 |
| 23 | ETS1 | 5 | 3 | 0.6 | Colon | GCC 6:45 |
| 23 | ETS1 | 1 | 0 | 0 | Lung | PN 91:5513 |
| 23 | ETS1 | 4 | 0 | 0 | Lung | PN 91:5513 |
| 23 | ETS1 | 5 | 0 | 0 | Lung | PN 91:5513 |
| 23 | ETS1 | 1 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D11S910 | 22 | 3 | 0.14 | Head&Neck | CR 54:4756 |
| Unknown | D11S910 | 31 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D11S910 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | D11S910 | 30 | 5 | 0.17 | Melanoma | CR 56:589 |
| 22.3-23 | D11S968 | 33 | 14 | 0.42 | Breast | CR 54:4586 |
| 22.3-23 | D11S968 | 25 | 14 | 0.56 | Cervix | PNAS 91:6953 |
| 22.3-23 | D11S968 | 5 | 1 | 0.2 | Kidney | PNAS 92:2854 |
| 22.3-23 | D11S968 | 17 | 1 | 0.06 | Kidney | PNAS 92:2854 |

Chromosome 11 - q Arm

| | | | | | | |
|-----------|----------|------|-----|------|-----------|--------------|
| 22.3-23 | D11S969 | 17 | 1 | 0.06 | Kidney | PNAS 92:2854 |
| Unknown | Unknown | 16 | 1 | 0.06 | Brain | CR 50:5784 |
| 13 | Unknown | 25 | 1 | 0.04 | Breast | JNCI 84:506 |
| Unknown | D11S485 | 16 | 9 | 0.56 | Cervix | PNAS 91:6953 |
| 13 | Unknown | 7 | 0 | 0 | Endocrine | N 328:524 |
| Unknown | D11S129 | 7 | 1 | 0.14 | Endocrine | CR 51:1154 |
| Unknown | D11S1383 | 5 | 4 | 0.8 | Endocrine | CR 56:599 |
| Unknown | D11S460 | 7 | 3 | 0.43 | Endocrine | GCC 12:73 |
| Unknown | D11S476 | 2 | 1 | 0.5 | Endocrine | GCC 12:73 |
| Unknown | D11S527 | 7 | 5 | 0.71 | Endocrine | CR 56:599 |
| Unknown | D11S546 | 4 | 0 | 0 | Endocrine | GCC 12:73 |
| Unknown | D11S614 | 22 | 5 | 0.23 | Endocrine | CR 56:599 |
| Unknown | D11S787 | 6 | 4 | 0.67 | Endocrine | CR 56:599 |
| Unknown | D11S873 | 23 | 6 | 0.26 | Endocrine | CR 56:599 |
| Unknown | D11S874 | 13 | 3 | 0.23 | Endocrine | CR 56:599 |
| Unknown | D11S490 | 19 | 9 | 0.47 | Head&Neck | CR 54:1152 |
| 13 | Unknown | 7 | 0 | 0 | Liver | BJC 67:1007 |
| 13 | Unknown | 10 | 0 | 0 | Liver | BJC 64:1083 |
| 13-23 | D11S24 | 2 | 0 | 0 | Liver | JJ 81:108 |
| 14-22.3 | D11S1240 | 53 | 12 | 0.23 | Lung | GCC 13:40 |
| 13.1-13.4 | D11S1253 | 67 | 13 | 0.19 | Lung | GCC 13:40 |
| 21-23.2 | D11S1256 | 67 | 21 | 0.31 | Lung | GCC 13:40 |
| 14-22.3 | D11S1260 | 20 | 8 | 0.4 | Lung | GCC 13:40 |
| 13.4-14 | D11S1261 | 39 | 11 | 0.28 | Lung | GCC 13:40 |
| 23.2-23.3 | D11S1263 | 65 | 11 | 0.17 | Lung | GCC 13:40 |
| 23.2-23.3 | D11S1265 | 50 | 14 | 0.28 | Lung | GCC 13:40 |
| 14-22.3 | D11S1268 | 30 | 10 | 0.33 | Lung | GCC 13:40 |
| 13-23 | D11S24 | 2 | 0 | 0 | Lung | PN 84:9252 |
| 24 | D11S488 | 17 | 5 | 0.29 | Ovary | GO 55:245 |
| Unknown | D11S85 | 15 | 5 | 0.33 | Ovary | CR 53:2393 |
| 13 | FOLR1 | 14 | 1 | 0.07 | Ovary | BJC 67:268 |
| 13 | Unknown | 8 | 3 | 0.38 | Pancreas | BJC 65:809 |
| Unknown | D11S1818 | 38 | 11 | 0.29 | Stomach | CR 56:268 |
| 13-23 | D11S24 | 2 | 0 | 0 | Stomach | CR 48:2988 |
| 13-23 | D11S24 | 1 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | D11S420 | 19 | 0 | 0 | Uterus | CR 54:4294 |
| SUM | | 2978 | 764 | 0.26 | | |

Chromosome 12 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|---------------|-------|-------------|-----------|-------------------|--------------|
| 12.1 | KRAS2 | 3 | 0 | 0 | Uterus | CR 51:5632 |
| Unknown | D12S16 | 16 | 1 | 0.06 | Brain | CR 50:5784 |
| Unknown | D12S16 | 12 | 2 | 0.17 | Breast | CR 50:7184 |
| Unknown | D12S16 | 23 | 2 | 0.09 | Breast | CR 53:4356 |
| Unknown | D12S2 | 16 | 2 | 0.12 | Cervix | CR 54:4481 |
| Unknown | D12S87 | 24 | 2 | 0.08 | Cervix | CR 56:197 |
| Unknown | D12S89 | 25 | 2 | 0.08 | Cervix | CR 56:197 |
| 12.1 | KRAS2 | 7 | 0 | 0 | Colon | N 331:273 |
| Unknown | D12S77 | 18 | 2 | 0.11 | Endocrine | CR 56:599 |
| Unknown | D12S16 | 26 | 1 | 0.04 | Esophageal | CR 54:2996 |
| Unknown | D12S16 | 7 | 2 | 0.29 | Esophageal | GCC 10:177 |
| Unknown | D12S62 | 28 | 5 | 0.18 | Head&Neck | CR 54:1152 |
| Unknown | D12S98 | 19 | 1 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D12S98 | 17 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D12S16 | 10 | 0 | 0 | Kidney | CR 51:820 |
| Unknown | D12S94-D12S77 | 5 | 1 | 0.2 | Kidney | PNAS 92:2854 |
| Unknown | D12S94-D12S77 | 20 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D12S98 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | Unknown | 43 | 8 | 0.19 | Leukemia | B 86:3869 |
| Unknown | Unknown | 35 | 8 | 0.23 | Leukemia | B 86:3869 |
| Unknown | D12S58 | 44 | 9 | 0.2 | Leukemia | B 86:3869 |
| Unknown | D12S64 | 54 | 7 | 0.13 | Leukemia | B 86:3869 |
| Unknown | D12S69 | 46 | 4 | 0.09 | Leukemia | B 86:3869 |
| Unknown | D12S89 | 82 | 21 | 0.26 | Leukemia | B 87:3368 |
| Unknown | D12S89 | 50 | 11 | 0.22 | Leukemia | B 86:3869 |
| Unknown | D12S91 | 48 | 9 | 0.19 | Leukemia | B 86:3869 |
| Unknown | D12S94-D12S77 | 51 | 6 | 0.12 | Leukemia | B 86:3869 |
| Unknown | D12S:89-91 | 50 | 13 | 0.26 | Leukemia | CR 55:5377 |
| Unknown | D12S16 | 12 | 1 | 0.08 | Liver | CR 51:89 |
| 12.1 | KRAS2 | 4 | 0 | 0 | Liver | CCG 48:72 |
| Unknown | D12S16 | 25 | 5 | 0.2 | Lung | CR 52:2478 |
| 12.1 | KRAS2 | 3 | 1 | 0.33 | Lung | PN 84:9252 |
| Unknown | D12S98 | 19 | 0 | 0 | Melanoma | CR 56:589 |
| 12.1 | KRAS2 | 2 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| 13.3-12.3 | A2M | 10 | 1 | 0.1 | Ovary | IJC 54:546 |
| Unknown | D12S16 | 8 | 3 | 0.38 | Ovary | CR 51:5118 |
| 12-PTER | PRVWF | 16 | 1 | 0.06 | Ovary | BJC 69:429 |
| 12.1 | KRAS2 | 7 | 0 | 0 | Ovary | CR 50:2724 |
| Unknown | PRB1 | 23 | 2 | 0.09 | Ovary | CR 53:2393 |
| Unknown | D12S16 | 9 | 1 | 0.11 | Prostate | G 11:530 |
| 12.1 | KRAS2 | 4 | 1 | 0.25 | Stomach | CR 48:2988 |
| 12.1 | KRAS2 | 7 | 0 | 0 | Testis | GCC 13:249 |
| Unknown | PRB1-PRB4 | 11 | 2 | 0.18 | Testis | LI 73:606 |
| Unknown | D12S61 | 14 | 1 | 0.07 | Uterus | CR 54:4294 |
| 12.1 | KRAS2 | 3 | 0 | 0 | Uterus | CR 51:5632 |

Chromosome 12 - p Arm

| | | | |
|-----|-----|-----|------|
| SUM | 959 | 141 | 0.15 |
|-----|-----|-----|------|

Chromosome 12 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|---------------|-------|-------------|-----------|------------|--------------|
| Unknown | IGF1 | 11 | 1 | 0.09 | Uterus | CR 54:4294 |
| Unknown | Unknown | 14 | 1 | 0.07 | Brain | CR 50:5784 |
| Unknown | D12S17 | 19 | 1 | 0.05 | Breast | CR 50:7184 |
| 14-24.1 | D12S7 | 35 | 2 | 0.06 | Breast | GCC 2:191 |
| Unknown | D12S17 | 8 | 1 | 0.12 | Cervix | GCC 9:119 |
| Unknown | D12S7 | 31 | 1 | 0.03 | Cervix | CR 54:4481 |
| Unknown | D12S78 | 31 | 6 | 0.19 | Cervix | CR 56:197 |
| Unknown | D12S83 | 22 | 1 | 0.05 | Cervix | CR 56:197 |
| Unknown | D12S17 | 19 | 1 | 0.05 | Colon | CCG 48:167 |
| Unknown | D12S17 | 17 | 4 | 0.24 | Colon | IJC 53:382 |
| 14-24.1 | D12S7 | 22 | 3 | 0.14 | Colon | N 331:273 |
| 14-qter | D12S8 | 24 | 4 | 0.17 | Colon | N 331:273 |
| 24.3-qter | D12S11 | 13 | 0 | 0 | Endocrine | N 328:524 |
| Unknown | D12S392 | 16 | 1 | 0.06 | Endocrine | CR 56:599 |
| Unknown | D12S43 | 23 | 0 | 0 | Endocrine | GCC 13:9 |
| Unknown | D12S14 | 18 | 3 | 0.17 | Esophageal | CR 54:2996 |
| Unknown | D12S17 | 9 | 1 | 0.11 | Esophageal | CR 51:2113 |
| Unknown | D12S17 | 34 | 3 | 0.09 | Esophageal | GCC 10:177 |
| Unknown | D12S17 | 23 | 2 | 0.09 | Esophageal | CR 54:2996 |
| Unknown | D12S60 | 24 | 6 | 0.25 | Head&Neck | CR 54:1152 |
| Unknown | D12S86 | 24 | 4 | 0.17 | Head&Neck | CR 54:4756 |
| Unknown | D12S86 | 18 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D12S17 | 24 | 0 | 0 | Kidney | CR 51:820 |
| Unknown | D12S86 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | D12S97-D12S86 | 19 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D12S97-D12S86 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| 24.3-qter | Unknown | 12 | 1 | 0.08 | Liver | BJC 64:1083 |
| 24.3-qter | Unknown | 7 | 0 | 0 | Liver | BJC 67:1007 |
| Unknown | D12S17 | 14 | 1 | 0.07 | Liver | CR 51:89 |
| Unknown | D12S17 | 15 | 1 | 0.07 | Liver | JJCR 81:108 |
| Unknown | D12S17 | 29 | 4 | 0.14 | Lung | CR 52:2478 |
| Unknown | D12S86 | 23 | 0 | 0 | Melanoma | CR 56:589 |
| Unknown | D12S17 | 25 | 6 | 0.24 | Ovary | CR 53:2393 |
| Unknown | D12S17 | 15 | 5 | 0.33 | Ovary | CR 51:5118 |
| Unknown | D12S60 | 15 | 2 | 0.13 | Ovary | BJC 69:429 |
| 22-24.2 | PAH | 26 | 2 | 0.08 | Ovary | IJC 54:546 |
| 24.3-qter | Unknown | 13 | 0 | 0 | Pancreas | BJC 65:809 |
| 24.3-qter | Unknown | 6 | 3 | 0.5 | Pancreas | CR 54:2761 |
| Unknown | D12S17 | 6 | 0 | 0 | Pancreas | CR 54:2761 |
| 14-24.1 | D12S7 | 17 | 1 | 0.06 | Prostate | G 11:530 |
| Unknown | D12S17 | 26 | 5 | 0.19 | Sarcoma | CR 52:2419 |
| CEN-q14 | D12S4 | 5 | 1 | 0.2 | Sarcoma | CR 52:2419 |
| 2.4-ter | Unknown | 11 | 6 | 0.55 | Stomach | BJC 59:750 |
| 24.3-qter | D12S11 | 32 | 5 | 0.16 | Stomach | HG 92:244 |
| Unknown | D12S17 | 41 | 11 | 0.27 | Stomach | CR 51:2926 |
| 12-13.2 | COL2A1 | 11 | 0 | 0 | Testis | GCC 13:249 |

Chromosome 12 - q Arm

| | | | | | | |
|-----------|--------|------|-----|------|--------|------------|
| 24.3-qter | D12S11 | 30 | 0 | 0 | Testis | GCC 13:249 |
| Unknown | D12S12 | 15 | 7 | 0.47 | Testis | O 9:2245 |
| Unknown | D12S14 | 19 | 3 | 0.16 | Testis | O 9:2245 |
| Unknown | D12S15 | 14 | 1 | 0.07 | Testis | O 9:2245 |
| Unknown | D12S17 | 26 | 7 | 0.27 | Testis | O 9:2245 |
| CEN-q14 | D12S4 | 23 | 4 | 0.17 | Testis | O 9:2245 |
| Unknown | D12S6 | 17 | 7 | 0.41 | Testis | O 9:2245 |
| 14-24.1 | D12S7 | 6 | 1 | 0.17 | Testis | LI 73:606 |
| 14-24.1 | D12S7 | 15 | 0 | 0 | Testis | GCC 13:249 |
| Unknown | D12S7 | 1 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D12S7 | 3 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D12S7 | 1 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D12S7 | 19 | 8 | 0.42 | Testis | O 9:2245 |
| 14-qter | D12S8 | 8 | 1 | 0.12 | Testis | O 9:2245 |
| Unknown | D12S17 | 23 | 4 | 0.17 | Uterus | GCC 9:119 |
| Unknown | D12S60 | 17 | 1 | 0.06 | Uterus | CR 54:4294 |
| Unknown | IGF1 | 11 | 1 | 0.09 | Uterus | CR 54:4294 |
| SUM | | 1096 | 147 | 0.13 | | |

Chromosome 13 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------|-------|-------------|-----------|--------------|--------------|
| 12 | D13S36 | 19 | 5 | 0.26 | Ovary | IJC 54:546 |
| 12 | D13S36 | 19 | 3 | 0.16 | Ovary | IJC 52:575 |
| 12.3 | D13S11 | 9 | 3 | 0.33 | Ovary | IJC 54:546 |
| 12.3 | D13S11 | 6 | 5 | 0.83 | Sarcoma | CGC 53:45 |
| Unknown | D13S115 | 13 | 6 | 0.46 | Head&Neck | CR 54:1152 |
| Unknown | D13S115 | 16 | 2 | 0.12 | Ovary | BJC 69:429 |
| Unknown | D13S221 | 28 | 7 | 0.25 | Bladder | Unknown |
| Unknown | D13S221 | 39 | 17 | 0.44 | Breast | GCC 13:291 |
| 12.3 | D13S6 | 4 | 2 | 0.5 | Breast | PNAS 84:2372 |
| 12.3 | D13S6 | 13 | 5 | 0.38 | Colon | IJC 53:382 |
| 12.3 | D13S6 | 1 | 0 | 0 | Colon | CCG 48:167 |
| 12.3 | D13S6 | 8 | 2 | 0.25 | Ovary | IJC 54:546 |
| 12.3 | D13S6 | 9 | 0 | 0 | Stomach | G 2:180 |
| 12.3 | D13S6 | 7 | 2 | 0.29 | Uterus | CR 51:5632 |
| Unknown | D13S289 | 35 | 17 | 0.49 | Breast | GCC 13:291 |
| 12 | FLT1 | 7 | 0 | 0 | Brain | CR 54:1397 |
| 12 | FLT1 | 9 | 3 | 0.33 | Brain | CR 54:1397 |
| 12 | FLT1 | 18 | 6 | 0.33 | Ovary | CR 54:605 |
| 12 | FLT1 | 5 | 1 | 0.2 | Ovary | BJC 69:429 |
| 12.3 | D13S33 | 21 | 4 | 0.19 | Ovary | IJC 54:546 |
| 12.3 | D13S33 | 23 | 6 | 0.26 | Ovary | IJC 52:575 |
| 12 | D13S260 | 43 | 13 | 0.3 | Breast | GCC 13:291 |
| 13 | D13S1 | 94 | 26 | 0.28 | Bladder | O 6:2305 |
| 14-12 | D13S1 | 34 | 7 | 0.21 | Breast | GE 5:554 |
| 13 | D13S1 | 8 | 3 | 0.38 | Breast | PNAS 84:2372 |
| 13 | D13S1 | 13 | 4 | 0.31 | Breast | GCC 2:191 |
| 13 | D13S1 | 7 | 2 | 0.29 | Cervix | CR 49:3598 |
| 14-12 | D13S1 | 11 | 1 | 0.09 | Colon | JNCI 84:1100 |
| 13 | D13S1 | 15 | 7 | 0.47 | Colon | IJC 53:382 |
| 12 | D13S1 | 12 | 1 | 0.08 | Colon | CCG 48:167 |
| 13 | D13S1 | 14 | 4 | 0.29 | Esophageal | CR 54:2996 |
| 13 | D13S1 | 10 | 2 | 0.2 | Kidney | CR 51:1071 |
| 13 | D13S1 | 25 | 5 | 0.2 | Liver | JJCR 84:893 |
| 14-12 | D13S1 | 15 | 5 | 0.33 | Liver | CR 54:281 |
| 14-12 | D13S1 | 5 | 2 | 0.4 | Liver | CCG 48:12 |
| 12 | D13S1 | 9 | 0 | 0 | Liver | JJCR 81:108 |
| 14-12 | D13S1 | 9 | 6 | 0.67 | Liver | CR 51:4367 |
| 13 | D13S1 | 19 | 8 | 0.42 | Lung | PN 84:9252 |
| 14-12 | D13S1 | 8 | 7 | 0.88 | Lung | CR 49:5130 |
| 12 | D13S1 | 1 | 0 | 0 | Lung | PN 84:9252 |
| 13 | D13S1 | 5 | 0 | 0 | Neuroblastom | CR 49:1095 |
| 13 | D13S1 | 15 | 2 | 0.13 | Ovary | IJC 54:546 |
| 13 | D13S1 | 12 | 9 | 0.75 | Sarcoma | CR 52:2419 |
| 13 | D13S1 | 6 | 0 | 0 | Stomach | HG 89:445 |
| 14-12 | D13S1 | 10 | 1 | 0.1 | Stomach | CR 48:2988 |

Chromosome 13 - q Arm

| | | | | | | |
|-----------|---------|-----|----|------|------------|--------------|
| 14-12 | D13S1 | 11 | 1 | 0.09 | Testis | LI 73:606 |
| 13 | D13S1 | 3 | 0 | 0 | Testis | CCG 52:72 |
| 13 | D13S1 | 3 | 1 | 0.33 | Testis | CCG 52:72 |
| 13 | D13S1 | 1 | 0 | 0 | Testis | CCG 52:72 |
| 13 | D13S1 | 8 | 1 | 0.12 | Uterus | CR 51:5632 |
| 12 | D13S267 | 32 | 16 | 0.5 | Breast | GCC 13:291 |
| 14 | D13S218 | 140 | 33 | 0.24 | Leukemia | CR 55:2044 |
| 12 | D13S263 | 45 | 20 | 0.44 | Breast | GCC 13:291 |
| 14 | D13S22 | 17 | 5 | 0.29 | Breast | GE 5:554 |
| 14 | D13S22 | 11 | 3 | 0.27 | Breast | GE 5:554 |
| 14 | D13S22 | 12 | 0 | 0 | Pediatric | CR 50:3279 |
| 14 | D13S22 | 8 | 7 | 0.88 | Sarcoma | GCC 53:45 |
| 14 | D13S153 | 42 | 15 | 0.36 | Breast | GCC 13:291 |
| 14.3 | D13S133 | 18 | 10 | 0.56 | Head&Neck | CR 54:152 |
| 14.3 | D13S133 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| 14.3 | D13S133 | 140 | 5 | 0.04 | Leukemia | CR 55:2044 |
| 14.3 | D13S133 | 11 | 0 | 0 | Ovary | CR 54:605 |
| 14.3 | D13S133 | 18 | 11 | 0.61 | Ovary | CR 54:605 |
| 14.3 | D13S133 | 21 | 7 | 0.33 | Prostate | HUPATH 27:28 |
| 14.3-21.1 | D13S31 | 29 | 9 | 0.31 | Ovary | IJC 52:575 |
| 14.3-21 | D13S31 | 26 | 6 | 0.23 | Ovary | IJC 54:546 |
| 14 | RB | 94 | 28 | 0.3 | Bladder | O 6:2305 |
| 14 | RB | 9 | 4 | 0.44 | Brain | O 6:445 |
| 14 | RB | 20 | 3 | 0.15 | Breast | AJP 140:215 |
| 14 | RB | 38 | 6 | 0.16 | Breast | CR 53:4356 |
| 14.1 | RB | 14 | 5 | 0.36 | Breast | JNCI 84:506 |
| 14 | RB | 10 | 4 | 0.4 | Breast | GCC 4:113 |
| 14 | RB | 32 | 12 | 0.38 | Breast | GE 5:554 |
| 14 | RB | 37 | 12 | 0.32 | Breast | GCC 4:113 |
| 14 | RB | 90 | 23 | 0.26 | Breast | CR 52:2991 |
| 14 | RB | 14 | 0 | 0 | Cervix | BJC 67:71 |
| 14 | RB | 27 | 9 | 0.33 | Colon | CR 52:741 |
| 14 | RB | 25 | 12 | 0.48 | Colon | IJC 53:382 |
| 14.1 | RB | 156 | 18 | 0.12 | Colon | BJC 64:475 |
| 14 | RB | 39 | 10 | 0.26 | Colon | GAST 104:163 |
| 14 | RB | 8 | 0 | 0 | Colon | JNCI 84:1100 |
| 14 | RB | 6 | 0 | 0 | Colon | JNCI 84:1100 |
| 14 | RB | 42 | 0 | 0 | Endocrine | C 74:693 |
| 14 | RB | 29 | 17 | 0.59 | Esophageal | C 73:2472 |
| 14 | RB | 40 | 19 | 0.47 | Esophageal | CR 51:5766 |
| 14 | RB | 8 | 1 | 0.12 | Esophageal | CR 51:2113 |
| 14 | RB | 16 | 5 | 0.31 | Esophageal | CR 54:2996 |
| 14 | RB | 50 | 24 | 0.48 | Esophageal | CR 52:6525 |
| 14 | RB | 29 | 17 | 0.59 | Head&Neck | C 73:2472 |
| 14 | RB | 11 | 4 | 0.36 | Liver | CR 54:281 |
| 14 | RB | 11 | 3 | 0.27 | Liver | CR 51:4367 |

Chromosome 13 - q Arm

| | | | | | | |
|-----------|---------|----|----|------|------------|--------------|
| 14 | RB | 9 | 1 | 0.11 | Liver | CR 51:4367 |
| 14 | RB | 67 | 13 | 0.19 | Lung | O 8:1913 |
| 14 | RB | 16 | 0 | 0 | Lung | O 9:39 |
| 14 | RB | 7 | 2 | 0.29 | Lung | CR 54:5643 |
| 14 | RB | 20 | 12 | 0.6 | Lung | O 8:1913 |
| 14 | RB | 8 | 0 | 0 | Lung | S 241:353 |
| 14 | RB | 3 | 2 | 0.67 | Lung | CL 71:67 |
| 14 | RB | 8 | 6 | 0.75 | Lung | O 9:39 |
| 14 | RB | 76 | 28 | 0.37 | Lung | O 8:1913 |
| 14 | RB | 27 | 14 | 0.52 | Lung | CR 54:5643 |
| 14 | RB | 59 | 22 | 0.37 | Lung | O 10:937 |
| 14 | RB | 5 | 4 | 0.8 | Lung | CR 54:5643 |
| 14 | RB | 2 | 1 | 0.5 | Lung | CL 71:67 |
| 14 | RB | 7 | 1 | 0.14 | Ovary | GO 55:245 |
| 14 | RB | 13 | 8 | 0.62 | Ovary | IJC 58:663 |
| 14 | RB | 31 | 23 | 0.74 | Ovary | CR 54:610 |
| 14 | RB | 39 | 13 | 0.33 | Ovary | IJC 54:546 |
| 14.1 | RB | 17 | 2 | 0.12 | Ovary | CR 54:610 |
| 14 | RB | 33 | 9 | 0.27 | Ovary | IJC 52:575 |
| 14 | RB | 48 | 25 | 0.52 | Ovary | CR 54:610 |
| 14 | RB | 9 | 0 | 0 | Pediatric | CR 50:3279 |
| 14 | RB | 13 | 3 | 0.23 | Prostate | PNAS 87:8751 |
| 14.1 | RB | 9 | 6 | 0.67 | Prostate | BJU 73:390 |
| 14 | RB | 19 | 7 | 0.37 | Prostate | HUPATH 27:28 |
| 14 | RB | 40 | 24 | 0.6 | Prostate | BJC 70:1252 |
| 14 | RB | 7 | 5 | 0.71 | Sarcoma | CR 52:2419 |
| 14 | RB | 13 | 4 | 0.31 | Stomach | LI 74:835 |
| 14 | RB | 31 | 12 | 0.39 | Testis | O 9:2245 |
| Unknown | D13S155 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | D13S155 | 32 | 3 | 0.09 | Melanoma | CR 56:589 |
| 14.1 | D13S118 | 21 | 7 | 0.33 | Prostate | HUPATH 27:28 |
| 21.1-21.2 | D13S26 | 27 | 17 | 0.63 | Ovary | GO 47:137 |
| 21-qter | D13S12 | 7 | 1 | 0.14 | Liver | PNAS 86:8852 |
| 21-qter | D13S12 | 4 | 4 | 1 | Sarcoma | CCG 53:45 |
| 22 | D13S2 | 94 | 26 | 0.28 | Bladder | O 6:2305 |
| Unknown | D13S2 | 6 | 1 | 0.17 | Breast | GCC 2:191 |
| 22 | D13S2 | 7 | 3 | 0.43 | Breast | PNAS 84:2372 |
| 22 | D13S2 | 2 | 0 | 0 | Cervix | CR 49:3598 |
| 22 | D13S2 | 4 | 1 | 0.25 | Cervix | CR 54:4481 |
| 22 | D13S2 | 10 | 3 | 0.3 | Colon | IJC 53:382 |
| 22 | D13S2 | 8 | 0 | 0 | Colon | CCG 48:167 |
| 22 | D13S2 | 4 | 1 | 0.25 | Colon | CCG 48:167 |
| 22 | D13S2 | 17 | 7 | 0.41 | Esophageal | CR 54:2996 |
| 22 | D13S2 | 6 | 2 | 0.33 | Kidney | CR 51:1071 |
| 22 | D13S2 | 6 | 4 | 0.67 | Liver | CCG 48:72 |
| 22 | D13S2 | 13 | 3 | 0.23 | Liver | CR 51:89 |

Chromosome 13 - q Arm

| | | | | | | |
|---------|---------|----|----|------|-------------------|--------------|
| Unknown | D13S2 | 13 | 0 | 0 | Liver | JJCR 81:108 |
| 22 | D13S2 | 21 | 12 | 0.57 | Lung | PN 84:9252 |
| 22 | D13S2 | 12 | 2 | 0.17 | Lung | JJCR 80:924 |
| Unknown | D13S2 | 9 | 7 | 0.78 | Lung | CR 49:5130 |
| 22 | D13S2 | 7 | 1 | 0.14 | Neuroblastom a | CR 49:1095 |
| Unknown | D13S2 | 10 | 3 | 0.3 | Ovary | IJC 54:546 |
| 22 | D13S2 | 8 | 6 | 0.75 | Sarcoma | CR 52:2419 |
| 22 | D13S2 | 10 | 3 | 0.3 | Stomach | CR 52:3099 |
| 22 | D13S2 | 9 | 1 | 0.11 | Stomach | HG 92:244 |
| 22 | D13S2 | 11 | 2 | 0.18 | Stomach | CR 48:2988 |
| 22 | D13S2 | 6 | 4 | 0.67 | Stomach | G 2:180 |
| Unknown | D13S2 | 7 | 1 | 0.14 | Stomach | HG 89:445 |
| Unknown | D13S2 | 14 | 4 | 0.29 | Testis | O 9:2245 |
| 22 | D13S2 | 4 | 1 | 0.25 | Uterus | CR 51:5632 |
| 22-31 | D13S170 | 47 | 11 | 0.23 | Breast | GCC 13:291 |
| 22-31 | D13S170 | 29 | 11 | 0.38 | Head&Neck | CR 54:4756 |
| 22-31 | D13S170 | 20 | 0 | 0 | Head&Neck | CR 54:4756 |
| 31 | D13S4 | 1 | 1 | 1 | Breast | GCC 2:191 |
| Unknown | D13S4 | 26 | 3 | 0.12 | Breast | GE 5:554 |
| Unknown | D13S4 | 5 | 2 | 0.4 | Breast | PNAS 84:2372 |
| Unknown | D13S4 | 10 | 0 | 0 | Cervix | CR 49:3598 |
| 31 | D13S4 | 8 | 0 | 0 | Colon | JNCI 84:1100 |
| Unknown | D13S4 | 1 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D13S4 | 19 | 12 | 0.63 | Colon | IJC 53:382 |
| Unknown | D13S4 | 12 | 4 | 0.33 | Esophageal | SA 4:2996 |
| Unknown | D13S4 | 4 | 0 | 0 | Liver | JJCR 81:108 |
| 31 | D13S4 | 19 | 10 | 0.53 | Lung | PN 84:9252 |
| 31 | D13S4 | 16 | 3 | 0.19 | Lung | JJCR 80:924 |
| Unknown | D13S4 | 5 | 5 | 1 | Lung | CR 49:5130 |
| 31 | D13S4 | 8 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| Unknown | D13S4 | 15 | 11 | 0.73 | Sarcoma | CR 52:2419 |
| 31 | D13S4 | 14 | 3 | 0.21 | Stomach | HG 92:244 |
| Unknown | D13S4 | 11 | 2 | 0.18 | Stomach | G 2:180 |
| Unknown | D13S4 | 17 | 2 | 0.12 | Stomach | CR 48:2988 |
| Unknown | D13S4 | 12 | 0 | 0 | Uterus | CR 51:5632 |
| 22-34 | D13S5 | 26 | 6 | 0.23 | Breast | GE 5:554 |
| 21.3-32 | D13S5 | 4 | 1 | 0.25 | Breast | PNAS 84:2372 |
| 21.3-32 | D13S5 | 15 | 4 | 0.27 | Colon | IJC 53:382 |
| 21.3-32 | D13S5 | 4 | 0 | 0 | Colon | CCG 48:167 |
| 22-34 | D13S5 | 1 | 0 | 0 | Colon | JNCI 84:1100 |
| 22-34 | D13S5 | 22 | 9 | 0.41 | Ovary | IJC 54:546 |
| 21.3-32 | D13S5 | 10 | 4 | 0.4 | Stomach | G 2:180 |
| 22-34 | D13S5 | 7 | 1 | 0.14 | Stomach | G 2:180 |
| 21.3-32 | D13S5 | 5 | 0 | 0 | Uterus | CR 51:5632 |
| 22-34 | D13S5 | 3 | 0 | 0 | Uterus | CR 51:5632 |

Chromosome 13 - q Arm

| | | | | | | |
|---------|---------|-----|----|------|--------------|--------------|
| 21 | D13S71 | 15 | 2 | 0.13 | Brain | CR 54:1397 |
| 21 | D13S71 | 7 | 0 | 0 | Brain | CR 54:1397 |
| 32-34 | D13S128 | 34 | 12 | 0.35 | Ovary | CR 54:605 |
| 34 | D13S34 | 12 | 5 | 0.42 | Ovary | IJC 52:575 |
| 34 | D13S34 | 15 | 7 | 0.47 | Ovary | IJC 54:546 |
| 34 | D13S32 | 28 | 11 | 0.39 | Ovary | IJC 54:546 |
| 34 | D13S32 | 26 | 12 | 0.46 | Ovary | IJC 52:575 |
| 22-31 | D13S173 | 39 | 7 | 0.18 | Breast | GCC 13:291 |
| 34 | D13S3 | 94 | 26 | 0.28 | Bladder | O 6:2305 |
| Unknown | D13S3 | 20 | 3 | 0.15 | Breast | GCC 2:191 |
| 34 | D13S3 | 26 | 4 | 0.15 | Breast | GE 5:554 |
| 34 | D13S3 | 7 | 2 | 0.29 | Breast | PNAS 84:2372 |
| 33-34 | D13S3 | 27 | 3 | 0.11 | Cervix | CR 54:4401 |
| 34 | D13S3 | 18 | 4 | 0.22 | Cervix | CR 49:3598 |
| 34 | D13S3 | 15 | 6 | 0.4 | Colon | IJC 53:382 |
| Unknown | D13S3 | 6 | 0 | 0 | Colon | JNCI 84:1100 |
| Unknown | D13S3 | 4 | 0 | 0 | Liver | JOCR 81:108 |
| 33-34 | D13S3 | 2 | 1 | 0.5 | Liver | CCG 48:72 |
| 34 | D13S3 | 8 | 4 | 0.5 | Liver | CR 51:4367 |
| 34 | D13S3 | 9 | 4 | 0.44 | Lung | PNAS 86:5099 |
| Unknown | D13S3 | 23 | 7 | 0.3 | Lung | PN 84:9252 |
| 34 | D13S3 | 11 | 10 | 0.91 | Lung | CR 49:5130 |
| 34 | D13S3 | 24 | 9 | 0.38 | Lung | PN 84:9252 |
| 34 | D13S3 | 9 | 4 | 0.44 | Lung | PNAS 86:5099 |
| 34 | D13S3 | 7 | 1 | 0.14 | Neuroblastom | CR 49:1095 |
| 34 | D13S3 | 21 | 3 | 0.14 | Ovary | IJC 52:575 |
| 34 | D13S3 | 19 | 4 | 0.21 | Ovary | IJC 54:546 |
| Unknown | D13S3 | 9 | 4 | 0.44 | Sarcoma | CR 52:2419 |
| 34 | D13S3 | 5 | 0 | 0 | Stomach | HG 89:445 |
| 34 | D13S3 | 20 | 5 | 0.25 | Stomach | G 2:180 |
| 33-34 | D13S3 | 9 | 1 | 0.11 | Stomach | HG 92:244 |
| Unknown | D13S3 | 19 | 5 | 0.26 | Stomach | G 2:180 |
| 33-34 | D13S3 | 17 | 2 | 0.12 | Stomach | CR 48:2988 |
| Unknown | D13S3 | 1 | 0 | 0 | Testis | CCG 52:72 |
| 34 | D13S3 | 20 | 8 | 0.4 | Testis | O 9:2245 |
| Unknown | D13S3 | 4 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D13S3 | 2 | 0 | 0 | Testis | CCG 52:72 |
| 34 | D13S3 | 7 | 1 | 0.14 | Uterus | CR 51:5632 |
| 34 | D13S35 | 17 | 2 | 0.12 | Ovary | IJC 54:546 |
| 34 | D13S35 | 18 | 2 | 0.11 | Ovary | IJC 52:575 |
| Unknown | D13S52 | 33 | 7 | 0.21 | Breast | CR 50:7184 |
| Unknown | D13S52 | 132 | 34 | 0.26 | Breast | CR 51:5794 |
| Unknown | D13S52 | 53 | 23 | 0.43 | Esophageal | GCC 10:177 |
| Unknown | D13S52 | 16 | 3 | 0.19 | Esophageal | CR 51:2113 |
| Unknown | D13S52 | 22 | 10 | 0.45 | Esophageal | CR 54:2996 |
| Unknown | D13S52 | 20 | 3 | 0.15 | Kidney | CR 51:820 |

Chromosome 13 - q Arm

| | | | | | | |
|---------|--|----|----|------|-----------|--------------|
| Unknown | D13S52 | 26 | 4 | 0.15 | Liver | CR 51:89 |
| Unknown | D13S52 | 2 | 1 | 0.5 | Lung | CR 52:2478 |
| Unknown | D13S52 | 9 | 5 | 0.56 | Lung | CR 52:2478 |
| Unknown | D13S52 | 26 | 5 | 0.19 | Lung | CR 52:2478 |
| Unknown | D13S52 | 1 | 1 | 1 | Lung | CR 52:2478 |
| Unknown | D13S52 | 27 | 6 | 0.22 | Ovary | CR 51:5118 |
| 34 | F7 | 11 | 2 | 0.18 | Ovary | IJC 54:546 |
| 34 | F7 | 11 | 2 | 0.18 | Ovary | IJC 54:546 |
| Unknown | BRAC2 (D13S:263-219-220-267-171-260-217) | 1 | 1 | 1 | Bladder | CR 55:4830 |
| Unknown | D13S30 | 3 | 0 | 0 | Bladder | CR 51:5405 |
| Unknown | D13S:133-170 | 30 | 15 | 0.5 | Bladder | CR 55:5213 |
| Unknown | Unknown | 7 | 1 | 0.14 | Brain | CR 49:6572 |
| Unknown | Unknown | 14 | 2 | 0.14 | Brain | CR 50:5784 |
| 32 | D13S193 | 13 | 2 | 0.15 | Brain | CR 54:1397 |
| 32 | D13S193 | 13 | 0 | 0 | Brain | CR 54:1397 |
| Unknown | RB1-D13S4-D13S63 | 7 | 0 | 0 | Brain | CGC 73:122 |
| Unknown | RB1-D13S4-D13S63 | 18 | 2 | 0.11 | Brain | CGC 73:122 |
| Unknown | RB1-D13S4-D13S63 | 10 | 0 | 0 | Brain | CGC 73:122 |
| Unknown | BRAC2 (D13S:263-219-220-267-171-260-217) | 1 | 1 | 1 | Breast | CR 55:4830 |
| Unknown | BRAC2 (D13S:263-219-220-267-171-260-217) | 33 | 28 | 0.85 | Breast | CR 55:4830 |
| Unknown | D13S7 | 2 | 1 | 0.5 | Breast | PNAS 84:2372 |
| Unknown | BRAC2 (D13S:263-219-220-267-171-260-217) | 1 | 1 | 1 | Cervix | CR 55:4830 |
| Unknown | | 6 | 0 | 0 | Colon | JNCI 84:1100 |
| Unknown | BRAC2 (D13S:263-219-220-267-171-260-217) | 1 | 1 | 1 | Colon | CR 55:4830 |
| Unknown | D13S10 | 5 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D13S37 | 21 | 1 | 0.05 | Colon | CCG 48:167 |
| Unknown | ESD | 19 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D13S168 | 18 | 2 | 0.11 | Endocrine | CR 56:599 |
| Unknown | D13S174-D13S173 | 20 | 1 | 0.05 | Kidney | PNAS 92:2854 |
| Unknown | D13S174-D13S173 | 5 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D13S:156-158-164-217-221 | 24 | 3 | 0.12 | Leukemia | CR 55:5377 |
| Unknown | Unknown | 11 | 0 | 0 | Liver | BJC 64:1083 |
| Unknown | Unknown | 5 | 0 | 0 | Liver | BJC 67:1007 |
| Unknown | 14.2 | 7 | 0 | 0 | Liver | BJC 67:1007 |
| p11-q11 | D13S11 | 1 | 1 | 1 | Liver | PNAS 86:8852 |
| Unknown | Unknown | 24 | 18 | 0.75 | Lung | CR 54:2322 |
| 33-qter | Unknown | 3 | 1 | 0.33 | Lung | PN 86:5099 |
| 33-qter | Unknown | 9 | 4 | 0.44 | Lung | PN 86:5099 |

Chromosome 13 - q Arm

| | | | | | | |
|---------|--|------|------|------|----------|--------------|
| 33-qter | Unknown | 9 | 4 | 0.44 | Lung | PN 86:5099 |
| Unknown | BRAC2 (D13S:263- 219-220-267-171- 260-217) | 6 | 5 | 0.83 | Ovary | CR 55:4830 |
| Unknown | D13S3-2-1-RB1 | 32 | 18 | 0.56 | Ovary | CR 53:2393 |
| Unknown | Unknown | 7 | 0 | 0 | Pancreas | BJC 65:809 |
| Unknown | 14.2 | 10 | 0 | 0 | Pancreas | BJC 65:809 |
| Unknown | Unknown | 13 | 3 | 0.23 | Prostate | CSurveys 11: |
| Unknown | BRAC2 (D13S:263- 219-220-267-171- 260-217) | 7 | 6 | 0.86 | Prostate | CR 55:4830 |
| Unknown | D13S3-D13S5 | 11 | 1 | 0.09 | Prostate | G 11:530 |
| Unknown | D13S103 | 32 | 5 | 0.16 | Stomach | RG 92:244 |
| Unknown | D13S409 | 14 | 2 | 0.14 | Stomach | CR 55:1933 |
| Unknown | Unknown | 15 | 3 | 0.2 | Testis | G 5:134 |
| Unknown | D13S103 | 9 | 1 | 0.11 | Testis | GCC 13:249 |
| Unknown | D13S70 | 13 | 3 | 0.23 | Testis | GCC 13:249 |
| Unknown | D13S120 | 15 | 0 | 0 | Uterus | CR 54:4294 |
| Unknown | D13S122 | 18 | 2 | 0.11 | Uterus | CR 54:4294 |
| SUM | | 5208 | 1509 | 0.29 | | |

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|--------|-------|-------------|-----------|------------|------------|
| Unknown | D14S22 | 24 | 2 | 0.08 | Esophageal | CR 54:2996 |
| SUM | | 24 | 2 | 0.08 | | |

Chromosome 14 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|-----------------|-------|-------------|-----------|------------|------------|
| Unknown | TCRD | 31 | 6 | 0.19 | Uterus | CR 54:4294 |
| Unknown | D14S:267-268-51 | 30 | 21 | 0.7 | Bladder | CR 55:5213 |
| Unknown | Unknown | 19 | 3 | 0.16 | Brain | CR 50:5784 |
| 32 | D14S13 | 14 | 1 | 0.07 | Brain | CR 49:6572 |
| 32.1-32.2 | D14S13 | 26 | 1 | 0.04 | Brain | CR 55:4696 |
| 32.1-32.2 | D14S13 | 26 | 1 | 0.04 | Brain | CR 55:4696 |
| 32 | D14S16 | 26 | 1 | 0.04 | Brain | CR 55:4696 |
| 32 | D14S16 | 26 | 1 | 0.04 | Brain | CR 55:4696 |
| 32.32-33 | D14S23 | 26 | 0 | 0 | Brain | CR 55:4696 |
| 32.32-33 | D14S23 | 26 | 0 | 0 | Brain | CR 55:4696 |
| 24.3 | D14S43 | 26 | 5 | 0.19 | Brain | CR 55:4696 |
| 24.3 | D14S43 | 26 | 5 | 0.19 | Brain | CR 55:4696 |
| 32.1-32.2 | D14S45 | 26 | 1 | 0.04 | Brain | CR 55:4696 |
| 32.1-32.2 | D14S45 | 26 | 1 | 0.04 | Brain | CR 55:4696 |
| 24.3-31 | D14S48 | 26 | 8 | 0.31 | Brain | CR 55:4696 |
| 24.3-31 | D14S48 | 26 | 8 | 0.31 | Brain | CR 55:4696 |
| 32.1-32.2 | D14S51 | 26 | 3 | 0.12 | Brain | CR 55:4696 |
| 32.1-32.2 | D14S51 | 26 | 3 | 0.12 | Brain | CR 55:4696 |
| 12.0-13.0 | D14S54 | 26 | 2 | 0.08 | Brain | CR 55:4696 |
| 12.0-13.0 | D14S54 | 26 | 2 | 0.08 | Brain | CR 55:4696 |
| 23-31 | D14S59 | 26 | 10 | 0.38 | Brain | CR 55:4696 |
| 23-31 | D14S59 | 26 | 10 | 0.38 | Brain | CR 55:4696 |
| 12.0-13.0 | D14S70 | 26 | 8 | 0.31 | Brain | CR 55:4696 |
| 12.0-13.0 | D14S70 | 26 | 8 | 0.31 | Brain | CR 55:4696 |
| 24.3-31 | D14S76 | 26 | 6 | 0.23 | Brain | CR 55:4696 |
| 24.3-31 | D14S76 | 26 | 6 | 0.23 | Brain | CR 55:4696 |
| 12 | D14S80 | 26 | 7 | 0.27 | Brain | CR 55:4696 |
| 12 | D14S80 | 26 | 7 | 0.27 | Brain | CR 55:4696 |
| 31 | D14S81 | 26 | 7 | 0.27 | Brain | CR 55:4696 |
| 31 | D14S81 | 26 | 7 | 0.27 | Brain | CR 55:4696 |
| 32.3 | IGH | 26 | 9 | 0.35 | Brain | CR 55:4696 |
| 32.3 | IGH | 26 | 9 | 0.35 | Brain | CR 55:4696 |
| 32 | D14S13 | 60 | 7 | 0.12 | Breast | CR 53:4356 |
| 32 | D14S13 | 29 | 7 | 0.24 | Breast | GCC 2:191 |
| 32 | D14S16 | 47 | 6 | 0.13 | Breast | CR 50:7184 |
| 32 | D14S16 | 17 | 2 | 0.12 | Breast | GCC 2:191 |
| 32.3 | IGH | 6 | 2 | 0.33 | Breast | CR 53:3804 |
| 32.32-33 | D14S1 | 10 | 2 | 0.2 | Cervix | CR 49:3598 |
| 32.33 | D14S20 | 10 | 1 | 0.1 | Cervix | CR 54:4481 |
| Unknown | D14S3 | 7 | 0 | 0 | Cervix | GCC 9:119 |
| 32.1 | ARCT | 26 | 6 | 0.23 | Colon | O 8:671 |
| 32.32-33 | AKT1 | 10 | 4 | 0.4 | Colon | O 8:671 |
| 32.32-33 | D14S1 | 42 | 14 | 0.33 | Colon | O 8:671 |
| 32.33 | D14S1 | 28 | 12 | 0.43 | Colon | IJC 53:382 |
| 32 | D14S13 | 35 | 14 | 0.4 | Colon | IJC 53:382 |
| Unknown | D14S16 | 17 | 2 | 0.12 | Colon | CCG 48:167 |

Chromosome 14 - q Arm

| | | | | | | |
|-------------|---------------|----|----|------|--------------|------------|
| 32 | D14S16 | 14 | 7 | 0.5 | Colon | IJC 53:382 |
| 32 | D14S16 | 37 | 18 | 0.49 | Colon | O 8:671 |
| 32.32-.33 | D14S17 | 12 | 5 | 0.42 | Colon | IJC 53:382 |
| 32.32-.33 | D14S17 | 20 | 7 | 0.35 | Colon | O 8:671 |
| 32.1-32.32 | D14S18 | 1 | 1 | 1 | Colon | IJC 53:382 |
| 32.32-32.33 | D14S19 | 39 | 22 | 0.56 | Colon | O 8:671 |
| 32.33 | D14S19 | 14 | 4 | 0.29 | Colon | IJC 53:382 |
| 32.33 | D14S20 | 20 | 10 | 0.5 | Colon | O 8:671 |
| 32.1-32.32 | D14S21 | 2 | 2 | 1 | Colon | IJC 53:382 |
| 32.1-32.32 | D14S21 | 23 | 6 | 0.26 | Colon | O 8:671 |
| 32.32-.33 | D14S23 | 23 | 9 | 0.39 | Colon | IJC 53:382 |
| 32.32-.33 | D14S23 | 42 | 21 | 0.5 | Colon | O 8:671 |
| 32.3 | IGH | 47 | 26 | 0.55 | Colon | O 8:671 |
| 32.1 | PI | 6 | 0 | 0 | Colon | O 8:671 |
| Unknown | D14S174 | 21 | 0 | 0 | Endocrine | GCC 13:9 |
| 32.1-32.2 | D14S45 | 23 | 0 | 0 | Endocrine | CR 56:599 |
| 32 | D14S13 | 23 | 4 | 0.17 | Esophageal | CR 51:2113 |
| 32 | D14S13 | 64 | 9 | 0.14 | Esophageal | GCC 10:177 |
| 32 | D14S13 | 26 | 4 | 0.15 | Esophageal | CR 54:2996 |
| Unknown | D14S51 | 23 | 9 | 0.39 | Head&Neck | CR 54:1152 |
| Unknown | D14S73 | 20 | 1 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D14S73 | 18 | 1 | 0.06 | Head&Neck | CR 54:4756 |
| 32 | D14S13 | 36 | 3 | 0.08 | Kidney | CR 51:820 |
| Unknown | D14S65-D14S81 | 6 | 1 | 0.17 | Kidney | PNAS 92:28 |
| Unknown | D14S65-D14S81 | 22 | 5 | 0.23 | Kidney | PNAS 92:28 |
| Unknown | Unknown | 10 | 0 | 0 | Liver | BJC 64:108 |
| Unknown | Unknown | 5 | 0 | 0 | Liver | BJC 67:100 |
| 32.32-.33 | D14S1 | 3 | 0 | 0 | Liver | CCG 48:72 |
| 32.32-.33 | D14S1 | 17 | 6 | 0.35 | Liver | JJCR 81:10 |
| 32 | D14S13 | 46 | 5 | 0.11 | Liver | CR 51:89 |
| Unknown | D14S15 | 2 | 0 | 0 | Liver | PNAS 86:88 |
| 32.32-.33 | D14S1 | 1 | 1 | 1 | Lung | CR 54:5643 |
| 32.32-.33 | D14S1 | 17 | 7 | 0.41 | Lung | CR 54:5643 |
| 32.32-.33 | D14S1 | 8 | 1 | 0.12 | Lung | CR 54:5643 |
| 32.32-.33 | D14S1 | 23 | 2 | 0.09 | Lung | PN 84:9252 |
| 32 | D14S13 | 50 | 6 | 0.12 | Lung | CR 52:2478 |
| 32.33 | D14S1 | 22 | 7 | 0.32 | Neuroblastom | O 7:1185 |
| 32.32-.33 | D14S1 | 16 | 8 | 0.5 | Neuroblastom | CR 49:1095 |
| 32.32-.33 | D14S1 | 19 | 4 | 0.21 | Neuroblastom | O 7:1185 |
| 32.1-32.2 | D14S13 | 24 | 5 | 0.21 | Neuroblastom | O 7:1185 |
| 32 | D14S16 | 13 | 8 | 0.62 | Neuroblastom | O 7:1185 |
| 32.32-.33 | D14S17 | 18 | 1 | 0.06 | Neuroblastom | O 7:1185 |

Chromosome 14 - q Arm

| | | | | | | |
|-------------|---------|------|-----|------|--------------|------------|
| 32.32-32.33 | D14S19 | 20 | 4 | 0.2 | Neuroblastom | O 7:1185 |
| 32.1-32.32 | D14S21 | 18 | 1 | 0.06 | Neuroblastom | O 7:1185 |
| 11.2-13 | MYH6 | 17 | 0 | 0 | Neuroblastom | O 7:1185 |
| 32.32-.33 | D14S1 | 26 | 2 | 0.08 | Ovary | IJC 54:546 |
| 32 | D14S13 | 28 | 5 | 0.18 | Ovary | CR 51:5118 |
| 32 | D14S16 | 15 | 7 | 0.47 | Ovary | CR 53:2393 |
| 32.33 | D14S20 | 9 | 3 | 0.33 | Ovary | O 7:1059 |
| Unknown | D14S34 | 13 | 7 | 0.54 | Ovary | BJC 69:429 |
| 24.3-31 | D14S48 | 9 | 3 | 0.33 | Ovary | BJC 69:429 |
| Unknown | D14S49 | 20 | 5 | 0.25 | Ovary | BJC 69:429 |
| Unknown | D14S50 | 10 | 3 | 0.3 | Ovary | BJC 69:429 |
| Unknown | D14S51 | 17 | 4 | 0.24 | Ovary | BJC 69:429 |
| Unknown | Unknown | 6 | 0 | 0 | Pancreas | BJC 65:809 |
| 32 | D14S13 | 4 | 0 | 0 | Pancreas | CR 54:2761 |
| 32.32-.33 | D14S1 | 7 | 0 | 0 | Prostate | G 11:530 |
| 32 | D14S13 | 29 | 1 | 0.03 | Sarcoma | CR 52:2419 |
| 32.32-.33 | D14S1 | 16 | 1 | 0.06 | Sarcoma | CR 52:2419 |
| Unknown | D14S44 | 32 | 5 | 0.16 | Stomach | CR 48:2986 |
| 32.33 | D14S20 | 8 | 1 | 0.12 | Stomach | HG 92:244 |
| Unknown | D14S44 | 21 | 2 | 0.1 | Testis | O 9:2245 |
| 32.32-.33 | D14S1 | 10 | 0 | 0 | Testis | GCC 13:249 |
| Unknown | D14S3 | 12 | 1 | 0.08 | Uterus | CR 51:5632 |
| 24.3-31 | D14S76 | 28 | 3 | 0.11 | Uterus | GCC 9:119 |
| 11.2-13 | MYH6 | 18 | 2 | 0.11 | Uterus | CR 54:4294 |
| Unknown | TCRD | 31 | 6 | 0.19 | Uterus | CR 54:4294 |
| SUM | | 2442 | 542 | 0.22 | | |

Chromosome 15 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|--------|-------|-------------|-----------|------------|------------|
| Unknown | D15S25 | 26 | 4 | 0.15 | Esophageal | CR 54:2996 |
| Unknown | D15S25 | 9 | 0 | 0 | Colon | CCG 48:167 |
| Unknown | D15S25 | 26 | 4 | 0.15 | Esophageal | CR 54:2996 |
| SUM | | 35 | 4 | 0.11 | | |

Chromosome 15 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|----------|-----------------|-------|-------------|-----------|--------------|--------------|
| 26.1 | FES | 36 | 5 | 0.14 | Uterus | CR 54:4294 |
| Unknown | Unknown | 18 | 3 | 0.17 | Brain | CR 50:5784 |
| Unknown | D15S27 | 7 | 1 | 0.14 | Brain | CR 49:6572 |
| 14-21 | D15S1 | 28 | 1 | 0.04 | Breast | GCC 2:191 |
| 11-12.0 | D15S11 | 34 | 3 | 0.09 | Breast | CR 53:4356 |
| pter-q13 | D15S24 | 2 | 1 | 0.5 | Breast | CR 53:3904 |
| Unknown | D15S28 | 12 | 2 | 0.17 | Breast | CR 50:7184 |
| Unknown | D15S29 | 16 | 4 | 0.25 | Breast | GCC 2:191 |
| 14-21 | D15S1 | 6 | 0 | 0 | Cervix | CR 49:3598 |
| pter-q13 | D15S24 | 23 | 0 | 0 | Cervix | CR 54:4481 |
| 14-21 | D15S1 | 6 | 1 | 0.17 | Colon | N 331:273 |
| Unknown | ACTC | 36 | 6 | 0.17 | Endocrine | CR 56:599 |
| Unknown | CYP19 | 33 | 5 | 0.15 | Endocrine | CR 56:599 |
| 14-21 | D15S1 | 5 | 4 | 0.8 | Endocrine | CR 56:599 |
| Unknown | D15S100 | 31 | 5 | 0.16 | Endocrine | CR 56:599 |
| Unknown | D15S107 | 8 | 6 | 0.75 | Endocrine | CR 56:599 |
| Unknown | D15S109 | 8 | 3 | 0.38 | Endocrine | CR 56:599 |
| Unknown | D15S114 | 4 | 4 | 1 | Endocrine | CR 56:599 |
| Unknown | D15S116 | 21 | 7 | 0.33 | Endocrine | CR 56:599 |
| Unknown | D15S118 | 16 | 5 | 0.31 | Endocrine | CR 56:599 |
| Unknown | D15S125 | 24 | 5 | 0.21 | Endocrine | CR 56:599 |
| Unknown | D15S127 | 10 | 7 | 0.7 | Endocrine | CR 56:599 |
| Unknown | D15S144 | 9 | 7 | 0.78 | Endocrine | CR 56:599 |
| Unknown | D15S165 | 32 | 7 | 0.22 | Endocrine | CR 56:599 |
| Unknown | D15S87 | 20 | 7 | 0.35 | Endocrine | CR 56:599 |
| Unknown | D15S97 | 32 | 8 | 0.25 | Endocrine | CR 56:599 |
| Unknown | GABRB3 | 31 | 7 | 0.23 | Endocrine | CR 56:599 |
| Unknown | D15S27 | 17 | 2 | 0.12 | Esophageal | GCC 10:177 |
| Unknown | D15S27 | 27 | 2 | 0.07 | Esophageal | CR 54:2996 |
| Unknown | D15S117 | 21 | 1 | 0.05 | Head&Neck | CR 54:1152 |
| Unknown | D15S118 | 17 | 1 | 0.06 | Head&Neck | CR 54:4756 |
| Unknown | D15S118 | 15 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D15S118 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | D15S120-D15S127 | 21 | 1 | 0.05 | Kidney | PNAS 92:2854 |
| Unknown | D15S120-D15S127 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D15S28 | 18 | 2 | 0.11 | Kidney | CR 51:820 |
| 14-21 | D15S1 | 10 | 1 | 0.1 | Liver | JJCR 81:108 |
| pter-q13 | D15S24 | 26 | 3 | 0.12 | Liver | CR 51:89 |
| 14-21 | D15S1 | 4 | 0 | 0 | Lung | NEJ 317:1109 |
| 14-21 | D15S1 | 8 | 0 | 0 | Lung | PN 84:9252 |
| 14-21 | D15S1 | 5 | 2 | 0.4 | Lung | NEJ 317:1109 |
| 14-21 | D15S1 | 2 | 0 | 0 | Lung | NEJ 317:1109 |
| Unknown | D15S28 | 18 | 2 | 0.11 | Lung | CR 52:2478 |
| Unknown | D15S118 | 24 | 4 | 0.17 | Melanoma | CR 56:589 |
| 14-21 | D15S1 | 7 | 0 | 0 | Neuroblastom | CR 49:1095 |

Chromosome 15 - q Arm

| | | | | | | |
|----------|--------------|------|-----|------|----------|------------|
| 11-12.0 | D15S11 | 13 | 1 | 0.08 | Ovary | IJC 54:546 |
| Unknown | D15S2 | 11 | 4 | 0.36 | Ovary | CR 53:2393 |
| pter-q13 | D15S24 | 31 | 2 | 0.06 | Ovary | IJC 54:546 |
| Unknown | D15S28 | 9 | 1 | 0.11 | Ovary | CR 51:5118 |
| 26.1 | FES | 15 | 6 | 0.4 | Ovary | BJC 69:429 |
| pter-q13 | D15S24 | 1 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | D15S29-D15S1 | 9 | 0 | 0 | Prostate | G 11:530 |
| 14-21 | D15S1 | 9 | 4 | 0.44 | Sarcoma | CR 52:2419 |
| Unknown | D15S27 | 12 | 5 | 0.42 | Sarcoma | CR 52:2419 |
| 14-21 | D15S1 | 13 | 0 | 0 | Stomach | CR 48:2988 |
| Unknown | D15S86 | 32 | 5 | 0.16 | Stomach | HG 92:244 |
| pter-q13 | D15S24 | 46 | 4 | 0.09 | Testis | Q 9:2245 |
| Unknown | D15S86 | 21 | 2 | 0.1 | Testis | GCC 13:249 |
| Unknown | CYP19 | 27 | 0 | 0 | Uterus | CR 54:4294 |
| 14-21 | D15S1 | 6 | 1 | 0.17 | Uterus | CR 51:5632 |
| 26.1 | FES | 36 | 5 | 0.14 | Uterus | CR 54:4294 |
| SUM | | 1015 | 173 | 0.17 | | |

Chromosome 16 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Refs |
|------------|---------|-------|-------------|-----------|------------|------|
| 13.3 | HBZP1 | 6 | 0 | 0 | Prostate | G1 |
| 13.3 | D16S85 | 7 | 0 | 0 | Breast | CR |
| 13.3 | D16S85 | 62 | 5 | 0.08 | Breast | GCC |
| 13.3 | D16S85 | 8 | 0 | 0 | Liver | BJC |
| 13.3 | D16S85 | 11 | 0 | 0 | Liver | BJC |
| 13.3 | D16S85 | 24 | 5 | 0.21 | Ovary | CR |
| 13.3 | D16S85 | 11 | 1 | 0.09 | Pancreas | BJC |
| 13.3 | D16S85 | 11 | 1 | 0.09 | Stomach | HG |
| 13.3 | D16S85 | 22 | 3 | 0.14 | Testis | GCC |
| 13.3 | D16S83 | 27 | 8 | 0.3 | Breast | GCC |
| 13.3 | D16S83 | 31 | 6 | 0.19 | Breast | CR |
| 13.3 | D16S83 | 16 | 2 | 0.12 | Esophageal | CR |
| 13.3 | D16S83 | 11 | 0 | 0 | Esophageal | CR |
| 13.3 | D16S83 | 19 | 5 | 0.26 | Liver | CR |
| 13.3 | D16S83 | 16 | 1 | 0.06 | Liver | CR |
| 13.3 | D16S83 | 15 | 6 | 0.4 | Sarcoma | CR |
| 13 | D16S84 | 21 | 1 | 0.05 | Breast | CR |
| 13 | D16S84 | 43 | 0 | 0 | Breast | CR |
| pter-p13.3 | D16S84 | 5 | 0 | 0 | Cervix | GCC |
| pter-p13.3 | D16S84 | 28 | 4 | 0.14 | Esophageal | GCC |
| pter-p13.3 | D16S84 | 14 | 1 | 0.07 | Kidney | CR |
| pter-p13.3 | D16S84 | 22 | 5 | 0.23 | Lung | CR |
| pter-p13.3 | D16S84 | 21 | 7 | 0.33 | Ovary | CR |
| pter-p13.3 | D16S84 | 9 | 2 | 0.22 | Uterus | GCC |
| 13.3 | HBAI | 22 | 5 | 0.23 | Breast | CR |
| 13.3 | HBAI | 47 | 1 | 0.02 | Breast | CR |
| 13.3 | HBAI | 22 | 5 | 0.23 | Breast | CR |
| 13.3 | HBAI | 11 | 9 | 0.82 | Liver | CR |
| 13.3 | HBAI | 36 | 16 | 0.44 | Liver | PNA |
| Unknown | D16S414 | 10 | 0 | 0 | Head&Neck | CR |
| Unknown | D16S414 | 19 | 3 | 0.16 | Head&Neck | CR |
| Unknown | D16S414 | 6 | 3 | 0.5 | Kidney | GCC |
| Unknown | D16S414 | 26 | 1 | 0.04 | Melanoma | CR |
| 13 | D16S292 | 12 | 0 | 0 | Ovary | BJC |
| pter-p13 | D16S32 | 21 | 3 | 0.14 | Breast | CR |
| pter-p13 | D16S32 | 26 | 8 | 0.31 | Liver | PNA |
| pter-p13 | D16S32 | 16 | 4 | 0.25 | Liver | JJC |
| pter-p13 | D16S32 | 8 | 7 | 0.88 | Liver | CR |
| 13.1 | MPP | 13 | 5 | 0.38 | Leukemia | LAN |
| 13.11 | D16S131 | 8 | 1 | 0.12 | Breast | CR |
| 13.11 | D16S131 | 13 | 6 | 0.46 | Liver | PNA |
| 12.2 | D16S159 | 34 | 6 | 0.18 | Breast | CR |
| P11-P13 | D16S159 | 29 | 1 | 0.03 | Breast | CR |
| Unknown | D16S159 | 22 | 1 | 0.05 | Liver | CR |
| Unknown | D16S159 | 22 | 1 | 0.05 | Liver | CR |
| Unknown | Unknown | 18 | 2 | 0.11 | Brain | CR |

Chromosome 16 - p Arm

| | | | | | | |
|----------|-------------------------|------|-----|------|-----------|-----|
| 12.2 | D16S23 | 36 | 5 | 0.14 | Breast | CR |
| 13.2 | D16S34 | 3 | 1 | 0.33 | Breast | CR |
| 13.2 | D16S34 | 21 | 7 | 0.33 | Breast | CR |
| PTER-P13 | D16S35 | 26 | 4 | 0.15 | Breast | CR |
| PTER-P13 | D16S35 | 20 | 4 | 0.2 | Cervix | CR |
| 12-pter | Unknown | 18 | 0 | 0 | Colon | BJC |
| Unknown | D16S418 | 22 | 0 | 0 | Endocrine | CR |
| Unknown | D16S404 | 20 | 2 | 0.1 | Head&Neck | CR |
| Unknown | D16S404-D16S403-D16S414 | 22 | 0 | 0 | Kidney | PNA |
| Unknown | D16S404-D16S403-D16S414 | 6 | 0 | 0 | Kidney | PNA |
| 13.2 | D16S34 | 20 | 9 | 0.45 | Liver | PNA |
| 13.2 | D16S34 | 8 | 5 | 0.62 | Liver | CR |
| 13.2 | D16S34 | 6 | 3 | 0.5 | Liver | CR |
| PTER-P13 | D16S35 | 7 | 4 | 0.57 | Liver | CR |
| PTER-P13 | D16S35 | 24 | 9 | 0.38 | Liver | PNA |
| pter-p13 | D16S37 | 2 | 0 | 0 | Liver | JJC |
| 13.2 | D16S34 | 27 | 4 | 0.15 | Ovary | JJC |
| PTER-P13 | D16S35 | 8 | 0 | 0 | Prostate | PNA |
| PTER-P13 | D16S35 | 8 | 0 | 0 | Prostate | CSu |
| 12-pter | Unknown | 5 | 0 | 0 | Stomach | BJC |
| PTER-P13 | D16S35 | 25 | 5 | 0.2 | Testis | OJ9 |
| Unknown | D16S291 | 18 | 1 | 0.06 | Uterus | CR |
| SUM | | 1231 | 213 | 0.17 | | |

Chromosome 16 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------|-------|-------------|-----------|------------|--------------|
| 16 | D16S137 | 37 | 5 | 0.14 | Breast | CR 54:513 |
| Unknown | D16S300 | 23 | 7 | 0.3 | Breast | GCC 14:171 |
| Unknown | D16S299 | 36 | 7 | 0.19 | Breast | GCC 14:171 |
| 12.1 | D16S304 | 24 | 12 | 0.5 | Breast | GCC 14:171 |
| 22.1 | TAT | 43 | 16 | 0.37 | Breast | CR 54:513 |
| 22.1 | TAT | 41 | 15 | 0.37 | Breast | GCC 9:101 |
| 22.1 | TAT | 8 | 5 | 0.62 | Liver | CR 52:1504 |
| 22.1 | TAT | 10 | 9 | 0.9 | Liver | CR 54:281 |
| 22.1 | TAT | 23 | 13 | 0.57 | Liver | PNAS 87:6791 |
| 22.1 | TAT | 25 | 13 | 0.52 | Liver | PNAS 87:6791 |
| 22.1 | TAT | 29 | 14 | 0.48 | Liver | PNAS 87:6791 |
| Unknown | D16S408 | 20 | 3 | 0.15 | Breast | JJCR 86:1054 |
| 13 | CET | 36 | 9 | 0.25 | Breast | CR 54:513 |
| 21 | CET | 44 | 20 | 0.45 | Liver | PNAS 87:6791 |
| 13-22.1 | MT2 | 36 | 15 | 0.42 | Liver | PNAS 87:6791 |
| 21 | D16S151 | 43 | 16 | 0.37 | Breast | CR 51:5794 |
| 21 | D16S151 | 18 | 6 | 0.33 | Breast | CR 54:513 |
| 21 | D16S151 | 43 | 8 | 0.19 | Esophageal | GCC 10:177 |
| Unknown | D16S151 | 8 | 2 | 0.25 | Liver | CR 51:89 |
| 21 | D16S265 | 70 | 24 | 0.34 | Breast | GCC 9:101 |
| 21 | D16S265 | 58 | 19 | 0.33 | Breast | BCRT 32:5 |
| 21 | D16S265 | 19 | 3 | 0.16 | Ovary | BJC 69:429 |
| 22.1 | D16S38 | 35 | 14 | 0.4 | Breast | CR 54:513 |
| 21-22.1 | D16S186 | 28 | 15 | 0.54 | Breast | GCC 14:171 |
| 21-22.1 | D16S186 | 33 | 13 | 0.39 | Breast | GCC 9:101 |
| 21-22.1 | D16S186 | 27 | 6 | 0.22 | Uterus | CR 54:4294 |
| 22.1 | D16S318 | 33 | 13 | 0.39 | Breast | GCC 9:101 |
| 22.1 | D16S318 | 29 | 14 | 0.48 | Breast | GCC 14:171 |
| Unknown | D16S421 | 12 | 2 | 0.17 | Breast | JJCR 86:1054 |
| Unknown | D16S421 | 27 | 14 | 0.52 | Breast | GCC 14:171 |
| 22.1 | D16S4 | 28 | 16 | 0.57 | Breast | CR 54:513 |
| 22.1 | D16S4 | 29 | 14 | 0.48 | Breast | GCC 9:101 |
| 22.1 | D16S4 | 31 | 12 | 0.39 | Liver | PNAS 87:6791 |
| 22.1 | D16S4 | 9 | 5 | 0.56 | Liver | CR 52:1504 |
| 22.1 | D16S4 | 17 | 6 | 0.35 | Ovary | CR 53:2393 |
| 22.1 | D16S152 | 21 | 4 | 0.19 | Breast | CR 54:513 |
| 22.1 | HP | 27 | 11 | 0.41 | Breast | CR 54:513 |
| 22.1 | HP | 21 | 12 | 0.57 | Breast | CR 51:5794 |
| 22.1 | HP | 29 | 15 | 0.52 | Breast | GCC 9:101 |
| 22.1 | HP | 9 | 1 | 0.11 | Cervix | CR 49:3598 |
| 22.1 | HP | 15 | 3 | 0.2 | Colon | IJC 53:382 |
| Unknown | HP | 7 | 1 | 0.14 | Liver | CR 51:89 |
| Unknown | HP | 10 | 4 | 0.4 | Liver | CR 52:1504 |
| 22.1 | HP | 28 | 10 | 0.36 | Liver | PNAS 87:6791 |
| 22.1 | HP | 14 | 8 | 0.57 | Liver | JJCR 81:108 |
| 22.1 | HP | 13 | 7 | 0.54 | Liver | JJCR 81:108 |

Chromosome 16 - q Arm

| | | | | | | |
|-----------|---------|-----|-----|------|--------------|--------------|
| 22.1 | HP | 20 | 5 | 0.25 | Lung | PN 84:9252 |
| 22.1 | HP | 4 | 0 | 0 | Neuroblastom | CR 49:1095 |
| Unknown | HP | 24 | 2 | 0.08 | Ovary | GO 47:137 |
| 22.1 | HP | 22 | 5 | 0.23 | Ovary | IJC 54:546 |
| 22.1 | HP | 4 | 0 | 0 | Prostate | G 11:530 |
| Unknown | HP | 11 | 1 | 0.09 | Stomach | CR 52:3099 |
| 22.1 | HP | 10 | 0 | 0 | Stomach | CR 48:2988 |
| 22.1 | HP | 2 | 0 | 0 | Testis | CCG 52:72 |
| 22.1 | HP | 2 | 0 | 0 | Testis | CCG 52:72 |
| 22.1 | HP | 2 | 0 | 0 | Testis | CCG 52:72 |
| 22.1 | HP | 4 | 0 | 0 | Uterus | CR 51:5632 |
| 22.3-23.2 | CTRB | 34 | 9 | 0.26 | Breast | CR 54:513 |
| 23.2 | CTRB | 4 | 2 | 0.5 | Breast | CR 51:5794 |
| 23.2 | CTRB | 9 | 5 | 0.56 | Liver | CR 52:1504 |
| 22.3-23.2 | CTRB | 38 | 17 | 0.45 | Liver | PNAS 87:6791 |
| 23.3-24.1 | D16S289 | 28 | 13 | 0.46 | Breast | GCC 14:171 |
| 23.3-24.1 | D16S289 | 57 | 21 | 0.37 | Breast | GCC 9:101 |
| 23.3-24.1 | D16S289 | 22 | 5 | 0.23 | Uterus | CR 54:4294 |
| 24.2 | D16S20 | 45 | 15 | 0.33 | Breast | CR 54:513 |
| 22.1-24 | D16S30 | 6 | 3 | 0.5 | Breast | CR 54:513 |
| Unknown | D16S511 | 32 | 15 | 0.47 | Breast | GCC 14:171 |
| Unknown | D16S402 | 12 | 5 | 0.42 | Breast | JJCR 86:1054 |
| Unknown | D16S402 | 38 | 20 | 0.53 | Breast | GCC 14:171 |
| Unknown | D16S402 | 13 | 2 | 0.15 | Head&Neck | CR 54:1152 |
| 24.2-24.3 | D16S157 | 21 | 9 | 0.43 | Breast | CR 54:513 |
| 22-23 | D16S157 | 9 | 4 | 0.44 | Breast | CR 51:5794 |
| 24.2-24.3 | D16S43 | 20 | 8 | 0.4 | Breast | CR 54:513 |
| Unknown | D16S155 | 11 | 2 | 0.18 | Breast | CR 54:513 |
| 23-24 | D16S156 | 61 | 30 | 0.49 | Breast | CR 51:5794 |
| 24 | APRT | 33 | 17 | 0.52 | Breast | CR 54:513 |
| 24 | APRT | 25 | 3 | 0.12 | Breast | CR 53:3707 |
| 24 | APRT | 25 | 3 | 0.12 | Breast | CR 53:4356 |
| 24 | APRT | 19 | 10 | 0.53 | Breast | GCC 2:191 |
| 24 | APRT | 12 | 7 | 0.58 | Breast | GCC 9:101 |
| 24 | APRT | 10 | 6 | 0.6 | Liver | CR 52:1504 |
| 24 | APRT | 26 | 17 | 0.65 | Liver | PNAS 87:6791 |
| Unknown | D16S7 | 10 | 1 | 0.1 | Brain | CR 49:6572 |
| 24 | D16S7 | 21 | 3 | 0.14 | Brain | CR 50:5784 |
| 24 | D16S7 | 42 | 19 | 0.45 | Breast | CR 50:7184 |
| 24 | D16S7 | 8 | 6 | 0.75 | Breast | CR 53:3804 |
| 24 | D16S7 | 354 | 164 | 0.46 | Breast | BJC 71:438 |
| 24 | D16S7 | 59 | 30 | 0.51 | Breast | GCC 9:101 |
| 24 | D16S7 | 57 | 18 | 0.32 | Breast | CR 53:4356 |
| 24 | D16S7 | 57 | 18 | 0.32 | Breast | CR 53:3707 |
| 24 | D16S7 | 269 | 120 | 0.45 | Breast | C 74:2281 |
| 24.3 | D16S7 | 68 | 32 | 0.47 | Breast | CR 54:513 |

Chromosome 16 - q Arm

| | | | | | | |
|---------|-----------------|-----|----|------|------------|--------------|
| 23-24 | D16S71 | 138 | 59 | 0.43 | Breast | CR 51:5794 |
| Unknown | D16S7 | 83 | 23 | 0.28 | Breast | JJCR 84:1159 |
| Unknown | D16S7 | 35 | 1 | 0.03 | Cervix | CR 54:4481 |
| 23-24 | D16S7 | 7 | 2 | 0.29 | Cervix | GCC 9:119 |
| 23-24 | D16S7 | 32 | 6 | 0.19 | Colon | IOC 53:3824 |
| 23-24 | D16S7 | 6 | 1 | 0.17 | Esophageal | CR 51:2113 |
| Unknown | D16S7 | 15 | 4 | 0.27 | Esophageal | CR 54:2996 |
| 24 | D16S7 | 29 | 3 | 0.1 | Kidney | CR 51:820 |
| Unknown | D16S7 | 33 | 12 | 0.36 | Liver | CR 51:89 |
| 24 | D16S7 | 53 | 24 | 0.45 | Liver | PNAS 87:6791 |
| 23-24 | D16S7 | 25 | 11 | 0.44 | Liver | CR 54:281 |
| 24 | D16S7 | 50 | 14 | 0.28 | Liver | JJCR 84:893 |
| 24 | D16S7 | 37 | 8 | 0.22 | Lung | CR 52:2478 |
| Unknown | D16S7 | 30 | 11 | 0.37 | Ovary | CR 51:5118 |
| 24 | D16S7 | 3 | 1 | 0.33 | Pancreas | CR 54:2761 |
| 24 | D16S7 | 15 | 4 | 0.27 | Prostate | PNAS 87:8751 |
| Unknown | D16S7 | 17 | 3 | 0.18 | Prostate | BJU 73:390 |
| 24 | D16S7 | 32 | 9 | 0.28 | Sarcoma | CR 52:2419 |
| 24 | D16S7 | 43 | 2 | 0.05 | Testis | O 9:2245 |
| Unknown | D16S7 | 16 | 0 | 0 | Uterus | GCC 9:119 |
| 24.3 | D16S413 | 41 | 21 | 0.51 | Breast | GCC 14:171 |
| 24.3 | D16S413 | 22 | 0 | 0 | Endocrine | CR 56:599 |
| 24.3 | D16S44 | 10 | 4 | 0.4 | Breast | CR 54:513 |
| 24.3 | D16S303 | 23 | 11 | 0.48 | Breast | GCC 14:171 |
| 24.3 | D16S303 | 42 | 18 | 0.43 | Breast | GCC 9:101 |
| 13 | MT2 | 29 | 9 | 0.31 | Breast | CR 54:513 |
| 13 | MT2 | 8 | 4 | 0.5 | Liver | CR 52:1504 |
| 13 | MT2 | 8 | 4 | 0.5 | Liver | CR 52:1504 |
| Unknown | D16S10 | 31 | 7 | 0.23 | Breast | GCC 9:101 |
| Unknown | D16S260 | 28 | 8 | 0.29 | Breast | GCC 9:101 |
| Unknown | D16S266 | 53 | 18 | 0.34 | Breast | GCC 9:101 |
| 12.1 | D16S27 | 26 | 7 | 0.27 | Breast | CR 54:513 |
| 12.1 | D16S27 | 27 | 9 | 0.33 | Breast | GCC 9:101 |
| Unknown | D16S301 | 38 | 16 | 0.42 | Breast | GCC 9:101 |
| Unknown | D16S305 | 58 | 20 | 0.34 | Breast | GCC 9:101 |
| Unknown | D16S320 | 65 | 20 | 0.31 | Breast | GCC 9:101 |
| Unknown | D16S398 | 56 | 16 | 0.29 | Breast | GCC 9:101 |
| Unknown | D16S5 | 29 | 11 | 0.38 | Breast | GCC 9:101 |
| 22.1 | E-cadherin | 28 | 16 | 0.57 | Breast | GCC 9:101 |
| 22.1 | E-cadherin | 41 | 27 | 0.66 | Breast | EMBO 14:6107 |
| Unknown | D16S422 | 21 | 4 | 0.19 | Head&Neck | CR 54:4756 |
| Unknown | D16S422 | 20 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | SPN | 22 | 3 | 0.14 | Head&Neck | CR 54:1152 |
| Unknown | D16S413-D16S402 | 21 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D16S413-D16S402 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D16S:422-419 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |

Chromosome 16 - q Arm

| | | | | | | |
|---------|-------------|------|------|------|----------|--------------|
| Unknown | Unknown | 3 | 0 | 0 | Liver | BJC 67:1007 |
| Unknown | Unknown | 6 | 0 | 0 | Liver | BJC 64:1083 |
| Unknown | D16S422-419 | 21 | 0 | 0 | Melanoma | CR 56:589 |
| Unknown | Unknown | 16 | 5 | 0.31 | Prostate | CSurveys 11: |
| SUM | | 4382 | 1588 | 0.36 | | |

Chromosome 17 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------|-------|-------------|-----------|------------|---------------------|
| Unknown | D17S34 | 35 | 5 | 0.14 | Brain | AJP 145:11 |
| 13.3 | D17S34 | 82 | 29 | 0.35 | Breast | AJP 140:21 |
| 13.3 | D17S34 | 77 | 52 | 0.68 | Breast | CR 54:4200 |
| 13-TER | D17S34 | 72 | 30 | 0.42 | Breast | CGC 76:106 |
| Unknown | D17S34 | 70 | 41 | 0.59 | Breast | O 8:781 |
| 13.3 | D17S34 | 44 | 33 | 0.75 | Breast | GCC 4:113 |
| 13.3 | D17S34 | 36 | 22 | 0.61 | Breast | CR 53:1637 |
| Unknown | D17S34 | 11 | 6 | 0.55 | Cervix | CGC 79:74 |
| 13.3 | D17S34 | 68 | 34 | 0.5 | Colon | EJC 30A:66 |
| 13.3 | D17S34 | 6 | 5 | 0.83 | Colon | Science Ap 1989:217 |
| 13.3 | D17S34 | 6 | 3 | 0.5 | Head&Neck | AJP 142:11 |
| Unknown | D17S34 | 12 | 1 | 0.08 | Head&Neck | CR 52:4787 |
| 13.3 | D17S34 | 20 | 2 | 0.1 | Liver | O 8:497 |
| 13.3 | D17S34 | 10 | 8 | 0.8 | Liver | BJC 64:108 |
| 13.3 | D17S34 | 9 | 4 | 0.44 | Liver | BJC 67:100 |
| 13.3 | D17S34 | 23 | 12 | 0.52 | Ovary | IJC 54:85 |
| 13.3 | D17S34 | 20 | 18 | 0.9 | Ovary | IJC 54:220 |
| Unknown | D17S34 | 43 | 18 | 0.42 | Ovary | CR 56:606 |
| 13.3 | D17S34 | 11 | 0 | 0 | Pancreas | CR 54:2761 |
| 13.3 | D17S34 | 17 | 3 | 0.18 | Prostate | CSurveys 1 |
| 13.3 | D17S34 | 18 | 3 | 0.17 | Prostate | PNAS 87:87 |
| 13.3 | D17S34 | 7 | 5 | 0.71 | Sarcoma | CR 53:468 |
| 13.3 | D17S34 | 9 | 0 | 0 | Sarcoma | CR 53:468 |
| 13.3 | D17S34 | 10 | 4 | 0.4 | Sarcoma | CR 53:468 |
| 13.3 | D17S34 | 4 | 2 | 0.5 | Sarcoma | CR 53:468 |
| 13.3 | D17S34 | 20 | 0 | 0 | Testis | GCC 13:249 |
| 13.3 | D17S849 | 26 | 16 | 0.62 | Breast | HMG 4:2047 |
| 13.3 | D17S926 | 12 | 7 | 0.58 | Breast | HMG 4:2047 |
| 13.3 | D17S30 | 54 | 20 | 0.37 | Breast | CR 53:1637 |
| 13.3 | D17S30 | 98 | 57 | 0.58 | Breast | Lan 336:76 |
| 13.3 | D17S30 | 59 | 30 | 0.51 | Breast | JNCI 84:50 |
| 13.3 | D17S30 | 52 | 27 | 0.52 | Breast | PNAS 88:38 |
| 13.3 | D17S30 | 51 | 8 | 0.16 | Breast | HG 91:6 |
| 13.3 | D17S30 | 34 | 16 | 0.47 | Breast | CR 50:7184 |
| 13.3 | D17S30 | 33 | 17 | 0.52 | Breast | ANYAS p 13 |
| 13.3 | D17S30 | 3 | 0 | 0 | Breast | CR 53:2947 |
| 13.3 | D17S30 | 6 | 3 | 0.5 | Cervix | GCC 9:119 |
| 13.3 | D17S30 | 39 | 27 | 0.69 | Colon | CR 50:7166 |
| 13.3 | D17S30 | 60 | 38 | 0.63 | Colon | EJC 30A:66 |
| 13.3 | D17S30 | 65 | 40 | 0.62 | Esophageal | GCC 10:177 |
| 13.3 | D17S30 | 51 | 36 | 0.71 | Head&Neck | O 10:1217 |
| 13.3 | D17S30 | 5 | 2 | 0.4 | Liver | BJC 67:100 |
| 13.3 | D17S30 | 26 | 14 | 0.54 | Liver | CR 51:897 |
| 13.3 | D17S30 | 37 | 23 | 0.62 | Lung | CR 52:2478 |
| 13.3 | D17S30 | 16 | 4 | 0.25 | Melanoma | GCC 7:169 |

Chromosome 17 - p Arm

| | | | | | | |
|---------|-----------|----|----|------|-----------|------------------------|
| 13.3 | D17S30 | 14 | 9 | 0.64 | Ovary | CR 50:2724 |
| 13.3 | D17S30 | 21 | 19 | 0.86 | Ovary | IJC 54:85 |
| 13.3 | D17S30 | 46 | 37 | 0.8 | Ovary | CR 56:606 |
| 13.3 | D17S30 | 41 | 27 | 0.66 | Ovary | O 7:1059 |
| 13.3 | D17S30 | 7 | 0 | 0 | Prostate | GCC 11:119 |
| 13.3 | D17S30 | 3 | 0 | 0 | Sarcoma | CR 53:468 |
| 13.3 | D17S30 | 6 | 4 | 0.67 | Sarcoma | CR 53:468 |
| 13.3 | D17S30 | 3 | 0 | 0 | Sarcoma | CR 53:468 |
| 13.3 | D17S30 | 6 | 0 | 0 | Sarcoma | CR 53:468 |
| 13.3 | D17S30 | 17 | 16 | 0.94 | Sarcoma | CR 49:6247 |
| 13.3 | D17S30 | 15 | 3 | 0.2 | Uterus | GCC 9:119 |
| 13.3 | D17S28 | 11 | 4 | 0.36 | Brain | CR 49:6572 |
| 13.3 | D17S28 | 22 | 3 | 0.14 | Brain | AJP 145:11 |
| 13.3 | D17S28 | 12 | 4 | 0.33 | Brain | CR 49:6572 |
| 13.3 | D17S28 | 27 | 11 | 0.41 | Breast | CR 54:6270 |
| 13.3 | D17S28 | 62 | 15 | 0.24 | Breast | GCC 76:106 |
| 13.3 | D17S28 | 37 | 26 | 0.7 | Breast | CR 54:4200 |
| 13.3 | D17S28 | 11 | 4 | 0.36 | Breast | HMG 4:2047 |
| 13.3 | D17S28 | 23 | 12 | 0.52 | Breast | CR 53:1637 |
| 13.3 | D17S28 | 27 | 4 | 0.15 | Cervix | CR 54:4481 |
| 13.3 | D17S28 | 14 | 1 | 0.07 | Cervix | BJC 67:71 |
| 13.3 | D17S28 | 7 | 5 | 0.71 | Colon | Science Ap 1989:217 |
| 13.3 | D17S28 | 13 | 8 | 0.62 | Colon | GCC 3:468 |
| 13.3 | D17S28 | 12 | 4 | 0.33 | Colon | CCG 48:167 |
| 13.3 | D17S28 | 2 | 0 | 0 | Head&Neck | CR 52:4787 |
| 13.3 | D17S28 | 11 | 0 | 0 | Kidney | JU 150:129 |
| 13.3 | D17S28 | 3 | 1 | 0.33 | Liver | CR 53:368 |
| 13.3 | D17S28 | 3 | 3 | 1 | Lung | CR 49:5130 |
| 13.3 | D17S28 | 16 | 2 | 0.12 | Ovary | IJC 52:575 |
| 13.3 | D17S28 | 8 | 6 | 0.75 | Ovary | CR 50:2724 |
| 13.3 | D17S28 | 23 | 15 | 0.65 | Ovary | CR 56:606 |
| 13.3 | D17S28 | 6 | 4 | 0.67 | Ovary | IJC 54:85 |
| 13.3 | D17S28 | 18 | 14 | 0.78 | Ovary | IJC 54:220 |
| 13.3 | D17S28 | 3 | 1 | 0.33 | Pancreas | CR 54:2761 |
| 13.3 | D17S28 | 3 | 0 | 0 | Pancreas | GCC 3:468 |
| 13.3 | D17S28 | 10 | 2 | 0.2 | Stomach | BJC 59:150 |
| 13.3 | D17S28 | 7 | 0 | 0 | Stomach | HG 89:445 |
| 13.3 | D17S28 | 29 | 12 | 0.41 | Testis | O 9:2245 |
| 13.3 | D17S28 | 1 | 1 | 1 | Uterus | CR 51:5632 |
| Unknown | Unknown | 20 | 10 | 0.5 | Bladder | JU 153:109 |
| Unknown | Unknown | 76 | 21 | 0.28 | Brain | CR 56:164 |
| 13.3 | D17S34-S5 | 13 | 7 | 0.54 | Brain | CR 54:1397 |
| 13.3 | D17S34-S5 | 20 | 11 | 0.55 | Brain | CR 54:1397 |
| 13.3 | D17S5 | 22 | 4 | 0.18 | Brain | AJP 145:11 |
| 13.3 | D17S5 | 16 | 6 | 0.38 | Brain | IJC 63:372 |
| 13.3 | D17S5 | 13 | 6 | 0.46 | Brain | CR 49:6572 |

Chromosome 17 - p Arm

| | | | | | | |
|------|-----------|-----|-----|------|------------|------------------------|
| 13.3 | D17S5 | 11 | 6 | 0.55 | Brain | CR 49:6572 |
| 13.3 | Unknown | 74 | 20 | 0.27 | Breast | AJP 140:721 |
| 13.3 | D17S5 | 62 | 26 | 0.42 | Breast | JJCR 84:11 |
| 13.3 | D17S5 | 68 | 37 | 0.54 | Breast | O 8:781 |
| 13.3 | D17S5 | 57 | 28 | 0.49 | Breast | BCRT 28:23 |
| 13.3 | D17S5 | 4 | 2 | 0.5 | Breast | CR 53:4804 |
| 13.3 | D17S5 | 29 | 16 | 0.55 | Breast | GCC 2:191 |
| 13.3 | D17S5 | 50 | 8 | 0.16 | Breast | CR 43:4356 |
| 13.3 | D17S5 | 465 | 224 | 0.48 | Breast | BJC 71:438 |
| 13.3 | D17S5 | 34 | 15 | 0.44 | Breast | HMC 4:2047 |
| 13.3 | D17S5 | 82 | 53 | 0.65 | Breast | CR 54:4200 |
| 13.3 | D17S5 | 75 | 21 | 0.28 | Breast | CGC 76:106 |
| 13.3 | D17S5 | 354 | 174 | 0.49 | Breast | C 74:2281 |
| 13.3 | D17S5 | 39 | 19 | 0.46 | Breast | IJC 53:41 |
| 13.3 | D17S5 | 42 | 25 | 0.6 | Breast | IJC 50:528 |
| 13.3 | D17S5 | 40 | 22 | 0.55 | Breast | GCC 4:1132 |
| 13.3 | D17S5 | 125 | 63 | 0.5 | Breast | CR 51:5794 |
| 13.3 | D17S5 | 61 | 26 | 0.43 | Breast | BG 90:635 |
| 13.3 | D17S5 | 52 | 27 | 0.52 | Breast | PNAS 88:38 |
| 13.3 | D17S5 | 15 | 4 | 0.27 | Cervix | CGC 79:74 |
| 13.3 | D17S5 | 12 | 1 | 0.08 | Cervix | BJC 67:71 |
| 13.3 | D17S5 | 32 | 5 | 0.16 | Cervix | CR 54:4481 |
| 13.3 | Unknown | 7 | 6 | 0.86 | Colon | Science Ap 1989:217 |
| 13.3 | D17S5 | 35 | 24 | 0.69 | Colon | BJC 59:750 |
| 13.3 | D17S5 | 19 | 7 | 0.37 | Colon | CCG 48:167 |
| 13.3 | D17S5 | 5 | 3 | 0.6 | Colon | O 9:991 |
| 13.3 | D17S5 | 27 | 21 | 0.78 | Colon | IJC 53:382 |
| 13.3 | D17S5 | 17 | 7 | 0.41 | Colon | GCC 3:468 |
| 13.3 | D17S5 | 26 | 10 | 0.38 | Colon | S 241:961 |
| 13.3 | D17S34-S5 | 24 | 11 | 0.46 | Esophageal | CR 52:6525 |
| 13.3 | D17S5 | 22 | 10 | 0.45 | Esophageal | CR 51:2113 |
| 13.3 | Unknown | 6 | 5 | 0.83 | Head&Neck | AJP 142:11 |
| 13.3 | D17S5 | 11 | 2 | 0.18 | Head&Neck | CR 52:1494 |
| 13.3 | D17S5 | 48 | 8 | 0.17 | Kidney | CR 51:5817 |
| 13.3 | D17S5 | 23 | 6 | 0.26 | Kidney | JU 150:129 |
| 13.3 | D17S5 | 15 | 5 | 0.33 | Kidney | CR 51:820 |
| 13.3 | D17S5 | 31 | 5 | 0.16 | Kidney | CR 51:1544 |
| 13.3 | D17S5 | 15 | 1 | 0.07 | Kidney | CR 51:1071 |
| 13.3 | D17S5 | 2 | 1 | 0.5 | Kidney | CR 51:1544 |
| 13.3 | D17S5 | 20 | 3 | 0.15 | Liver | O 6:491 |
| 13.3 | D17S5 | 14 | 3 | 0.21 | Liver | CR 51:4367 |
| 13.3 | D17S5 | 31 | 15 | 0.48 | Liver | CR 53:368 |
| 13.3 | D17S5 | 9 | 3 | 0.33 | Liver | BJC 64:108 |
| 13.3 | D17S34-S5 | 11 | 11 | 1 | Lung | CR 49:5130 |
| 13.3 | D17S5 | 6 | 6 | 1 | Lung | CR 55:28 |
| 13.3 | D17S34-S5 | 38 | 25 | 0.66 | Ovary | O 7:2069 |

Chromosome 17 - p Arm

| | | | | | | |
|---------|-----------|----|----|------|--------------|------------|
| 13.3 | D17S34-S5 | 6 | 2 | 0.33 | Ovary | O 7:2069 |
| 13.3 | D17S5 | 17 | 13 | 0.26 | Ovary | IJC 54:220 |
| 13.3 | D17S5 | 28 | 12 | 0.43 | Ovary | CR 51:5118 |
| 13.3 | D17S5 | 13 | 9 | 0.27 | Ovary | IJC 54:716 |
| 13.3 | D17S5 | 34 | 7 | 0.21 | Ovary | IJC 52:575 |
| 13.3 | D17S5 | 41 | 27 | 0.66 | Ovary | O 7:1059 |
| 13.3 | D17S5 | 28 | 15 | 0.54 | Ovary | GO 47:137 |
| 13.3 | D17S5 | 5 | 0 | 0 | Pancreas | GCC 3:468 |
| 13.3 | D17S5 | 8 | 0 | 0 | Pancreas | BJC 65:809 |
| 13.3 | D17S5 | 4 | 2 | 0.5 | Pancreas | CR 54:2361 |
| 13.3 | D17S5 | 27 | 1 | 0.04 | Pediatric | CR 50:3279 |
| 13.3 | D17S5 | 8 | 6 | 0.75 | Sarcoma | CGC 53:43 |
| 13.3 | D17S5 | 22 | 16 | 0.73 | Sarcoma | CR 52:2419 |
| 13.3 | D17S5 | 60 | 38 | 0.63 | Stomach | IA 77:232 |
| 13.3 | D17S5 | 38 | 19 | 0.5 | Stomach | CR 51:2926 |
| 13.3 | D17S5 | 14 | 2 | 0.14 | Stomach | GCC 3:468 |
| 13.3 | D17S5 | 24 | 9 | 0.38 | Stomach | HG 92:244 |
| 13.3 | D17S5 | 30 | 6 | 0.2 | Testis | O 9:2245 |
| 13.3 | D17S5 | 9 | 4 | 0.44 | Uterus | CR 51:5632 |
| 13.3 | D17S379 | 22 | 15 | 0.58 | Ovary | CR 55:606 |
| 13.3 | ABR | 29 | 6 | 0.21 | Ovary | CR 56:606 |
| Unknown | D17S65 | 16 | 10 | 0.62 | Breast | CR 54:4200 |
| 13 | D17S65 | 16 | 11 | 0.69 | Breast | GE 5:554 |
| 13 | D17S65 | 2 | 2 | 1 | Colon | S:April 16 |
| 13 | D17S1 | 15 | 3 | 0.2 | Brain | AJP 145:11 |
| 13 | D17S1 | 15 | 2 | 0.13 | Brain | AJP 145:11 |
| 13 | D17S1 | 21 | 4 | 0.19 | Breast | HG 91:6 |
| 13 | D17S1 | 20 | 9 | 0.45 | Breast | GCC 2:191 |
| 13 | D17S1 | 29 | 9 | 0.31 | Breast | CR 53:4356 |
| 13 | D17S1 | 7 | 2 | 0.29 | Cervix | CR 49:3598 |
| 13 | D17S1 | 14 | 6 | 0.43 | Colon | CR 50:7166 |
| 13 | D17S1 | 9 | 0 | 0 | Colon | N 331:275 |
| 13 | D17S1 | 2 | 2 | 1 | Colon | S:April 16 |
| 13 | D17S1 | 12 | 4 | 0.33 | Colon | S 241:961 |
| 13 | D17S1 | 30 | 13 | 0.43 | Head&Neck | O 10:1217 |
| 13 | D17S1 | 7 | 1 | 0.14 | Liver | JJCR 84:10 |
| 13 | D17S1 | 11 | 2 | 0.18 | Liver | CR 53:368 |
| 13 | D17S1 | 3 | 1 | 0.33 | Lung | PNAS 86:50 |
| 13 | D17S1 | 9 | 8 | 0.89 | Lung | PNAS 86:50 |
| 13 | D17S1 | 17 | 8 | 0.47 | Lung | PN 84:9252 |
| 13 | D17S1 | 7 | 7 | 1 | Lung | CR 49:5130 |
| 13 | D17S1 | 11 | 2 | 0.18 | Lung | PNAS 86:50 |
| 13 | D17S1 | 4 | 0 | 0 | Neuroblastom | CR 49:1095 |
| 13 | D17S1 | 5 | 0 | 0 | Sarcoma | CR 53:468 |
| 13 | D17S1 | 3 | 1 | 0.33 | Sarcoma | CR 53:468 |
| 13 | D17S1 | 3 | 0 | 0 | Sarcoma | CR 53:468 |

Chromosome 17 - p Arm

| | | | | | | |
|-----------|---------|----|----|------|------------|------------|
| 13 | D17S1 | 8 | 7 | 0.88 | Sarcoma | CR 52:2419 |
| 13 | D17S1 | 2 | 0 | 0 | Sarcoma | CR 52:408 |
| 13 | D17S1 | 13 | 12 | 0.92 | Sarcoma | CR 49:6247 |
| 13 | D17S1 | 5 | 4 | 0.2 | Stomach | CR 42:1099 |
| 13 | D17S1 | 10 | 0 | 0 | Stomach | CR 48:2988 |
| 13 | D17S1 | 6 | 1 | 0.17 | Uterus | CR 51:5732 |
| Unknown | D17S796 | 17 | 0 | 0 | Endocrine | CR 56:599 |
| Unknown | D17S796 | 41 | 14 | 0.34 | Head&Neck | CR 57:1786 |
| Unknown | D17S796 | 33 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D17S796 | 6 | 0 | 0.5 | Kidney | GC 302:16 |
| Unknown | D17S796 | 32 | 5 | 0.16 | Melanoma | CR 56:589 |
| 12.0-13 | D17S906 | 19 | 13 | 0.16 | Prostate | GC 302:218 |
| 13.1 | D17S31 | 9 | 2 | 0.22 | Brain | CR 49:6572 |
| 13.1 | D17S31 | 7 | 2 | 0.15 | Brain | HP 34:471 |
| 13.1 | D17S31 | 8 | 4 | 0.5 | Brain | CR 49:6572 |
| 13.1 | D17S31 | 21 | 7 | 0.33 | Breast | HG 97:267 |
| 13.1 | D17S31 | 54 | 24 | 0.44 | Breast | Lan 336:76 |
| 13.1 | D17S31 | 31 | 22 | 0.65 | Breast | CR 51:1200 |
| 13.1 | D17S31 | 87 | 37 | 0.43 | Breast | CR 51:5794 |
| 13.1-11.2 | D17S31 | 25 | 11 | 0.44 | Breast | IJC 50:528 |
| 13.1 | D17S31 | 2 | 1 | 0.5 | Breast | CR 53:2947 |
| 13.1 | D17S31 | 11 | 1 | 0.09 | Cervix | BJC 67:17 |
| 13.1-11.2 | D17S31 | 16 | 7 | 0.44 | Colon | CR 50:7166 |
| 13.1 | D17S31 | 6 | 6 | 1 | Colon | S:Apr 1:16 |
| 13.1 | D17S31 | 15 | 9 | 0.6 | Esophageal | CR 54:2996 |
| 13.1 | D17S31 | 29 | 18 | 0.62 | Head&Neck | O 10:1217 |
| 13.1-11.2 | D17S31 | 28 | 5 | 0.18 | Kidney | CR 51:5817 |
| 13.1 | D17S31 | 25 | 0 | 0 | Kidney | JO 150:129 |
| 13.1-11.2 | D17S31 | 16 | 6 | 0.38 | Liver | CR 51:89 |
| 13.1 | D17S31 | 21 | 12 | 0.57 | Liver | CR 53:1368 |
| 13.1 | D17S31 | 17 | 7 | 0.41 | Ovary | IJC 54:546 |
| 13.1 | D17S31 | 7 | 2 | 0.29 | Ovary | IJC 54:85 |
| 13.1 | D17S31 | 11 | 8 | 0.73 | Ovary | IJC 54:220 |
| 13.1 | D17S31 | 7 | 4 | 0.57 | Ovary | BJC 65:10 |
| 13.1 | D17S31 | 6 | 2 | 0.33 | Ovary | CR 56:606 |
| 13.1 | D17S31 | 3 | 1 | 0.33 | Pancreas | CR 54:2761 |
| 13.1-11.2 | D17S31 | 17 | 12 | 0.71 | Sarcoma | CR 52:2419 |
| 13.1 | D17S31 | 15 | 15 | 1 | Sarcoma | CR 49:6247 |
| 13.1 | D17S31 | 12 | 9 | 0.75 | Sarcoma | CR 52:2419 |
| 13.1 | TP53 | 7 | 0 | 0 | Bladder | HG 97:155 |
| 13.1 | TP53 | 21 | 9 | 0.43 | Brain | CR 54:1397 |
| Unknown | TP53 | 1 | 0 | 0 | Brain | AJP 145:11 |
| 13.1 | TP53 | 45 | 6 | 0.13 | Brain | O 6:1313 |
| 13.1 | TP53 | 6 | 2 | 0.33 | Brain | CR 49:6572 |
| 13.1 | TP53 | 22 | 9 | 0.41 | Brain | CGC 74:139 |
| 13.1 | TP53 | 38 | 11 | 0.29 | Brain | CR 52:1427 |

Chromosome 17 - p Arm

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|---------|------|-----|----|------|------------|------------|
| 13.1 | TP53 | 15 | 7 | 0.47 | Brain | CR 54:1397 |
| 13.1 | TP53 | 6 | 2 | 0.33 | Brain | CR 44:592 |
| 13.1 | TP53 | 31 | 22 | 0.71 | Breast | BJC 68:64 |
| Unknown | TP53 | 63 | 17 | 0.27 | Breast | BCRT 28:23 |
| 13.1 | TP53 | 61 | 14 | 0.23 | Breast | CGC 76:106 |
| Unknown | TP53 | 19 | 6 | 0.32 | Breast | CR 51:6194 |
| 13.1 | TP53 | 44 | 28 | 0.64 | Breast | HG 90:635 |
| 13.1 | TP53 | 35 | 13 | 0.37 | Breast | IJC 50:528 |
| 13.1 | TP53 | 70 | 26 | 0.37 | Breast | CR 51:5794 |
| 13.1 | TP53 | 65 | 13 | 0.22 | Breast | JCCR 36:47 |
| Unknown | TP53 | 11 | 6 | 0.55 | Breast | CR 52:2624 |
| 13.1 | TP53 | 81 | 22 | 0.27 | Breast | Jan 336:76 |
| 13.1 | TP53 | 25 | 10 | 0.4 | Breast | GCC 4:113 |
| 13.1 | TP53 | 36 | 10 | 0.28 | Breast | BJC 63:254 |
| 13.1 | TP53 | 12 | 5 | 0.42 | Breast | CR 53:2947 |
| 13.1 | TP53 | 110 | 72 | 0.65 | Breast | CR 54:4200 |
| 13.1 | TP53 | 36 | 15 | 0.42 | Breast | CR 53:1637 |
| 13.1 | TP53 | 17 | 9 | 0.53 | Breast | GCC 4:113 |
| 13.1 | TP53 | 41 | 34 | 0.83 | Breast | IJC 57:498 |
| Unknown | TP53 | 16 | 0 | 0 | Cervix | CGC 79:74 |
| 13.1 | TP53 | 9 | 1 | 0.11 | Cervix | BJC 67:71 |
| Unknown | TP53 | 6 | 3 | 0.5 | Cervix | GCC 9:119 |
| 13.1 | TP53 | 21 | 5 | 0.24 | Cervix | CR 54:4481 |
| 13.1 | TP53 | 17 | 8 | 0.47 | Colon | CR 52:741 |
| 13.1 | TP53 | 6 | 5 | 0.83 | Colon | GAST 107:3 |
| Unknown | TP53 | 23 | 15 | 0.65 | Colon | EJC 30A:26 |
| Unknown | TP53 | 48 | 38 | 0.79 | Colon | O 8:1391 |
| Unknown | TP53 | 26 | 22 | 0.85 | Colon | GAS 103:16 |
| 13.1 | TP53 | 30 | 17 | 0.57 | Colon | GAST 104:1 |
| Unknown | TP53 | 6 | 4 | 0.67 | Colon | O 9:991 |
| 13.1 | TP53 | 25 | 12 | 0.48 | Colon | HP 25:1069 |
| 13.1 | TP53 | 14 | 8 | 0.57 | Colon | CR 50:7166 |
| 13.1 | TP53 | 17 | 8 | 0.47 | Colon | JNCI 84:11 |
| 13.1 | TP53 | 17 | 7 | 0.41 | Colon | JNCI 84:11 |
| 13.1 | TP53 | 17 | 10 | 0.59 | Colon | IJC 53:382 |
| 13.1 | TP53 | 25 | 14 | 0.56 | Colon | CR 52:3965 |
| 13.1 | TP53 | 12 | 10 | 0.83 | Colon | CR 51:4436 |
| 13.1 | TP53 | 27 | 15 | 0.56 | Esophageal | C 73:2472 |
| 13.1 | TP53 | 14 | 10 | 0.71 | Esophageal | C 71:1933 |
| Unknown | TP53 | 47 | 27 | 0.57 | Esophageal | CR 52:6525 |
| 13.1 | TP53 | 14 | 7 | 0.5 | Head&Neck | CR 54:1152 |
| Unknown | TP53 | 32 | 14 | 0.44 | Head&Neck | O 9:2077 |
| 13.1 | TP53 | 27 | 15 | 0.56 | Head&Neck | C 73:2472 |
| 13.1 | TP53 | 39 | 21 | 0.54 | Head&Neck | O 10:1217 |
| 13.1 | TP53 | 20 | 4 | 0.2 | Kidney | CR 51:5817 |
| Unknown | TP53 | 40 | 5 | 0.12 | Kidney | BJC 69:230 |

Chromosome 17 - p Arm

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|---------|------|----|----|------|----------|------------|
| 13.1 | TP53 | 2 | 0 | 0 | Kidney | GCC 12:76 |
| 13.1 | TP53 | 10 | 6 | 0.6 | Kidney | IJC 64:899 |
| 13.1 | TP53 | 16 | 3 | 0.19 | Kidney | CR 51:820 |
| Unknown | TP53 | 65 | 9 | 0.14 | Leukemia | B 86:4587 |
| 13.1 | TP53 | 50 | 14 | 0.28 | Liver | JJCR 84:89 |
| 13.1 | TP53 | 7 | 6 | 0.86 | Liver | CR 51:6920 |
| Unknown | TP53 | 4 | 1 | 0.25 | Liver | CARC 17:14 |
| 13.1 | TP53 | 64 | 37 | 0.58 | Liver | C 73:42 |
| Unknown | TP53 | 19 | 11 | 0.58 | Liver | CR 54:281 |
| 13.1 | TP53 | 5 | 1 | 0.2 | Liver | O 8:2903 |
| 13.1 | TP53 | 7 | 3 | 0.43 | Liver | CR 51:89 |
| 13.1 | TP53 | 24 | 17 | 0.71 | Lung | CR 54:5643 |
| 13.1 | TP53 | 57 | 21 | 0.37 | Lung | O 10:937 |
| 13.1 | TP53 | 7 | 5 | 0.71 | Lung | CR 51:5643 |
| 13.1 | TP53 | 3 | 2 | 0.67 | Lung | CR 54:5643 |
| 13.1 | TP53 | 3 | 0 | 0 | Melanoma | GCC 74:169 |
| Unknown | TP53 | 28 | 7 | 0.25 | Melanoma | BJC 69:253 |
| 13.1 | TP53 | 42 | 19 | 0.45 | Ovary | CR 56:506 |
| 13.1 | TP53 | 12 | 5 | 0.42 | Ovary | IJC 54:546 |
| 13.1 | TP53 | 18 | 10 | 0.56 | Ovary | BJC 69:40 |
| 13.1 | TP53 | 9 | 6 | 0.67 | Ovary | IJC 54:85 |
| 13.1 | TP53 | 9 | 2 | 0.22 | Ovary | IJC 52:575 |
| 13.1 | TP53 | 23 | 18 | 0.78 | Ovary | IJC 54:220 |
| 13.1 | TP53 | 18 | 12 | 0.67 | Ovary | BJC 69:429 |
| 13.1 | TP53 | 12 | 3 | 0.25 | Ovary | CR 51:5118 |
| 13.1 | TP53 | 20 | 16 | 0.8 | Ovary | CR 51:5171 |
| Unknown | TP53 | 35 | 26 | 0.74 | Ovary | BJC 72:883 |
| 13.1 | TP53 | 7 | 1 | 0.14 | Ovary | O 7:2069 |
| 13.1 | TP53 | 2 | 1 | 0.5 | Ovary | O 7:2069 |
| 13.1 | TP53 | 32 | 18 | 0.56 | Ovary | O 7:2069 |
| 13.1 | TP53 | 13 | 3 | 0.23 | Ovary | O 7:2069 |
| 13.1 | TP53 | 7 | 5 | 0.71 | Pancreas | GCC 15:157 |
| 13.1 | TP53 | 27 | 3 | 0.11 | Prostate | AJP 145:28 |
| 13.1 | TP53 | 8 | 3 | 0.38 | Prostate | JU 151:107 |
| 13.1 | TP53 | 4 | 0 | 0 | Prostate | AJP 147:11 |
| Unknown | TP53 | 5 | 3 | 0.6 | Sarcoma | CR 53:468 |
| Unknown | TP53 | 4 | 1 | 0.25 | Sarcoma | CR 53:468 |
| Unknown | TP53 | 7 | 1 | 0.14 | Sarcoma | CR 53:468 |
| Unknown | TP53 | 12 | 6 | 0.5 | Sarcoma | CR 53:468 |
| Unknown | TP53 | 63 | 23 | 0.37 | Stomach | LI 72:232 |
| 13.1 | TP53 | 16 | 5 | 0.31 | Stomach | CGC 75:45 |
| Unknown | TP53 | 5 | 1 | 0.2 | Testis | GCC 6:92 |
| 13.1 | TP53 | 7 | 3 | 0.43 | Testis | O 9:2245 |
| 13.1 | TP53 | 9 | 2 | 0.22 | Uterus | GCC 9:119 |
| 13.1 | TP53 | 3 | 1 | 0.33 | Uterus | CR 51:5632 |
| 13.1 | TP53 | 4 | 1 | 0.25 | Uterus | CR 51:5632 |

Chromosome 17 - p Arm

| | | | | | | |
|---------|----------|----|----|------|-----------|---------------------|
| Unknown | TP53 | 28 | 3 | 0.11 | Uterus | CR 54:4294 |
| 13.1 | D17S286 | 27 | 1 | 0.15 | Cervix | CR 56:1397 |
| 13.1 | D17S786 | 2 | 0 | 0 | Kidney | GCC 12:76 |
| 12 | D17S520 | 14 | 7 | 0.5 | Brain | CR 54:1397 |
| 12 | D17S520 | 20 | 13 | 0.65 | Brain | CR 54:1397 |
| 13.1 | D17S520 | 31 | 15 | 0.49 | Head&Neck | O 9:2077 |
| 12 | D17S520 | 19 | 11 | 0.58 | Ovary | BJC 69:429 |
| 13.1 | D17S520 | 26 | 2 | 0.08 | Uterus | CR 54:4294 |
| 13.1 | MYH2 | 10 | 5 | 0.5 | Brain | CR 49:6572 |
| 13.1 | MYH2 | 8 | 2 | 0.25 | Brain | CR 49:6572 |
| 13.1 | MYH2 | 14 | 1 | 0.07 | Brain | AJP 145:11 |
| 13.1 | MYH2 | 14 | 10 | 0.71 | Colon | IJC 53:382 |
| 13.1 | MYH2 | 5 | 2 | 0.4 | Liver | CR 53:368 |
| 13.1 | MYH2 | 10 | 2 | 0.2 | Liver | GCC 48:82 |
| 13.1 | MYH2 | 10 | 10 | 1 | Lung | CR 49:5130 |
| 13.1 | MYH2 | 14 | 3 | 0.21 | Ovary | IJC 51:46 |
| 13.1 | MYH2 | 15 | 12 | 0.8 | Sarcoma | CR 49:6247 |
| 13.1 | MYH2 | 17 | 6 | 0.5 | Sarcoma | CR 52:2619 |
| 13.1 | MYH2 | 19 | 8 | 0.42 | Stomach | CR 52:3099 |
| 13.1 | MYH2 | 20 | 6 | 0.3 | Uterus | CR 51:5632 |
| 12 | D17S67 | 8 | 4 | 0.5 | Brain | AJP 145:11 |
| 12 | D17S67 | 35 | 22 | 0.63 | Breast | CR 54:4200 |
| 12 | D17S67 | 12 | 11 | 0.92 | Breast | GE 5:554 |
| 12 | D17S67 | 1 | 1 | 1 | Colon | Science Ap 1989:217 |
| 12 | D17S67 | 22 | 10 | 0.45 | Ovary | IJC 54:546 |
| 12 | D17S67 | 16 | 7 | 0.46 | Ovary | CR 56:606 |
| 13.1 | EW505 | 3 | 2 | 0.67 | Colon | Science Ap 1989:217 |
| 13.1 | UC 10-41 | 4 | 3 | 0.78 | Colon | Science Ap 1989:217 |
| 13.1 | EW401 | 3 | 1 | 0.33 | Colon | Science Ap 1989:217 |
| 13.1 | EW402 | 2 | 1 | 0.5 | Colon | Science Ap 1989:217 |
| 13.1 | EW405 | 3 | 1 | 0.33 | Colon | Science Ap 1989:217 |
| 13.1 | D17S29 | 15 | 1 | 0.07 | Brain | CR 49:6572 |
| 13.1 | D17S29 | 9 | 1 | 0.11 | Brain | CR 49:6572 |
| 13.1 | D17S29 | 2 | 0 | 0 | Colon | Science Ap 1989:217 |
| 13.1 | CHRNA1 | 26 | 14 | 0.54 | Head&Neck | O 9:2077 |
| 13.1 | CHRNA1 | 22 | 8 | 0.36 | Head&Neck | CR 54:1397 |
| 13.1 | CHRNA1 | 28 | 14 | 0.5 | Ovary | CR 56:606 |
| 11.2-12 | D17S261 | 6 | 2 | 0.33 | Brain | CR 54:1397 |
| 11.2-12 | D17S261 | 7 | 3 | 0.43 | Brain | CR 54:1397 |
| 11.2-12 | D17S261 | 19 | 8 | 0.42 | Leukemia | BJC 34:49 |
| 12-11.2 | D17S71 | 15 | 2 | 0.13 | Brain | AJP 145:11 |

Chromosome 17 - p Arm

| | | | | | | |
|--------------|-------------|----|----|------|-----------|---------------------|
| 12-11.2 | D17S71 | 3 | 2 | 0.61 | Breast | GE 5:554 |
| 12-11.2 | D17S71 | 18 | 15 | 0.83 | Colon | IJC 53:382 |
| 12-11.2 | D17S71 | 7 | 1 | 0.13 | Bladder | CR 53:568 |
| 12-11.2 | D17S71 | 10 | 10 | 1 | Lung | CR 49:5130 |
| 12-11.2 | D17S71 | 20 | 11 | 0.55 | Ovary | GO 47:137 |
| 12-11.2 | D17S71 | 17 | 6 | 0.35 | Sarcoma | CR 52:2419 |
| 12-11.2 | D17S71 | 9 | 5 | 0.56 | Sarcoma | CR 52:2419 |
| 12-11.2 | D17S71 | 13 | 5 | 0.38 | Uterine | CR 53:568 |
| 13.1 | D17S122 | 23 | 4 | 0.17 | Brain | AJP 145:11 |
| 13.1 | D17S122 | 28 | 11 | 0.38 | Head&Neck | CR 53:568 |
| 13.1 | D17S122 | 12 | 7 | 0.58 | Head&Neck | CR 54:1152 |
| Unknown | D17S58 | 17 | 2 | 0.12 | Brain | AJP 145:11 |
| 11.2-11.1 | D17S58 | 21 | 7 | 0.33 | Breast | GE 5:554 |
| 11.2-11.1 | D17S58 | 63 | 35 | 0.56 | Breast | CR 53:568 |
| Unknown | D17S58 | 35 | 14 | 0.4 | Breast | O 8:781 |
| 11.2-11.1 | D17S58 | 10 | 1 | 0.1 | Cervix | HMG 4:2047 |
| 11.2-11.1 | D17S58 | 5 | 1 | 0.2 | Colon | Science Ap 1989:217 |
| Unknown | D17S58 | 9 | 0 | 0 | Head&Neck | CR 52:4787 |
| 11.2-11.1 | D17S58 | 11 | 9 | 0.82 | Ovary | IJC 54:85 |
| Unknown | D17S58 | 19 | 12 | 0.63 | Ovary | CR 56:606 |
| Unknown | D17Z1 | 27 | 1 | 0.04 | Breast | GE 5:554 |
| Unknown | D17Z1 | 27 | 1 | 0.04 | Breast | GE 5:554 |
| D17S5-D17S58 | Unknown | 21 | 8 | 0.38 | Bladder | CR 51:5405 |
| Unknown | CHRNA1-TP53 | 30 | 18 | 0.6 | Bladder | CR 55:5213 |
| Unknown | Unknown | 32 | 13 | 0.41 | Brain | CR 50:5784 |
| 12-11.2 | D17S121 | 17 | 3 | 0.18 | Brain | AJP 145:11 |
| Unknown | D17S5:28-31 | 14 | 0 | 0 | Brain | CGC 73:122 |
| Unknown | D17S5:28-31 | 25 | 6 | 0.24 | Brain | CGC 73:122 |
| Unknown | D17S5:28-31 | 15 | 5 | 0.33 | Brain | CGC 73:122 |
| Unknown | D17S66 | 15 | 2 | 0.13 | Brain | AJP 145:11 |
| 13.3 | Unknown | 28 | 10 | 0.36 | Breast | HMG 4:2047 |
| 13 | Unknown | 51 | 17 | 0.33 | Breast | Lan 336:76 |
| 13.3 | Unknown | 27 | 16 | 0.59 | Breast | HMG 4:2047 |
| 13.3 | Unknown | 22 | 9 | 0.41 | Breast | HMG 4:2047 |
| 13.1-13.3 | Unknown | 88 | 38 | 0.43 | Breast | CR 51:5794 |
| 13.1 | Unknown | 16 | 6 | 0.38 | Breast | CR 53:1637 |
| 13.3 | Unknown | 21 | 7 | 0.33 | Breast | HMG 4:2047 |
| 13.3 | D17S1174 | 7 | 3 | 0.43 | Breast | HMG 4:2047 |
| 13 | D17S513 | 17 | 6 | 0.35 | Breast | CR 53:2947 |
| Unknown | D17S66 | 7 | 0 | 1 | Breast | CR 54:4200 |
| 13 | Unknown | 15 | 0 | 0 | Cervix | BJC 67:71 |
| 13.3 | Unknown | 1 | 1 | 1 | Colon | S:April 16 |
| 13.3 | Unknown | 3 | 3 | 1 | Colon | S:April 16 |
| 13.3 | Unknown | 1 | 1 | 1 | Colon | S:April 16 |
| 13.3 | Unknown | 4 | 4 | 1 | Colon | S:April 16 |

Chromosome 17 - p Arm

| | | | | | | |
|-----------|---|-------|------|------|------------|------------|
| 13.1 | Unknown | 2 | 2 | 1 | Colon | Science 26 |
| Unknown | HF-12 | 12 | 6 | 0.5 | Colon | JNCI 84:11 |
| 13 | D17S513 | 32 | 20 | 0.62 | Esophageal | C 73:2472 |
| 13 | D17S513 | 32 | 20 | 0.62 | Head&Neck | C 73:2472 |
| 13 | D17S513 | 32 | 20 | 0.62 | Head&Neck | C 73:2472 |
| 13.2 | CI17-732 | 35 | 1 | 0.03 | Kidney | BJC 69:230 |
| Unknown | D17S849-D17S796 | 6 | 0 | 0 | Kidney | PNAS 92:28 |
| Unknown | D17S849-D17S796 | 21 | 1 | 0.05 | Kidney | PNAS 92:28 |
| Unknown | D17S786-799 | 23 | 4 | 0.17 | Leukemia | CR 55:577 |
| Unknown | Unknown | 30 | 28 | 0.93 | Lung | CR 54:2322 |
| 13 | Unknown | 19 | 10 | 0.53 | Ovary | BJC 65:40 |
| Unknown | D17S1-D17S28 | 15 | 2 | 0.13 | Ovary | IJC 54:546 |
| 13.1 | D17S260 | 21 | 10 | 0.48 | Ovary | CR 55:546 |
| 13.1-13.3 | D17S34-D17S28- D17S5-D17S379- P53-D17S513 | 7 | 7 | 1 | Ovary | AJHG 55:66 |
| 13.1-13.3 | D17S34-D17S28- D17S5-D17S379- P53-D17S513 | 2 | 2 | 1 | Ovary | AJHG 55:66 |
| 13.1-13.3 | D17S34-D17S28- D17S5-D17S379- P53-D17S513 | 12 | 12 | 1 | Ovary | AJHG 55:66 |
| 13.1-13.3 | D17S34-D17S28- D17S5-D17S379- P53-D17S513 | 1 | 1 | 1 | Ovary | AJHG 55:66 |
| Unknown | D17S5-34-71- MYH2 | 36 | 29 | 0.81 | Ovary | CR 53:2393 |
| 13 | D17S513 | 36 | 16 | 0.44 | Ovary | CR 56:606 |
| 13.3 | D17S578 | 29 | 12 | 0.41 | Ovary | CR 56:606 |
| 13.3 | D17S654 | 27 | 17 | 0.63 | Ovary | CR 56:606 |
| 13.3 | D17S695 | 41 | 18 | 0.44 | Ovary | CR 56:606 |
| Unknown | D17S34-5-28-31 | 19 | 12 | 0.63 | Ovary | CGC 85:43 |
| Unknown | TP53-D17S:515- 520-513 | 18 | 9 | 0.5 | Ovary | BJC 72:133 |
| Unknown | D17S1-D17S28 | 7 | 0 | 0 | Prostate | G 11:530 |
| 12.0-13 | D17S1149 | 15 | 4 | 0.27 | Prostate | GCC 13:278 |
| Unknown | D17S1-D17S28 | 8 | 2 | 0.25 | Stomach | GCC 3:468 |
| Unknown | Unknown | 19 | 2 | 0.11 | Testis | G 5:134 |
| Unknown | D17S134 | 17 | 0 | 0 | Testis | GCC 13:249 |
| Unknown | D17S30-D17S787 | 24 | 2 | 0.08 | Testis | LI 73:606 |
| Unknown | 12G6 | 22 | 2 | 0.09 | Uterus | CR 54:4294 |
| SUM | | 10343 | 4539 | 0.44 | | |

Chromosome 17 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------|-------|-------------|-----------|------------|--------------|
| Unknown | D17S146 | 6 | 4 | 0.67 | Ovary | IJC 54:220 |
| 11.2-12 | D17S33 | 8 | 1 | 0.12 | Brain | CR 49:6572 |
| 11.2-12 | D17S33 | 9 | 0 | 0 | Brain | CR 49:6572 |
| 11.2-12 | D17S33 | 59 | 13 | 0.22 | Breast | CR 51:5794 |
| 11.2-12 | D17S33 | 7 | 1 | 0.14 | Ovary | CR 51:5794 |
| 11.2-12 | D17S33 | 7 | 2 | 0.29 | Sarcoma | CR 52:2419 |
| 11.2-12 | D17S33 | 9 | 2 | 0.22 | Sarcoma | CR 52:2419 |
| 11.2-12 | CRYB1 | 13 | 0 | 0 | Brain | AJP 145:1175 |
| 11.2-12 | CRYB1 | 28 | 2 | 0.07 | Breast | GCC 4:115 |
| 11.2-12 | CRYB1 | 16 | 0 | 0 | Colon | JNCI 84:1100 |
| Unknown | D17S117 | 15 | 6 | 0.4 | Breast | CR 53:5617 |
| Unknown | D17S73 | 25 | 6 | 0.24 | Breast | O 8:781 |
| CEN-12 | D17S73 | 27 | 10 | 0.37 | Breast | CR 53:5617 |
| CEN-12 | D17S73 | 7 | 3 | 0.43 | Ovary | IJC 54:85 |
| 11.2-12 | D17S907 | 18 | 1 | 0.06 | Prostate | GCC 13:278 |
| 11.2-12 | THRA1 | 37 | 10 | 0.27 | Breast | CR 54:2549 |
| 11.2-12 | THRA1 | 66 | 17 | 0.26 | Breast | GCC 11:58 |
| 11.2-12 | THRA1 | 14 | 11 | 0.79 | Breast | CR 52:2624 |
| 11.2-12 | THRA1 | 17 | 7 | 0.41 | Breast | AJOG 172:908 |
| 11.2-12 | THRA1 | 13 | 5 | 0.38 | Esophageal | CL 97:129 |
| 11.2-12 | THRA1 | 17 | 12 | 0.71 | Ovary | AJOG 172:908 |
| 11.2-12 | THRA1 | 20 | 1 | 0.05 | Ovary | IJC 54:220 |
| 13.1 | TCF2 | 26 | 7 | 0.27 | Head&Neck | O 9:2077 |
| 21.1 | RARA | 11 | 6 | 0.55 | Ovary | IJC 54:85 |
| 11.2-12 | D17S250 | 1 | 0 | 0 | Bladder | HG 94:231 |
| 21 | D17S250 | 5 | 1 | 0.2 | Breast | CR 54:6069 |
| 21 | D17S250 | 81 | 17 | 0.21 | Breast | CR 54:2549 |
| 21 | D17S250 | 78 | 18 | 0.23 | Breast | GCC 11:58 |
| 11.2-12 | D17S250 | 26 | 5 | 0.19 | Breast | O 8:781 |
| 11.2-12 | D17S250 | 6 | 1 | 0.17 | Breast | HG 94:231 |
| 11.2-12 | D17S250 | 14 | 7 | 0.5 | Breast | CR 52:2624 |
| 21 | D17S250 | 11 | 2 | 0.18 | Esophageal | CL 97:129 |
| 11.2-12 | D17S250 | 19 | 5 | 0.26 | Head&Neck | CR 54:1152 |
| 11.2-12 | D17S250 | 2 | 0 | 0 | Ovary | HG 94:231 |
| 11.2-12 | D17S250 | 22 | 14 | 0.64 | Ovary | BUC 69:429 |
| 11.2-12 | D17S250 | 20 | 2 | 0.1 | Prostate | O 11:1241 |
| 21 | D17S250 | 20 | 2 | 0.1 | Prostate | CR 55:1002 |
| 21 | PHB | 4 | 3 | 0.75 | Ovary | IJC 54:85 |
| Unknown | PHB | 9 | 9 | 1 | Ovary | IJC 54:220 |
| 21 | D17S800 | 1 | 0 | 0 | Bladder | HG 94:231 |
| 21 | D17S800 | 7 | 6 | 0.86 | Breast | CR 54:6069 |
| 21 | D17S800 | 4 | 0 | 0 | Breast | HG 94:231 |
| 21 | D17S902 | 37 | 10 | 0.27 | Breast | CR 54:2549 |
| 21 | D17S902 | 16 | 4 | 0.25 | Prostate | GCC 13:278 |
| 21 | D17S579 | 1 | 0 | 0 | Bladder | HG 94:231 |
| 21 | D17S579 | 19 | 11 | 0.58 | Breast | CR 52:2624 |

Chromosome 17 - q Arm

| | | | | | | |
|---------|---------|----|----|------|------------|--------------|
| 21 | D17S579 | 7 | 5 | 0.71 | Breast | CR 54:6069 |
| 21 | D17S579 | 34 | 7 | 0.21 | Breast | O 8:781 |
| 21 | D17S579 | 85 | 20 | 0.24 | Breast | GCC 11:58 |
| 21 | D17S579 | 16 | 5 | 0.31 | Breast | AJOG 172:908 |
| 21 | D17S579 | 94 | 12 | 0.13 | Breast | CR 54:2549 |
| 21 | D17S579 | 4 | 1 | 0.25 | Breast | HG 94:231 |
| 21 | D17S579 | 52 | 21 | 0.4 | Breast | BCRT 32:1 |
| 21 | D17S579 | 14 | 4 | 0.29 | Esophageal | CL 97:129 |
| 21 | D17S579 | 26 | 8 | 0.31 | Head&Neck | CR 54:1152 |
| 21 | D17S579 | 17 | 13 | 0.76 | Ovary | AJOG 172:908 |
| 21 | D17S579 | 23 | 9 | 0.39 | Ovary | GO 55:215 |
| 21 | D17S579 | 2 | 0 | 0 | Ovary | HG 94:231 |
| 21 | D17S579 | 18 | 14 | 0.78 | Ovary | IJC 54:220 |
| 21 | D17S579 | 37 | 22 | 0.59 | Ovary | CR 56:606 |
| 21 | D17S579 | 9 | 11 | 0.34 | Ovary | IJC 54:85 |
| 21 | D17S579 | 20 | 2 | 0.1 | Prostate | CR 55:1002 |
| 21 | D17S579 | 20 | 2 | 0.1 | Prostate | O 11:1241 |
| 21 | D17S579 | 25 | 0 | 0 | Uterus | CR 54:4294 |
| Unknown | D17S509 | 75 | 18 | 0.24 | Breast | CR 53:4356 |
| Unknown | D17S509 | 26 | 3 | 0.12 | Breast | HG 91:6 |
| Unknown | D17S509 | 11 | 5 | 0.45 | Liver | CR 51:89 |
| 21 | HOX2 | 19 | 1 | 0.05 | Prostate | O 11:1241 |
| Unknown | PPY | 20 | 5 | 0.25 | Breast | CR 53:5617 |
| Unknown | D17S806 | 26 | 2 | 0.08 | Cervix | CR 56:197 |
| 21.3-22 | COL1A1 | 24 | 10 | 0.42 | Breast | O 8:781 |
| 22 | D17S41 | 43 | 21 | 0.49 | Breast | CR 53:5617 |
| 12.0-24 | D17S41 | 20 | 8 | 0.4 | Breast | O 8:781 |
| 22 | D17S41 | 11 | 7 | 0.64 | Ovary | IJC 54:85 |
| 12.0-24 | D17S41 | 20 | 5 | 0.25 | Ovary | IJC 54:546 |
| 12.0-24 | D17S41 | 8 | 7 | 0.88 | Ovary | IJC 54:220 |
| 21.3-22 | NM23 | 23 | 6 | 0.26 | Breast | GCC 11:113 |
| 21.3-22 | NM23 | 61 | 8 | 0.13 | Breast | ANYAS p.137 |
| 21.3-22 | NM23 | 29 | 3 | 0.1 | Colon | CR 54:3979 |
| 21.3-22 | NM23 | 17 | 3 | 0.18 | Colon | EJC 30A:664 |
| 21.3-22 | NM23 | 7 | 0 | 0 | Melanoma | GCC 7:169 |
| 21.3-22 | NM23 | 20 | 13 | 0.65 | Ovary | IJC 54:85 |
| 21.3-22 | NM23 | 23 | 2 | 0.09 | Stomach | IJC 84:184 |
| 21.3-22 | NM23 | 7 | 0 | 0 | Uterus | C 73:1686 |
| Unknown | NME1 | 55 | 25 | 0.45 | Breast | CR 53:5617 |
| Unknown | NME1 | 68 | 20 | 0.29 | Breast | GCC 11:58 |
| Unknown | NME1 | 17 | 5 | 0.29 | Breast | CR 52:2624 |
| Unknown | NME1 | 45 | 10 | 0.22 | Breast | BCRT 28:231 |
| Unknown | NME1 | 48 | 7 | 0.15 | Breast | IJC 84:1159 |
| Unknown | NME1 | 18 | 1 | 0.06 | Cervix | CR 54:4481 |
| Unknown | NME1 | 27 | 2 | 0.07 | Esophageal | C 73:2472 |
| Unknown | NME1 | 27 | 2 | 0.07 | Head&Neck | C 73:2472 |

Chromosome 17 - q Arm

| | | | | | | |
|------------|----------|-----|----|------|------------|--------------|
| Unknown | NME1 | 21 | 1 | 0.05 | Ovary | CR 51:224 |
| Unknown | NME1 | 21 | 1 | 0.05 | Prostate | JU 151:1073 |
| Unknown | NME1 | 18 | 8 | 0.44 | Testis | O 9:2245 |
| Unknown | D17S74 | 16 | 7 | 0.19 | Breast | CR 53:3382 |
| 22 | D17S74 | 50 | 10 | 0.2 | Breast | BCRT 28:231 |
| 22 | D17S74 | 58 | 22 | 0.37 | Breast | CR 53:3382 |
| 22 | D17S74 | 67 | 13 | 0.19 | Breast | HG 91:6 |
| Unknown | D17S74 | 32 | 2 | 0.08 | Breast | CR 53:3382 |
| 22 | D17S74 | 106 | 49 | 0.46 | Breast | CR 54:4200 |
| Unknown | D17S74 | 33 | 29 | 0.71 | Breast | CR 53:3382 |
| 23 | D17S74 | 49 | 12 | 0.24 | Breast | CR 53:3382 |
| Unknown | D17S74 | 76 | 22 | 0.29 | Breast | CR 53:3382 |
| Unknown | D17S74 | 57 | 10 | 0.18 | Breast | JJCR 84:1159 |
| 23 | D17S74 | 52 | 20 | 0.37 | Esophageal | CR 53:3382 |
| Unknown | D17S74 | 54 | 20 | 0.37 | Esophageal | GCC 10:177 |
| Unknown | D17S74 | 29 | 5 | 0.17 | Esophageal | CR 53:3382 |
| Unknown | D17S74 | 30 | 3 | 0.1 | Kidney | CR 51:820 |
| Unknown | D17S74 | 21 | 2 | 0.1 | Liver | CR 53:3382 |
| Unknown | D17S74 | 12 | 2 | 0.17 | Liver | CR 53:3382 |
| 22 | D17S74 | 7 | 7 | 1 | Lung | CR 49:5130 |
| 22 | D17S74 | 9 | 8 | 0.89 | Lung | PN 86:5099 |
| 22 | D17S74 | 3 | 1 | 0.33 | Lung | PN 86:5099 |
| 22 | D17S74 | 11 | 2 | 0.18 | Lung | PN 86:5099 |
| Unknown | D17S74 | 39 | 8 | 0.21 | Lung | CR 52:2479 |
| Unknown | D17S74 | 24 | 10 | 0.42 | Ovary | IJC 54:546 |
| Unknown | D17S74 | 23 | 16 | 0.7 | Ovary | IJC 54:220 |
| Unknown | D17S74 | 26 | 10 | 0.38 | Ovary | CR 51:5118 |
| 23 | D17S74 | 6 | 0 | 0 | Ovary | CR 53:3382 |
| 23 | D17S74 | 8 | 1 | 0.12 | Ovary | CR 53:3382 |
| 22 | D17S74 | 10 | 2 | 0.2 | Ovary | IJC 52:575 |
| 23 | D17S74 | 17 | 6 | 0.35 | Ovary | CR 53:3382 |
| 23 | D17S74 | 16 | 2 | 0.2 | Ovary | CR 53:3382 |
| 22 | D17S74 | 17 | 12 | 0.71 | Ovary | IJC 54:85 |
| Unknown | D17S74 | 18 | 4 | 0.22 | Sarcoma | CR 49:6247 |
| Unknown | D17S74 | 22 | 3 | 0.14 | Sarcoma | CR 52:2419 |
| Unknown | MPO | 11 | 4 | 0.36 | Breast | CR 52:2624 |
| Unknown | MPO | 31 | 5 | 0.16 | Head&Neck | O 9:2077 |
| Unknown | MPO | 20 | 1 | 0.05 | Prostate | O 11:3241 |
| Unknown | D17S86 | 44 | 9 | 0.2 | Breast | CR 53:5617 |
| 21-12-21.2 | C117-24 | 36 | 13 | 0.36 | Esophageal | CR 54:1638 |
| 12-21.1 | C117-316 | 37 | 11 | 0.3 | Breast | CR 53:3382 |
| 12-21.1 | C117-316 | 32 | 9 | 0.28 | Esophageal | CR 54:1638 |
| 12-21.1 | C117-316 | 13 | 6 | 0.46 | Ovary | CR 53:3382 |
| 12-21.1 | C117-316 | 1 | 0 | 0 | Ovary | CR 53:3382 |
| 12-21.1 | C117-316 | 9 | 1 | 0.11 | Ovary | CR 53:3382 |

Chromosome 17 - q Arm

| | | | | | | |
|---------|----------|-----|----|------|------------|--------------|
| 12-21.1 | CI17-316 | 3 | 0 | 0 | Ovary | CR 53:3382 |
| 21.3 | CI17-477 | 32 | 22 | 0.69 | Esophageal | CR 54:1638 |
| 21.3 | CI17-28 | 7 | 3 | 0.43 | Esophageal | CR 54:1638 |
| 21.3 | CI17-28 | 26 | 15 | 0.58 | Esophageal | CR 54:1638 |
| 21.3 | CI17-592 | 18 | 8 | 0.44 | Breast | CR 53:3382 |
| 21.3 | CI17-592 | 17 | 6 | 0.35 | Esophageal | CR 54:1638 |
| 21.3 | CI17-592 | 4 | 2 | 0.5 | Ovary | CR 53:3382 |
| 21.3 | CI17-592 | 1 | 0 | 0 | Ovary | CR 53:3382 |
| 21.3 | CI17-592 | 3 | 2 | 0.67 | Ovary | CR 53:3382 |
| 21.3 | CI17-592 | 1 | 0 | 0 | Ovary | CR 53:3382 |
| 21.3 | CI17-701 | 138 | 48 | 0.35 | Breast | CR 53:3382 |
| 21.3 | CI17-701 | 38 | 21 | 0.55 | Esophageal | CR 54:1638 |
| 21.3 | CI17-701 | 12 | 5 | 0.42 | Ovary | CR 53:3382 |
| 21.3 | CI17-701 | 7 | 0 | 0 | Ovary | CR 53:3382 |
| 21.3 | CI17-701 | 15 | 9 | 0.6 | Ovary | CR 53:3382 |
| 21.3 | CI17-701 | 12 | 2 | 0.17 | Ovary | CR 53:3382 |
| 21.3 | CI17-730 | 96 | 36 | 0.38 | Breast | CR 53:3382 |
| 21.3 | CI17-730 | 35 | 20 | 0.57 | Esophageal | CR 54:1638 |
| 21.3 | CI17-730 | 4 | 0 | 0 | Ovary | CR 53:3382 |
| 21.3 | CI17-730 | 4 | 0 | 0 | Ovary | CR 53:3382 |
| 21.3 | CI17-730 | 12 | 6 | 0.5 | Ovary | CR 53:3382 |
| 21.3 | CI17-730 | 4 | 2 | 0.5 | Ovary | CR 53:3382 |
| 21.3 | CI17-507 | 25 | 7 | 0.28 | Breast | CR 53:3382 |
| 21.3 | CI17-507 | 18 | 10 | 0.56 | Esophageal | CR 54:1638 |
| 21.3 | CI17-507 | 3 | 1 | 0.33 | Ovary | CR 53:3382 |
| 21.3 | CI17-507 | 5 | 2 | 0.4 | Ovary | CR 53:3382 |
| 21.3 | CI17-507 | 7 | 6 | 0.86 | Ovary | CR 53:3382 |
| 21.3 | CI17-507 | 3 | 1 | 0.33 | Ovary | CR 53:3382 |
| 21.3 | CI17-533 | 93 | 25 | 0.27 | Breast | CR 53:3382 |
| 21.3 | CI17-533 | 42 | 21 | 0.5 | Esophageal | CR 54:1638 |
| 21.3 | CI17-533 | 9 | 4 | 0.44 | Ovary | CR 53:3382 |
| 21.3 | CI17-533 | 9 | 3 | 0.33 | Ovary | CR 53:3382 |
| 21.3 | CI17-533 | 11 | 6 | 0.55 | Ovary | CR 53:3382 |
| 21.3 | CI17-533 | 7 | 1 | 0.14 | Ovary | CR 53:3382 |
| 21-23 | D17S78 | 14 | 0 | 0 | Brain | AJP 145:1175 |
| 21-23 | D17S78 | 25 | 5 | 0.2 | Ovary | IJC 54:546 |
| 22-24 | GH | 39 | 13 | 0.33 | Breast | O 8:781 |
| 22-24 | GH | 16 | 4 | 0.25 | Breast | CR 52:2624 |
| 22-24 | GH | 59 | 13 | 0.22 | Breast | CR 53:5617 |
| 22-24 | GH | 12 | 1 | 0.08 | Lung | CR 49:5130 |
| 22-24 | GH | 14 | 7 | 0.5 | Ovary | GO 55:245 |
| 22-24 | GH | 15 | 1 | 0.07 | Uterus | CR 51:5632 |
| Unknown | 66 E6 | 11 | 4 | 0.36 | Breast | O 8:781 |
| 23-24 | D17S40 | 23 | 10 | 0.43 | Breast | CR 53:5617 |
| Unknown | D17S40 | 14 | 5 | 0.36 | Breast | O 8:781 |
| 23-24 | D17S40 | 15 | 9 | 0.6 | Ovary | IJC 54:85 |

Chromosome 17 - q Arm

| | | | | | | |
|---------|---------|-----|----|------|------------|--------------|
| Unknown | D17S40 | 18 | 4 | 0.22 | Ovary | IJC 54:546 |
| 23-qter | D17S21 | 15 | 0 | 0 | Brain | AJP 145:1175 |
| 23-qter | D17S21 | 20 | 7 | 0.35 | Breast | CR 53:5617 |
| 23-qter | D17S21 | 25 | 13 | 0.52 | Ovary | IJC 54:546 |
| Unknown | D17S515 | 32 | 6 | 0.19 | Head&Neck | O 9:2077 |
| Unknown | D17S801 | 32 | 4 | 0.12 | Cervix | CR 56:197 |
| Unknown | D17S785 | 37 | 1 | 0.03 | Head&Neck | CR 54:4756 |
| Unknown | D17S785 | 37 | 16 | 0.43 | Head&Neck | CR 54:4756 |
| Unknown | D17S785 | 6 | 3 | 0.5 | Kidney | GCC 12:76 |
| Unknown | D17S785 | 27 | 1 | 0.04 | Melanoma | CR 56:589 |
| Unknown | CACNLB1 | 19 | 2 | 0.11 | Prostate | O 11:1241 |
| Unknown | D17S20 | 72 | 5 | 0.07 | Breast | CR 53:5617 |
| 23-25.5 | D17S4 | 9 | 0 | 0 | Brain | CR 49:6572 |
| 23-25.5 | D17S4 | 14 | 3 | 0.21 | Brain | CR 49:6572 |
| 23-25.5 | D17S4 | 34 | 1 | 0.03 | Brain | AJP 145:1175 |
| 23-25.5 | D17S4 | 47 | 6 | 0.13 | Breast | HG 91:6 |
| 23-25.4 | D17S4 | 42 | 18 | 0.43 | Breast | BJC 69:754 |
| 23-25.3 | D17S4 | 51 | 21 | 0.41 | Breast | CR 54:4200 |
| 23-25.3 | D17S4 | 34 | 10 | 0.29 | Breast | IJC 53:11 |
| 23-25.3 | D17S4 | 104 | 28 | 0.27 | Breast | CR 51:5794 |
| 23-25.3 | D17S4 | 63 | 24 | 0.38 | Breast | CR 53:5617 |
| 23-25.3 | D17S4 | 34 | 10 | 0.29 | Breast | GCC 4:113 |
| 23-25.5 | D17S4 | 47 | 16 | 0.34 | Breast | Lan 336:761 |
| 23-25.3 | D17S4 | 36 | 7 | 0.19 | Breast | ANYAS p.137 |
| 23-25.5 | D17S4 | 35 | 3 | 0.09 | Cervix | CR 54:4481 |
| 23-25 | D17S4 | 13 | 0 | 0 | Cervix | BJC 67:71 |
| 23-25.3 | D17S4 | 20 | 3 | 0.15 | Colon | JNCI 84:1100 |
| 23-25.3 | D17S4 | 23 | 0 | 0 | Colon | CCG 48:167 |
| 23-25.5 | D17S4 | 25 | 5 | 0.2 | Colon | CR 50:7166 |
| 23-25.5 | D17S4 | 14 | 1 | 0.07 | Esophageal | CR 51:2113 |
| 23-25.3 | D17S4 | 23 | 7 | 0.3 | Esophageal | CR 54:2996 |
| 23-25.5 | D17S4 | 14 | 1 | 0.07 | Kidney | CR 51:1071 |
| 23-25.5 | D17S4 | 8 | 2 | 0.25 | Liver | CR 53:368 |
| 23-25.3 | D17S4 | 5 | 0 | 0 | Liver | PNAS 86:8852 |
| 23-25.3 | D17S4 | 2 | 0 | 0 | Lung | CR 49:5130 |
| 23-25.3 | D17S4 | 16 | 11 | 0.69 | Ovary | O 7:2069 |
| 23-25.3 | D17S4 | 16 | 2 | 0.12 | Ovary | O 7:2069 |
| 23-25.3 | D17S4 | 41 | 30 | 0.73 | Ovary | O 7:2069 |
| 23-25.3 | D17S4 | 7 | 4 | 0.57 | Ovary | Unknown |
| 23-25.3 | D17S4 | 29 | 11 | 0.38 | Ovary | IJC 54:546 |
| 23-25.3 | D17S4 | 21 | 2 | 0.1 | Ovary | CR 51:5118 |
| 23-25.3 | D17S4 | 30 | 11 | 0.37 | Ovary | IJC 52:575 |
| 23-25 | D17S4 | 15 | 10 | 0.67 | Ovary | IJC 54:85 |
| 23-25.5 | D17S4 | 15 | 10 | 0.67 | Ovary | IJC 54:85 |
| 23-25.3 | D17S4 | 19 | 12 | 0.63 | Ovary | IJC 54:220 |
| 23-25 | D17S4 | 4 | 0 | 0 | Pancreas | CR 54:2761 |

Chromosome 17 - q Arm

| | | | | | | |
|---------|----------|----|----|------|----------|--------------|
| 23-25 | D17S4 | 11 | 0 | 0 | Prostate | GCC 11:119 |
| 23-25 | D17S4 | 9 | 2 | 0.22 | Sarcoma | CR 52:2419 |
| 23-25.5 | D17S4 | 12 | 9 | 0.75 | Sarcoma | CR 52:2419 |
| 23-25.3 | D17S4 | 14 | 3 | 0.21 | Sarcoma | CR 49:6247 |
| 23-25 | D17S4 | 7 | 0 | 0 | Stomach | CR 51:2926 |
| 23-25.5 | D17S4 | 42 | 17 | 0.4 | Testis | O 9:2245 |
| 23-25.3 | TK1 | 21 | 1 | 0.05 | Breast | CR 53:5617 |
| 23-qter | D17S77 | 31 | 2 | 0.06 | Brain | AJP 145:1175 |
| 23-qter | D17S77 | 30 | 11 | 0.37 | Breast | CR 53:5617 |
| Unknown | D17S26 | 9 | 0 | 0 | Breast | CR 53:5617 |
| Unknown | D17S26 | 16 | 5 | 0.31 | Ovary | CR 50:2724 |
| 23-25 | D17S75 | 71 | 23 | 0.32 | Breast | CR 51:5794 |
| 23-25.3 | D17S24 | 23 | 0 | 0 | Brain | AJP 145:1175 |
| Unknown | D17S24 | 34 | 12 | 0.35 | Breast | GCC 4:113 |
| Unknown | D17S24 | 59 | 27 | 0.46 | Breast | CR 53:5617 |
| Unknown | D17S24 | 59 | 20 | 0.34 | Breast | O 8:781 |
| 23-25.3 | D17S24 | 40 | 17 | 0.42 | Breast | CR 54:4200 |
| 23-25 | D17S24 | 42 | 10 | 0.24 | Breast | CR 51:5794 |
| 23-25.3 | D17S24 | 40 | 17 | 0.42 | Breast | CR 54:4200 |
| 23-25.3 | D17S24 | 20 | 8 | 0.4 | Breast | GCC 2:191 |
| 23-25.3 | D17S24 | 4 | 2 | 0.5 | Breast | CR 53:3804 |
| Unknown | D17S24 | 21 | 2 | 0.1 | Colon | JNCI 84:1100 |
| 23-25.3 | D17S24 | 18 | 11 | 0.61 | Ovary | IJC 54:85 |
| Unknown | D17S24 | 16 | 8 | 0.5 | Ovary | IJC 54:546 |
| 23-25.3 | D17S24 | 18 | 11 | 0.61 | Ovary | IJC 54:85 |
| 23-25 | D17S24 | 3 | 0 | 0 | Ovary | CR 51:5118 |
| Unknown | D17S24 | 9 | 1 | 0.11 | Prostate | G 11:530 |
| 23-25 | D17S27 | 17 | 6 | 0.35 | Breast | CR 51:5794 |
| Unknown | D17S79 | 9 | 2 | 0.22 | Breast | CR 53:5617 |
| Unknown | D17S79 | 9 | 2 | 0.22 | Breast | CR 53:5617 |
| Unknown | D17S587 | 1 | 0 | 0 | Bladder | HG 94:231 |
| 12.0-21 | D17S588 | 1 | 0 | 0 | Bladder | HG 94:231 |
| Unknown | Unknown | 28 | 3 | 0.11 | Brain | CR 50:5784 |
| 25.1 | Unknown | 31 | 9 | 0.29 | Breast | CR 53:3382 |
| 23 | Unknown | 31 | 10 | 0.32 | Breast | CR 53:3382 |
| 22 | Unknown | 41 | 14 | 0.34 | Breast | CR 53:3382 |
| 25.3 | Unknown | 45 | 13 | 0.29 | Breast | CR 53:3382 |
| 21 | D173700 | 54 | 10 | 0.19 | Breast | CR 54:2549 |
| 21 | D17S1184 | 11 | 2 | 0.18 | Breast | CR 54:6069 |
| 21 | D17S1322 | 11 | 10 | 0.91 | Breast | CR 54:6069 |
| 21 | D17S1325 | 11 | 11 | 1 | Breast | CR 54:6069 |
| 21 | D17S1328 | 6 | 5 | 0.83 | Breast | CR 54:6069 |
| 21 | D17S183 | 36 | 8 | 0.22 | Breast | CR 54:2549 |
| Unknown | D17S2 | 4 | 0 | 0 | Breast | GCC 2:191 |
| Unknown | D17S293 | 15 | 3 | 0.2 | Breast | AJOG 172:908 |
| Unknown | D17S306 | 23 | 9 | 0.39 | Breast | O 8:781 |

Chromosome 17 - q Arm

| | | | | | | |
|---------|---|-----|-----|------|------------|--------------|
| Unknown | D17S5-D17S1- D17S31-D17S509- D17S74-D17S4 | 75 | 18 | 0.24 | Breast | CR 53:3707 |
| Unknown | D17S587 | 6 | 1 | 0.17 | Breast | HG 94:231 |
| 12.0-21 | D17S588 | 9 | 2 | 0.22 | Breast | O 8:781 |
| 12.0-21 | D17S588 | 6 | 1 | 0.17 | Breast | HG 94:231 |
| 12.0-21 | D17S588 | 17 | 8 | 0.47 | Breast | AJOG 172:908 |
| 21 | D17S648 | 39 | 7 | 0.18 | Breast | CR 54:2549 |
| Unknown | D17S68 | 23 | 16 | 0.7 | Breast | CR 54:4200 |
| 21 | D17S702 | 92 | 21 | 0.23 | Breast | CR 54:2549 |
| Unknown | D17S702 | 80 | 24 | 0.3 | Breast | GCC 11:58 |
| Unknown | D17S733 | 65 | 18 | 0.28 | Breast | GCC 11:58 |
| 21 | D17S746 | 36 | 10 | 0.28 | Breast | CR 54:2549 |
| 21 | D17S750 | 59 | 14 | 0.24 | Breast | CR 54:2549 |
| 23-qter | D17S77 | 30 | 11 | 0.37 | Breast | CR 53:5617 |
| Unknown | D17S773 | 9 | 2 | 0.22 | Breast | CR 53:5617 |
| 21 | D17S776 | 10 | 6 | 0.6 | Breast | CR 54:6069 |
| 21 | D17S776 | 70 | 17 | 0.24 | Breast | GCC 11:58 |
| 21 | D17S776 | 63 | 19 | 0.3 | Breast | CR 54:2549 |
| 21 | D17S846 | 74 | 24 | 0.32 | Breast | CR 54:2549 |
| 21 | D17S855 | 30 | 8 | 0.27 | Breast | CR 54:2549 |
| 21 | D17S855 | 86 | 21 | 0.24 | Breast | GCC 11:58 |
| 21 | D17S855 | 10 | 8 | 0.8 | Breast | CR 54:6069 |
| 21 | D17S856 | 53 | 10 | 0.19 | Breast | CR 54:2549 |
| 21 | D17S857 | 68 | 17 | 0.25 | Breast | CR 54:2549 |
| 21 | D17S859 | 17 | 2 | 0.12 | Breast | CR 54:2549 |
| 21 | D17S870 | 441 | 173 | 0.39 | Breast | BJC 71:438 |
| 21 | D17S870-C117-730 | 289 | 98 | 0.34 | Breast | C 74:2281 |
| Unknown | EDH17B-HSD-A3T | 19 | 7 | 0.37 | Breast | GCC 11:58 |
| Unknown | EDH17B-HSD-DEL | 20 | 9 | 0.45 | Breast | GCC 11:58 |
| Unknown | EPB3 | 15 | 6 | 0.4 | Breast | CR 53:5617 |
| 21 | GAS | 50 | 13 | 0.26 | Breast | CR 54:2549 |
| Unknown | PROH1B | 6 | 1 | 0.17 | Cervix | GCC 9:119 |
| Unknown | D17S791 | 22 | 1 | 0.05 | Endocrine | CR 56:599 |
| 25.3 | Unknown | 40 | 11 | 0.28 | Esophageal | CR 54:1638 |
| 22 | Unknown | 33 | 16 | 0.48 | Esophageal | CR 54:1638 |
| 25.1 | Unknown | 26 | 14 | 0.54 | Esophageal | CR 54:1638 |
| Unknown | D17S874 | 35 | 20 | 0.57 | Esophageal | GCC 10:177 |
| Unknown | GP3A | 15 | 6 | 0.4 | Head&Neck | O 9:2077 |
| 12.0-21 | D17S588 | 34 | 2 | 0.06 | Kidney | BJC 69:230 |
| Unknown | D17S802-805-809 | 22 | 5 | 0.23 | Leukemia | CR 55:5377 |
| Unknown | D17S32 | 13 | 0 | 0 | Liver | CR 53:368 |
| 25.3 | Unknown | 7 | 3 | 0.43 | Ovary | CR 53:3382 |
| 22 | Unknown | 3 | 1 | 0.33 | Ovary | CR 53:3382 |
| 25.1 | Unknown | 7 | 0 | 0 | Ovary | CR 53:3382 |
| 25.1 | Unknown | 17 | 6 | 0.35 | Ovary | CR 53:3382 |
| 22 | Unknown | 3 | 0 | 0 | Ovary | CR 53:3382 |

Chromosome 17 - q Arm

| | | | | | | |
|---------|---|-----|----|------|-------|--------------|
| 25.3 | Unknown | 8 | 3 | 0.38 | Ovary | CR 53:3382 |
| 25.3 | Unknown | 8 | 4 | 0.5 | Ovary | CR 53:3382 |
| 22 | Unknown | 5 | 4 | 0.8 | Ovary | CR 53:3382 |
| 25.3 | Unknown | 6 | 0 | 0 | Ovary | CR 53:3382 |
| 22 | Unknown | 1 | 0 | 0 | Ovary | CR 53:3382 |
| 23 | Unknown | 3 | 0 | 0 | Ovary | CR 53:3382 |
| 23 | Unknown | 5 | 5 | 1 | Ovary | CR 53:3382 |
| 25.1 | Unknown | 11 | 6 | 0.55 | Ovary | CR 53:3382 |
| 25.1 | Unknown | 10 | 1 | 0.1 | Ovary | CR 53:3382 |
| 23 | Unknown | 2 | 0 | 0 | Ovary | CR 53:3382 |
| 23 | Unknown | 8 | 3 | 0.38 | Ovary | CR 53:3382 |
| Unknown | 46E6-HOX2B-D17S250-588-579 | 18 | 10 | 0.56 | Ovary | BJC 72:1330 |
| Unknown | D17S136 | 6 | 5 | 0.83 | Ovary | IJC 54:220 |
| Unknown | D17S174 | 10 | 8 | 0.8 | Ovary | IJC 54:220 |
| Unknown | D17S180 | 6 | 4 | 0.67 | Ovary | IJC 54:220 |
| Unknown | D17S250-579-588-NM23-GH | 120 | 64 | 0.53 | Ovary | CR 53:1218 |
| 12.0-21 | D17S250-THRA1-D17S846-D17S856-D17S855-D17S183-D17S579-D17S588 | 3 | 2 | 0.67 | Ovary | AJHG 55:666 |
| 12.0-21 | D17S250-THRA1-D17S846-D17S856-D17S855-D17S183-D17S579-D17S588 | 14 | 12 | 0.86 | Ovary | AJHG 55:666 |
| 12.0-21 | D17S250-THRA1-D17S846-D17S856-D17S855-D17S183-D17S579-D17S588 | 11 | 8 | 0.73 | Ovary | AJHG 55:666 |
| 12.0-21 | D17S250-THRA1-D17S846-D17S856-D17S855-D17S183-D17S579-D17S588 | 1 | 1 | 1 | Ovary | AJHG 55:666 |
| Unknown | D17S293 | 11 | 9 | 0.82 | Ovary | IJC 54:220 |
| Unknown | D17S293 | 18 | 14 | 0.78 | Ovary | AJCG 172:908 |
| Unknown | D17S308 | 17 | 14 | 0.82 | Ovary | IJC 54:220 |
| Unknown | D17S587 | 2 | 0 | 0 | Ovary | HG 94:231 |
| 12.0-21 | D17S588 | 11 | 6 | 0.55 | Ovary | BJC 69:429 |
| 12.0-21 | D17S588 | 20 | 14 | 0.7 | Ovary | AJCG 172:908 |
| 12.0-21 | D17S588 | 2 | 0 | 0 | Ovary | HG 94:231 |
| Unknown | D17S73-41-4-77 | 37 | 28 | 0.76 | Ovary | CR 53:2393 |
| 22-23 | NME1-D17S74-GH-D17S40-D17S4-D17S75 | 11 | 11 | 1 | Ovary | AJHG 55:666 |
| 22-23 | NME1-D17S74-GH-D17S40-D17S4-D17S75 | 3 | 3 | 1 | Ovary | AJHG 55:666 |

Chromosome 17 - q Arm

| | | | | | | |
|---------|--|------|------|------|----------|-------------|
| 22-23 | NME1-D17S74-GH- D17S40-D17S4- D17S75 | 1 | 1 | 1 | Ovary | AJHG 55:666 |
| 22-23 | NME1-D17S74-GH- D17S40-D17S4- D17S75 | 14 | 14 | 1 | Ovary | AJHG 55:666 |
| Unknown | D17S1323 | 12 | 3 | 0.25 | Prostate | O 11:1241 |
| Unknown | D17S1327 | 15 | 2 | 0.13 | Prostate | O 11:1241 |
| 12.0-21 | D17S588 | 19 | 2 | 0.11 | Prostate | CR 55:1002 |
| 12.0-21 | D17S588 | 19 | 2 | 0.11 | Prostate | O 11:1241 |
| 21.3 | D17S752 | 14 | 1 | 0.07 | Prostate | GCC 13:278 |
| 21 | D17S776 | 12 | 5 | 0.42 | Prostate | O 11:1241 |
| 21 | D17S846 | 19 | 2 | 0.11 | Prostate | O 11:1241 |
| 21 | D17S855 | 19 | 8 | 0.44 | Prostate | O 11:1241 |
| 21 | D17S855 | 18 | 8 | 0.44 | Prostate | CR 55:1002 |
| 21 | D17S856 | 15 | 5 | 0.33 | Prostate | O 11:1241 |
| 21 | D17S856 | 15 | 6 | 0.4 | Prostate | CR 55:1002 |
| 21 | D17S857 | 20 | 2 | 0.1 | Prostate | O 11:1241 |
| 21 | D17S859 | 18 | 1 | 0.06 | Prostate | O 11:1241 |
| Unknown | KRT9 | 18 | 2 | 0.11 | Prostate | O 11:1241 |
| Unknown | D17S32 | 10 | 1 | 0.1 | Sarcoma | CR 49:6247 |
| Unknown | D17S32 | 14 | 2 | 0.14 | Sarcoma | CR 52:2419 |
| Unknown | D17S293 | 19 | 0 | 0 | Uterus | CR 54:4294 |
| Unknown | PROHIB | 2 | 1 | 0.5 | Uterus | GCC 9:119 |
| SUM | | 9605 | 3006 | 0.31 | | |

Chromosome 18 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|--------|-------|-------------|-----------|------------|--------------|
| 11.2-12.1 | TTR | 19 | 9 | 0.5 | Colon | IJC 53:382 |
| 11.1-11.2 | D18S7 | 5 | 2 | 0.4 | Breast | CR 53:3804 |
| 11.1-11.2 | D18S7 | 7 | 2 | 0.29 | Colon | S 241:961 |
| 11.1-11.2 | D18S7 | 9 | 2 | 0.22 | Stomach | HG 92:244 |
| 11.1-11.2 | D18S7 | 17 | 8 | 0.47 | Stomach | CR 52:3099 |
| Unknown | D18S1 | 7 | 1 | 0.14 | Breast | GCC 2:191 |
| Unknown | D18S1 | 6 | 4 | 0.5 | Colon | IJC 53:382 |
| Unknown | D18S1 | 11 | 0 | 0 | Colon | N 331:273 |
| Unknown | D18S1 | 16 | 4 | 0.25 | Colon | CR 50:7166 |
| Unknown | D18S1 | 1 | 1 | 1 | Lung | PNAS 86:5099 |
| Unknown | D18S1 | 5 | 2 | 0.4 | Lung | PNAS 86:5099 |
| Unknown | D18S1 | 4 | 1 | 0.25 | Lung | PNAS 86:5099 |
| Unknown | D18S1 | 9 | 3 | 0.33 | Ovary | O 7:1059 |
| Unknown | D18S1 | 15 | 7 | 0.47 | Sarcoma | CR 52:2419 |
| Unknown | D18S1 | 6 | 2 | 0.33 | Uterus | CR 51:5632 |
| 11 | D18S6 | 8 | 2 | 0.25 | Bladder | BJC 70:697 |
| 11 | D18S6 | 12 | 2 | 0.17 | Breast | PNAS 87:7737 |
| 11-pter | D18S6 | 24 | 5 | 0.21 | Breast | JNCI 84:506 |
| 11 | D18S6 | 16 | 6 | 0.38 | Cervix | CR 54:4481 |
| 11 | D18S6 | 19 | 9 | 0.47 | Colon | CR 50:7166 |
| 11 | D18S6 | 6 | 0 | 0 | Colon | CCG 48:167 |
| 11 | D18S6 | 17 | 3 | 0.18 | Ovary | IJC 54:546 |
| 11 | D18S6 | 1 | 0 | 0 | Prostate | JU 151:1073 |
| 11 | D18S6 | 15 | 4 | 0.27 | Testis | O 9:2245 |
| 11 | D18S6 | 5 | 1 | 0.2 | Testis | GCC 13:249 |
| Unknown | D18S57 | 33 | 10 | 0.3 | Cervix | CR 56:197 |
| Unknown | D18S22 | 14 | 2 | 0.14 | Brain | CR 50:5784 |
| Unknown | D18S22 | 17 | 3 | 0.18 | Breast | GCC 2:191 |
| Unknown | D18S22 | 29 | 11 | 0.38 | Esophageal | CR 54:2996 |
| Unknown | D18S22 | 11 | 7 | 0.64 | Sarcoma | CR 52:2419 |
| 21.3 | D18S8 | 7 | 3 | 0.43 | Breast | CR 53:3804 |
| 21.3 | D18S8 | 27 | 9 | 0.33 | Colon | S 241:961 |
| 21.3 | D18S8 | 7 | 5 | 0.71 | Stomach | CR 52:3099 |
| 21.3 | D18S8 | 14 | 6 | 0.43 | Stomach | HG 92:244 |
| Unknown | D18S24 | 13 | 1 | 0.08 | Breast | CR 50:7166 |
| Unknown | D18S24 | 6 | 0 | 0 | Cervix | GCC 9:119 |
| Unknown | D18S24 | 4 | 0 | 0 | Kidney | CR 51:820 |
| Unknown | D18S24 | 17 | 4 | 0.24 | Lung | CR 52:2478 |
| Unknown | D18S24 | 8 | 0 | 0 | Ovary | CR 51:5118 |
| Unknown | D18S24 | 3 | 0 | 0 | Uterus | GCC 9:119 |
| 11.2-12.1 | PALB | 18 | 9 | 0.5 | Colon | CR 50:7166 |
| 11.2-12.1 | PALB | 11 | 2 | 0.18 | Colon | GCC 3:468 |
| 11.2-12.1 | PALB | 6 | 0 | 0 | Pancreas | GCC 3:468 |
| 11.2-12.1 | PALB | 8 | 2 | 0.25 | Stomach | GCC 3:468 |
| 11.2-12.1 | PALB | 3 | 0 | 0 | Uterus | CR 51:5632 |
| 21.3 | DCC | 28 | 8 | 0.29 | Bladder | CR 55:5213 |

Chromosome 18 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|------------|---------|-------|-------------|-----------|------------|--------------|
| 11.21-PTER | D18S40 | 25 | 3 | 0.12 | Uterus | CR 54:4294 |
| Unknown | Unknown | 12 | 1 | 0.08 | Brain | CR 50:5784 |
| Unknown | D18S16 | 22 | 0 | 0 | Breast | CR 53:4356 |
| 11.3 | D18S3 | 9 | 1 | 0.11 | Breast | CR 50:7184 |
| Unknown | D18S53 | 31 | 8 | 0.26 | Cervix | CR 56:187 |
| Unknown | D18S59 | 20 | 1 | 0.05 | Endocrine | CR 56:599 |
| Unknown | D18S21 | 20 | 2 | 0.1 | Esophageal | CR 54:2996 |
| Unknown | D18S21 | 15 | 1 | 0.07 | Esophageal | CR 51:2113 |
| Unknown | D18S3 | 18 | 2 | 0.11 | Esophageal | GCC 10:177 |
| 11.21-PTER | D18S40 | 22 | 6 | 0.27 | Head&Neck | CR 54:1152 |
| Unknown | D18S59 | 13 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D18S59 | 18 | 3 | 0.17 | Head&Neck | CR 54:4756 |
| 11.3 | D18S3 | 12 | 0 | 0 | Kidney | CR 51:820 |
| Unknown | D18S59 | 21 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D18S59 | 6 | 1 | 0.17 | Kidney | PNAS 92:2854 |
| Unknown | D18S54 | 19 | 1 | 0.05 | Leukemia | CR 55:5377 |
| 11.3 | D18S3 | 16 | 4 | 0.25 | Lung | CR 52:2478 |
| Unknown | D18S59 | 33 | 4 | 0.12 | Melanoma | CR 56:589 |
| 11.3 | D18S3 | 6 | 0 | 0 | Ovary | CR 51:5118 |
| 11.21-PTER | D18S40 | 15 | 4 | 0.27 | Ovary | BJC 72:1330 |
| Unknown | D18S6 | 10 | 1 | 0.1 | Ovary | CR 53:2393 |
| 11.3 | D18S3 | 15 | 0 | 0 | Prostate | G 11:530 |
| Unknown | D18S21 | 10 | 2 | 0.2 | Sarcoma | CR 52:2419 |
| 11.21-PTER | D18S40 | 25 | 3 | 0.12 | Uterus | CR 54:4294 |
| SUM | | 388 | 45 | 0.12 | | |

Chromosome 18 - q Arm

| | | | | | | |
|-----------|--------|----|----|------|------------|---------------|
| 21.3 | DCC | 15 | 8 | 0.53 | Bladder | BJC 70:697 |
| 21.3 | DCC | 26 | 2 | 0.08 | Breast | CR 53:4356 |
| 21.3 | DCC | 16 | 5 | 0.31 | Breast | BJC 68:64 |
| 21 | DCC | 5 | 1 | 0.2 | Cervix | BJC 67:71 |
| 21.3 | DCC | 12 | 3 | 0.25 | Cervix | BJC 67:71 |
| 21.3 | DCC | 48 | 18 | 0.38 | Colon | EJC 30A:664 |
| 21.3 | DCC | 25 | 13 | 0.52 | Colon | CR 54:3979 |
| 21.3 | DCC | 4 | 1 | 0.25 | Colon | O 9:991 |
| 21.3 | DCC | 41 | 29 | 0.71 | Colon | S 247:49 |
| 21.3 | DCC | 19 | 0 | 0 | Endocrine | GCC 13:9 |
| 21.3 | DCC | 44 | 10 | 0.23 | Esophageal | CR 54:3007 |
| 21.3 | DCC | 50 | 12 | 0.24 | Esophageal | CR 52:6525 |
| 21.3 | DCC | 5 | 1 | 0.2 | Kidney | GCC 12:76 |
| 21.3 | DCC | 19 | 11 | 0.58 | Leukemia | B 83:3449 |
| 21.3 | DCC | 26 | 8 | 0.31 | Leukemia | B 82:927 |
| 21.3 | DCC | 9 | 3 | 0.33 | Leukemia | B 82:927 |
| 21.3 | DCC | 11 | 1 | 0.09 | Liver | CR 51:89 |
| 21.3 | DCC | 6 | 2 | 0.33 | Ovary | BJC 71:462 |
| 21.3 | DCC | 34 | 15 | 0.44 | Ovary | O 7:1059 |
| 21.3 | DCC | 7 | 3 | 0.43 | Ovary | O 7:1059 |
| 21.3 | DCC | 2 | 2 | 1 | Pancreas | CR 54:2761 |
| 21 | DCC | 12 | 2 | 0.17 | Prostate | PNAS 87:8751 |
| 21.3 | DCC | 11 | 5 | 0.45 | Prostate | CR 53:2723 |
| 21.3 | DCC | 13 | 5 | 0.38 | Prostate | GCC 11:119 |
| 21.3 | DCC | 12 | 2 | 0.17 | Prostate | CSurveys 11:1 |
| 21 | DCC | 7 | 5 | 0.71 | Stomach | CR 52:3099 |
| 21.3 | DCC | 18 | 5 | 0.28 | Stomach | L1 74:835 |
| 21.3 | DCC | 10 | 5 | 0.5 | Stomach | CR 52:3099 |
| 21.3 | DCC | 51 | 17 | 0.33 | Uterus | CR 54:4294 |
| 21.3 | DCC | 8 | 1 | 0.12 | Uterus | CR 51:5632 |
| 21.3 | DCC | 5 | 1 | 0.2 | Uterus | CR 51:5633 |
| 21.2-21.3 | D18S35 | 22 | 0 | 0 | Uterus | CR 54:4294 |
| 21.3 | BCL2 | 14 | 1 | 0.07 | Breast | PNAS 87:7737 |
| 21.3 | BCL2 | 10 | 6 | 0.6 | Colon | JJCR 85:584 |
| 21.3 | BCL2 | 20 | 10 | 0.5 | Ovary | O 7:1059 |
| 21.3 | BCL2 | 7 | 2 | 0.29 | Prostate | GCC 11:119 |
| 21.3 | BCL2 | 17 | 4 | 0.24 | Stomach | JJCR 85:584 |
| Unknown | D18S68 | 23 | 8 | 0.35 | Cervix | CR 56:197 |
| Unknown | D18S19 | 22 | 9 | 0.41 | Breast | PNAS 87:7737 |
| Unknown | D18S19 | 8 | 3 | 0.38 | Prostate | GCC 11:119 |
| 21.3-qter | D18S5 | 9 | 4 | 0.44 | Bladder | BJC 70:697 |
| 12 | D18S5 | 17 | 4 | 0.24 | Bladder | CR 51:5405 |
| 21.3-qter | D18S5 | 70 | 11 | 0.16 | Breast | JJCR 84:1159 |
| 12 | D18S5 | 5 | 1 | 0.2 | Breast | GCC 2:191 |
| 21.3-qter | D18S5 | 43 | 6 | 0.14 | Breast | AJP 140:215 |
| 21.3-qter | D18S5 | 16 | 11 | 0.69 | Breast | PNAS 87:7737 |

Chromosome 18 - q Arm

| | | | | | | |
|-----------|-----------------|----|----|------|--------------|--------------|
| 21.3-qter | D18S5 | 21 | 2 | 0.1 | Cervix | CR 54:4481 |
| 12 | D18S5 | 7 | 0 | 0 | Cervix | CR 49:3598 |
| 21.3-qter | D18S5 | 6 | 2 | 0.33 | Colon | O 9:991 |
| 21.3-qter | D18S5 | 21 | 16 | 0.76 | Colon | IJC 53:382 |
| 12 | D18S5 | 19 | 12 | 0.63 | Colon | CR 50:7166 |
| 12 | D18S5 | 29 | 11 | 0.38 | Esophageal | GCC 10:177 |
| 12 | D18S5 | 19 | 1 | 0.05 | Kidney | CR 51:1544 |
| 12 | D18S5 | 18 | 1 | 0.06 | Liver | JJCR 81:108 |
| 12 | D18S5 | 28 | 3 | 0.11 | Lung | PN 84:9252 |
| 12 | D18S5 | 7 | 0 | 0 | Neuroblastom | CR 49:1095 |
| | | | | | a | |
| 21.3-qter | D18S5 | 16 | 4 | 0.25 | Ovary | IJC 54:546 |
| 21.3-qter | D18S5 | 15 | 9 | 0.6 | Ovary | O 7:1059 |
| 21.3-qter | D18S5 | 21 | 12 | 0.57 | Prostate | JO 151:1073 |
| 21.3-qter | D18S5 | 16 | 4 | 0.25 | Prostate | GCC 11:119 |
| 12 | D18S5 | 13 | 0 | 0 | Stomach | CR 48:2988 |
| 21.3-qter | D18S5 | 15 | 10 | 0.67 | Stomach | CR 52:3099 |
| 21.3-qter | D18S5 | 16 | 1 | 0.07 | Testis | GCC 13:249 |
| 12 | D18S5 | 42 | 16 | 0.38 | Testis | O 9:2245 |
| 12 | D18S5 | 9 | 2 | 0.22 | Uterus | CR 51:5632 |
| Unknown | D18S58-D18S61 | 6 | 1 | 0.17 | Kidney | PNAS 92:2854 |
| Unknown | D18S58-D18S61 | 22 | 0 | 0 | Kidney | PNAS 92:2854 |
| 23 | D18S11 | 67 | 17 | 0.25 | Breast | PNAS 87:7737 |
| 23 | D18S11 | 8 | 3 | 0.38 | Colon | GCC 3:468 |
| 23 | D18S11 | 25 | 8 | 0.32 | Ovary | IJC 54:546 |
| 23 | D18S11 | 35 | 21 | 0.6 | Ovary | O 7:1059 |
| 23 | D18S11 | 5 | 0 | 0 | Pancreas | GCC 3:468 |
| 23 | D18S11 | 13 | 2 | 0.15 | Prostate | GCC 11:119 |
| 23 | D18S11 | 13 | 2 | 0.15 | Stomach | GCC 3:468 |
| Unknown | D18S70 | 41 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D18S70 | 43 | 3 | 0.07 | Head&Neck | CR 54:4756 |
| Unknown | D18S70 | 21 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D18S70 | 6 | 1 | 0.17 | Kidney | PNAS 92:2854 |
| Unknown | D18S70 | 23 | 5 | 0.22 | Melanoma | CR 56:589 |
| Unknown | D18S70 | 23 | 5 | 0.22 | Melanoma | CR 56:589 |
| 12.1-21.1 | Unknown | 18 | 4 | 0.22 | Bladder | BJC 70:697 |
| 23 | Unknown | 11 | 4 | 0.36 | Bladder | BJC 70:697 |
| Unknown | D18S22 | 12 | 0 | 0 | Brain | CR 49:6572 |
| Unknown | D18S46 | 17 | 1 | 0.06 | Endocrine | CR 56:599 |
| Unknown | D18S34 | 26 | 6 | 0.23 | Head&Neck | CR 54:1152 |
| Unknown | D18S:58-67 | 23 | 4 | 0.17 | Leukemia | CR 55:5377 |
| Unknown | Unknown | 2 | 0 | 0 | Liver | BJC 67:1007 |
| Unknown | Unknown | 5 | 0 | 0 | Liver | BJC 64:1083 |
| Unknown | GCC-D18S34 | 28 | 12 | 0.43 | Ovary | CR 53:2393 |
| Unknown | MBP- D18S:34-35 | 15 | 6 | 0.4 | Ovary | BJC 72:1330 |
| Unknown | PLANH2 | 7 | 2 | 0.29 | Ovary | O 7:1059 |
| Unknown | Unknown | 6 | 4 | 0.67 | Pancreas | CR 54:2761 |

Chromosome 18 - q Arm

| | | | | | | |
|---------|---------|------|-----|------|----------|-------------|
| Unknown | Unknown | 1 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | Unknown | 6 | 0 | 0 | Pancreas | BJC 65:809 |
| 23 | Unknown | 2 | 2 | 1 | Prostate | GU 151:1073 |
| Unknown | D18S31 | 19 | 2 | 0.11 | Testis | GCC 13:249 |
| Unknown | JOSR4.4 | 20 | 5 | 0.25 | Testis | O 9:2245 |
| SUM | | 2301 | 659 | 0.29 | | |

Chromosome 19 - p Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|---------|-------|-------------|-----------|------------|--------------|
| Unknown | LFPE | 21 | 0 | 0 | Uterus | CR 54:4294 |
| 13.2-CEN | D19S11 | 36 | 2 | 0.06 | Brain | AJP 145:1175 |
| Unknown | D19S20 | 12 | 0 | 0 | Brain | CR 50:5784 |
| Unknown | D19S20 | 35 | 1 | 0.03 | Brain | AJP 145:1175 |
| Unknown | D19S20 | 8 | 0 | 0 | Brain | CR 49:6572 |
| 13.2 | D19S24 | 15 | 0 | 0 | Brain | AJP 145:1175 |
| 12-13.2 | D19S76 | 14 | 0 | 0 | Brain | CR 54:1397 |
| 12-13.2 | D19S76 | 11 | 1 | 0.09 | Brain | CR 54:1397 |
| 13.2-13.1 | LDLR | 3 | 1 | 0.33 | Brain | CR 54:1397 |
| 13.2-13.1 | LDLR | 11 | 0 | 0 | Brain | CR 54:1397 |
| 13.2-CEN | D19S11 | 26 | 7 | 0.27 | Breast | CR 53:4356 |
| Unknown | D19S20 | 36 | 7 | 0.19 | Breast | CR 50:7184 |
| 13.3-.2 | D19S22 | 35 | 1 | 0.03 | Breast | CR 53:4356 |
| 13.2-CEN | D19S11 | 45 | 1 | 0.02 | Cervix | CR 54:4481 |
| 13.3 | D19S177 | 27 | 4 | 0.15 | Cervix | CR 56:197 |
| Unknown | D19S20 | 8 | 0 | 0 | Cervix | GCC 9:119 |
| Unknown | D19S221 | 29 | 7 | 0.24 | Cervix | CR 56:197 |
| Unknown | D19S7 | 26 | 4 | 0.15 | Cervix | CR 54:4481 |
| Unknown | D19S216 | 22 | 1 | 0.05 | Endocrine | CR 56:599 |
| Unknown | D19S20 | 22 | 6 | 0.27 | Esophageal | CR 54:2996 |
| Unknown | D19S20 | 25 | 2 | 0.08 | Esophageal | GCC 10:177 |
| 13.3-.2 | D19S22 | 34 | 11 | 0.32 | Esophageal | GCC 10:177 |
| 13.3 | D19S177 | 16 | 4 | 0.25 | Head&Neck | CR 54:1152 |
| Unknown | D19S216 | 15 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D19S216 | 19 | 1 | 0.05 | Head&Neck | CR 54:4756 |
| Unknown | D19S221 | 19 | 6 | 0.32 | Head&Neck | CR 54:1152 |
| 13.3 | Unknown | 48 | 7 | 0.15 | Kidney | CR 51:5817 |
| Unknown | D19S20 | 40 | 8 | 0.2 | Kidney | CR 51:5817 |
| Unknown | D19S20 | 25 | 8 | 0.32 | Kidney | CR 51:520 |
| 13.3 | D19S21 | 30 | 3 | 0.1 | Kidney | CR 51:5817 |
| Unknown | D19S216 | 3 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D19S216 | 17 | 1 | 0.06 | Kidney | PNAS 92:2854 |
| 13.2-TER | C3 | 3 | 0 | 0 | Liver | CCG 48:72 |
| 13.3-.2 | D19S22 | 28 | 1 | 0.04 | Liver | CR 51:89 |
| Unknown | D19S7 | 11 | 0 | 0 | Liver | JJCR 81:108 |
| Unknown | D19S20 | 26 | 3 | 0.12 | Lung | CR 52:2478 |
| Unknown | D19S7 | 17 | 0 | 0 | Lung | PN 84:9252 |
| Unknown | D19S216 | 25 | 2 | 0.08 | Melanoma | CR 56:589 |
| Unknown | Unknown | 19 | 5 | 0.26 | Ovary | CR 51:5118 |
| 13.2-CEN | D19S11 | 16 | 3 | 0.19 | Ovary | IJC 54:546 |
| 13.2-CEN | D19S11 | 13 | 2 | 0.16 | Ovary | CR 53:2393 |
| 13.3 | D19S177 | 11 | 5 | 0.45 | Ovary | BJC 69:429 |
| Unknown | D19S20 | 13 | 5 | 0.38 | Ovary | GO 55:198 |
| Unknown | D19S20 | 24 | 8 | 0.33 | Ovary | CR 51:5118 |
| 13.3-13.2 | INSR | 21 | 5 | 0.24 | Ovary | IJC 54:546 |
| 13.3-.2 | D19S22 | 6 | 0 | 0 | Pancreas | CR 54:2761 |

Chromosome 19 - p Arm

| | | | | | | |
|-----------|--------|------|-----|------|----------|------------|
| 13.2-CEN | D19S11 | 3 | 0 | 0 | Prostate | G 11:530 |
| Unknown | D19S20 | 21 | 5 | 0.24 | Sarcoma | CR 52:2419 |
| Unknown | D19S7 | 3 | 1 | 0.33 | Sarcoma | CR 52:2419 |
| 13.2-CEN | D19S11 | 46 | 2 | 0.04 | Testis | O 9:2245 |
| Unknown | D19S20 | 20 | 1 | 0.05 | Testis | LT 73:606 |
| Unknown | D19S20 | 20 | 1 | 0.05 | Testis | G 5:134 |
| 13.3-13.2 | INSR | 2 | 0 | 0 | Testis | CCG 52:72 |
| 13.3-13.2 | INSR | 3 | 0 | 0 | Testis | CCG 52:72 |
| 13.3-13.2 | INSR | 1 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D19S20 | 14 | 0 | 0 | Uterus | GCC 9:119 |
| Unknown | LIPE | 21 | 0 | 0 | Uterus | CR 54:4294 |
| SUM | | 1099 | 143 | 0.13 | | |

Chromosome 19 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|---------|-------|-------------|-----------|------------|--------------|
| 13.2 | APOC2 | 11 | 0 | 0 | Uterus | CR 54:4294 |
| 13.2 | APOC2 | 33 | 19 | 0.58 | Brain | AJP 145:1175 |
| 13.2 | APOC2 | 22 | 8 | 0.36 | Brain | CR 54:1397 |
| 13.2 | APOC2 | 15 | 1 | 0.07 | Brain | CR 54:1397 |
| 13.1-13.2 | BC13 | 5 | 4 | 0.8 | Brain | CR 54:1397 |
| 13.1-13.2 | BC13 | 6 | 1 | 0.17 | Brain | CR 54:1397 |
| 13.3 | CKM | 34 | 19 | 0.56 | Brain | AJP 145:1175 |
| 13.2 | CYP2 | 24 | 13 | 0.54 | Brain | AJP 145:1175 |
| 13.2 | D19S178 | 12 | 1 | 0.08 | Brain | CR 54:1397 |
| 13.2 | D19S178 | 18 | 5 | 0.28 | Brain | CR 54:1397 |
| 13.4 | D19S180 | 21 | 9 | 0.43 | Brain | CR 54:1397 |
| 13.4 | D19S180 | 11 | 2 | 0.18 | Brain | CR 54:1397 |
| 13.1 | D19S191 | 23 | 6 | 0.26 | Brain | CR 54:1397 |
| 13.1 | D19S191 | 12 | 2 | 0.17 | Brain | CR 54:1397 |
| 13.4 | D19S22 | 18 | 1 | 0.06 | Brain | CR 50:5784 |
| 13.4 | D19S22 | 37 | 18 | 0.49 | Brain | AJP 145:1175 |
| 12-13.1 | D19S30 | 15 | 7 | 0.47 | Brain | AJP 145:1175 |
| 12-13.1 | D19S31 | 6 | 4 | 0.67 | Brain | AJP 145:1175 |
| 13.1 | D19S32 | 21 | 10 | 0.48 | Brain | AJP 145:1175 |
| 13.1-13.2 | D19S47 | 18 | 4 | 0.22 | Brain | CR 54:1397 |
| 13.1-13.2 | D19S47 | 11 | 2 | 0.18 | Brain | CR 54:1397 |
| 12-13.1 | D19S49 | 22 | 5 | 0.23 | Brain | CR 54:1397 |
| 12-13.1 | D19S49 | 12 | 1 | 0.08 | Brain | CR 54:1397 |
| 13.3 | D19S51 | 12 | 7 | 0.58 | Brain | AJP 145:1175 |
| 13.3 | D19S62 | 12 | 7 | 0.58 | Brain | AJP 145:1175 |
| 13.3 | D19S63 | 24 | 15 | 0.62 | Brain | AJP 145:1175 |
| 12 | D19S7 | 21 | 10 | 0.48 | Brain | AJP 145:1175 |
| 11-CEN | D19S74 | 7 | 4 | 0.57 | Brain | AJP 145:1175 |
| 12-13.1 | D19S75 | 11 | 1 | 0.09 | Brain | CR 54:1397 |
| 12-13.1 | D19S75 | 19 | 3 | 0.16 | Brain | CR 54:1397 |
| 13.2 | D19S8 | 21 | 14 | 0.67 | Brain | AJP 145:1175 |
| Unknown | D19S9 | 6 | 2 | 0.33 | Brain | AJP 145:1175 |
| 13.3 | ERCC1 | 32 | 18 | 0.56 | Brain | AJP 145:1175 |
| 13.3 | ERCC2 | 16 | 7 | 0.44 | Brain | AJP 145:1175 |
| 13.2 | APOC2 | 25 | 2 | 0.08 | Breast | GCC 2:191 |
| 13.4 | D19S22 | 19 | 3 | 0.16 | Breast | CR 50:7184 |
| 13.2 | APOC2 | 29 | 3 | 0.1 | Cervix | CR 56:197 |
| Unknown | D19S223 | 24 | 3 | 0.12 | Cervix | CR 56:197 |
| Unknown | D19S9 | 1 | 0 | 0 | Cervix | CR 49:3598 |
| 13.2 | APOC2 | 17 | 1 | 0.06 | Colon | CCG 48:167 |
| 12 | D19S7 | 21 | 16 | 0.76 | Colon | IJC 53:382 |
| Unknown | D19S210 | 18 | 1 | 0.06 | Endocrine | CR 56:599 |
| 13.4 | D19S22 | 23 | 7 | 0.3 | Esophageal | CR 54:2996 |
| Unknown | D19S210 | 22 | 7 | 0.32 | Head&Neck | CR 54:1152 |
| Unknown | D19S255 | 10 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D19S255 | 10 | 0 | 0 | Head&Neck | CR 54:4756 |

Chromosome 19 - q Arm

| | | | | | | |
|---------|-----------------|------|-----|------|-------------------|--------------|
| Unknown | D19S210-D19S224 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D19S210-D19S224 | 19 | 0 | 0 | Kidney | PNAS 92:2854 |
| 13.4 | D19S22 | 14 | 3 | 0.21 | Kidney | CR 51:820 |
| Unknown | D19S225 | 3 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D19S225 | 17 | 1 | 0.06 | Kidney | PNAS 92:2854 |
| 13.4 | D19S22 | 24 | 11 | 0.46 | Lung | CR 52:2478 |
| 13.4 | D19S22 | 3 | 2 | 0.67 | Lung | CR 52:2478 |
| 13.4 | D19S22 | 1 | 1 | 1 | Lung | CR 52:2478 |
| 13.4 | D19S22 | 9 | 9 | 1 | Lung | CR 52:2478 |
| Unknown | D19S225 | 22 | 0 | 0 | Melanoma | CR 56:589 |
| 12 | D19S7 | 3 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| Unknown | CYP1 | 7 | 1 | 0.14 | Ovary | CR 50:2724 |
| 13.4 | D19S22 | 16 | 4 | 0.25 | Ovary | CR 51:5378 |
| 12-13.1 | D19S49 | 13 | 3 | 0.23 | Ovary | BJC 69:429 |
| 13.2 | D19S8 | 23 | 5 | 0.22 | Ovary | IdC 54:546 |
| Unknown | D19S8-CYP2A | 23 | 4 | 0.17 | Ovary | CR 53:2393 |
| 13.2 | D19S8 | 12 | 0 | 0 | Prostate | G 11:530 |
| 13.4 | D19S22 | 9 | 3 | 0.33 | Sarcoma | CR 52:2419 |
| 12 | D19S7 | 16 | 1 | 0.06 | Stomach | CR 48:2988 |
| 12 | D19S7 | 19 | 2 | 0.11 | Testis | O 9:2245 |
| 13.2 | APOC2 | 11 | 0 | 0 | Uterus | CR 54:4294 |
| SUM | | 1066 | 323 | 0.3 | | |

Chromosome 20 - p Arm

| Band | Marker | Total | Cases with LOH | LOH Frequency | Tumor Type | Reference |
|---------|---------|-------|----------------|---------------|-------------------|--------------|
| 12 | D20S6 | 4 | 1 | 0.25 | Uterus | CR 51:5632 |
| Unknown | Unknown | 12 | 1 | 0.08 | Brain | CR 50:5784 |
| 12 | D20S6 | 8 | 0 | 0 | Brain | CR 49:6572 |
| Unknown | D20S19 | 6 | 0 | 0 | Breast | CR 53:3804 |
| Unknown | D20S19 | 37 | 2 | 0.05 | Breast | CR 50:7184 |
| 12 | D20S6 | 20 | 3 | 0.15 | Breast | GCC 2:191 |
| Unknown | D20S118 | 31 | 0 | 0 | Cervix | CR 56:197 |
| Unknown | D20S19 | 3 | 0 | 0 | Cervix | GCC 9:119 |
| 12 | D20S6 | 2 | 0 | 0 | Cervix | CR 49:3598 |
| 12 | D20S6 | 28 | 6 | 0.21 | Cervix | CR 54:4481 |
| Unknown | D20S98 | 16 | 2 | 0.12 | Cervix | CR 56:197 |
| Unknown | D20S95 | 16 | 0 | 0 | Endocrine | CR 56:599 |
| Unknown | D20S19 | 59 | 7 | 0.12 | Esophageal | GCC 10:177 |
| Unknown | D20S72 | 20 | 2 | 0.1 | Esophageal | CR 54:2996 |
| Unknown | D20S104 | 12 | 0 | 0 | Head&Neck | CR 54:4756 |
| Unknown | D20S104 | 23 | 2 | 0.09 | Head&Neck | CR 54:4756 |
| Unknown | D20S95 | 20 | 6 | 0.3 | Head&Neck | CR 54:1152 |
| Unknown | D20S104 | 17 | 1 | 0.06 | Kidney | PNAS 92:2854 |
| Unknown | D20S104 | 3 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D20S117 | 5 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D20S117 | 21 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D20S19 | 29 | 1 | 0.03 | Kidney | CR 51:820 |
| Unknown | D20S19 | 39 | 0 | 0 | Liver | CR 51:89 |
| Unknown | D20S19 | 40 | 6 | 0.2 | Lung | CR 52:2478 |
| Unknown | D20S104 | 23 | 2 | 0.09 | Melanoma | CR 56:589 |
| 12 | D20S6 | 2 | 0 | 0 | Neuroblastom a | CR 49:1095 |
| Unknown | Unknown | 16 | 0 | 0 | Ovary | CR 53:2393 |
| Unknown | D20S19 | 32 | 4 | 0.12 | Ovary | CR 51:5118 |
| 12 | D20S27 | 14 | 3 | 0.21 | Ovary | BJC 69:429 |
| 12 | D20S6 | 27 | 4 | 0.15 | Ovary | IJC 54:546 |
| Unknown | D20S19 | 5 | 0 | 0 | Pancreas | CR 54:2761 |
| 12 | D20S5 | 2 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | D20S5 | 6 | 0 | 0 | Prostate | G 11:530 |
| Unknown | D20S19 | 8 | 2 | 0.25 | Sarcoma | CR 52:2419 |
| 12 | D20S5 | 13 | 4 | 0.31 | Sarcoma | CR 52:2419 |
| Unknown | D20S19 | 15 | 3 | 0.2 | Stomach | CR 52:3099 |
| 12 | D20S6 | 22 | 9 | 0.41 | Testis | O 9:2245 |
| Unknown | D20S19 | 2 | 0 | 0 | Uterus | GCC 9:119 |
| 12 | D20S27 | 26 | 0 | 0 | Uterus | CR 54:4294 |
| 12 | D20S6 | 4 | 1 | 0.25 | Uterus | CR 51:5632 |
| 90M | | 684 | 73 | 0.11 | | |

Chromosome 20 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|---------|---------|-------|-------------|-----------|------------|--------------|
| 13.3 | CSPT1 | 20 | 1 | 0.05 | Uterus | CR 54:4294 |
| Unknown | Unknown | 20 | 0 | 0 | Brain | CR 50:5784 |
| 13.2 | D20S4 | 15 | 2 | 0.13 | Breast | GCC 2:191 |
| Unknown | D20S119 | 26 | 3 | 0.12 | Cervix | CR 56:197 |
| 13.2 | D20S4 | 23 | 2 | 0.09 | Cervix | CR 54:4481 |
| Unknown | D20S25 | 25 | 0 | 0 | Endocrine | CR 56:599 |
| Unknown | D20S19 | 19 | 3 | 0.16 | Esophageal | CR 54:2996 |
| Unknown | D20S100 | 18 | 1 | 0.06 | Head&Neck | CR 54:4756 |
| Unknown | D20S100 | 21 | 2 | 0.1 | Head&Neck | CR 54:4756 |
| Unknown | D20S110 | 16 | 1 | 0.06 | Head&Neck | CR 54:1152 |
| Unknown | D20S119 | 11 | 1 | 0.09 | Head&Neck | CR 54:1152 |
| Unknown | D20S100 | 16 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D20S100 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | Unknown | 5 | 1 | 0.2 | Liver | BJC 64:1083 |
| 13.2 | D20S4 | 15 | 0 | 0 | Liver | JJCR 81:108 |
| 13.2 | D20S4 | 4 | 0 | 0 | Liver | CCG 48:72 |
| 13.2 | D20S4 | 10 | 1 | 0.1 | Lung | PN 84:9252 |
| 13.2 | D20S4 | 10 | 4 | 0.4 | Lung | PN 86:5099 |
| 13.2 | D20S4 | 2 | 2 | 1 | Lung | PN 86:5099 |
| 13.2 | D20S4 | 6 | 2 | 0.33 | Lung | PN 86:5099 |
| Unknown | D20S100 | 30 | 0 | 0 | Melanoma | CR 56:589 |
| Unknown | D20S19 | 33 | 0 | 0 | Ovary | IJC 54:546 |
| 13.2 | D20S4 | 19 | 3 | 0.16 | Ovary | CR 53:2393 |
| Unknown | D20S46 | 14 | 3 | 0.21 | Ovary | BJC 69:429 |
| Unknown | D20S54 | 14 | 1 | 0.07 | Ovary | BJC 69:429 |
| 13.2 | D20S4 | 8 | 0 | 0 | Prostate | G 11:530 |
| 13.2 | D20S4 | 11 | 0 | 0 | Stomach | CR 48:2988 |
| Unknown | D20S19 | 31 | 0 | 0 | Testis | O 9:2245 |
| Unknown | D20S26 | 25 | 1 | 0.04 | Testis | GCC 13:249 |
| 13.2 | D20S4 | 36 | 4 | 0.11 | Testis | O 9:2245 |
| 13.3 | CSPT1 | 20 | 1 | 0.05 | Uterus | CR 54:4294 |
| SUM | | 509 | 38 | 0.07 | | |

Chromosome 21 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Refer |
|-----------|-------------------------|-------|-------------|-----------|------------|-------|
| 11.1 | D21S52 | 13 | 1 | 0.08 | Uterus | CR 51 |
| Unknown | Unknown | 14 | 0 | 0 | Brain | CR 50 |
| 22.3 | D21S113 | 5 | 0 | 0 | Brain | CR 49 |
| Unknown | BCEI | 15 | 2 | 0.13 | Breast | CR 53 |
| Unknown | D21S1 | 21 | 1 | 0.05 | Breast | GCC 2 |
| Unknown | D21S112 | 29 | 4 | 0.14 | Breast | CR 53 |
| 22.3 | D21S113 | 26 | 4 | 0.15 | Breast | CR 50 |
| 22.3 | D21S113 | 3 | 0 | 0 | Cervix | GCC 9 |
| 22.3 | D21S113 | 19 | 2 | 0.11 | Cervix | CR 54 |
| Unknown | D21S212 | 26 | 2 | 0.08 | Cervix | CR 56 |
| Unknown | D21S265 | 23 | 0 | 0 | Cervix | CR 56 |
| Unknown | D21S267 | 14 | 1 | 0.07 | Cervix | CR 56 |
| Unknown | D21S11 | 15 | 0 | 0 | Colon | GCC 4 |
| Unknown | D21S156 | 16 | 0 | 0 | Endocrine | CR 56 |
| 22.3 | D21S113 | 9 | 2 | 0.22 | Esophageal | CR 51 |
| 22.3 | D21S113 | 30 | 11 | 0.37 | Esophageal | GCC 1 |
| 22.3 | D21S113 | 20 | 5 | 0.25 | Esophageal | CR 54 |
| Unknown | D21S262 | 18 | 0 | 0 | Head&Neck | CR 54 |
| Unknown | D21S262 | 17 | 3 | 0.18 | Head&Neck | CR 54 |
| Unknown | D21S59 | 19 | 5 | 0.26 | Head&Neck | CR 54 |
| 22.3 | D21S113 | 19 | 3 | 0.16 | Kidney | CR 51 |
| Unknown | D21S262 | 6 | 0 | 0 | Kidney | PNAS |
| Unknown | D21S262 | 16 | 0 | 0 | Kidney | PNAS |
| Unknown | D21S267-D21S265-D21S263 | 19 | 1 | 0.05 | Kidney | PNAS |
| Unknown | D21S267-D21S265-D21S263 | 6 | 2 | 0.33 | Kidney | PNAS |
| 22.3 | D21S113 | 15 | 1 | 0.07 | Liver | CR 51 |
| 21.2-TER | D21S19 | 14 | 0 | 0 | Liver | CGC |
| 11.1 | D21S52 | 4 | 1 | 0.25 | Liver | JJCR |
| 22.3 | D21S113 | 28 | 5 | 0.18 | Lung | CR 52 |
| Unknown | D21S262 | 23 | 1 | 0.04 | Melanoma | CR 56 |
| 22.3 | D21S113 | 6 | 0 | 0 | Ovary | O 5:2 |
| 22.3 | D21S113 | 12 | 0 | 0 | Ovary | CR 51 |
| 22.3 | D21S113 | 25 | 2 | 0.08 | Ovary | IJC 5 |
| Unknown | D21S113-11 | 28 | 10 | 0.36 | Ovary | CR 53 |
| 11.2 | D21S120 | 12 | 4 | 0.33 | Ovary | BJC 6 |
| 22.3 | D21S167 | 13 | 7 | 0.54 | Ovary | BJC 6 |
| 22.3-QTER | D21S171 | 13 | 3 | 0.23 | Ovary | BJC 6 |
| 22.3 | D21S113 | 3 | 0 | 0 | Pancreas | CR 54 |
| Unknown | D21S9-D21S17 | 10 | 0 | 0 | Prostate | G 11 |
| Unknown | Unknown | 6 | 2 | 0.33 | Sarcoma | CGC 5 |
| 22.3 | D21S113 | 15 | 1 | 0.07 | Sarcoma | CR 52 |
| 22.3 | D21S113 | 21 | 3 | 0.14 | Testis | O 9:2 |
| 22.3 | D21S113 | 6 | 1 | 0.17 | Uterus | GCC 9 |
| 22.3 | D21S167 | 20 | 0 | 0 | Uterus | CR 54 |
| 11.1 | D21S52 | 13 | 1 | 0.08 | Uterus | CR 51 |

Chromosome 21 - q Arm

| | | | |
|-----|-----|----|------|
| SUM | 692 | 90 | 0.13 |
|-----|-----|----|------|

Chromosome 22 - q Arm

| Band | Marker | Total | Cases w/LOH | LOH Freq. | Tumor Type | Reference |
|-----------|----------|-------|-------------|-----------|------------|-------------|
| 11.2-13.1 | TOPIP2 | 15 | 1 | 0.07 | Uterus | CR 54:4294 |
| Unknown | BCR | 2 | 0 | 0 | Brain | CGC 53:271 |
| Unknown | CRYB | 7 | 1 | 0.14 | Brain | CR 50:6783 |
| Unknown | CYP2D | 6 | 4 | 0.67 | Brain | CR 53:2386 |
| Unknown | CYP2D | 6 | 6 | 1 | Brain | CR 53:2386 |
| 11.2-12 | D22S1 | 4 | 0 | 0 | Brain | CR 50:6783 |
| 11.2-12 | D22S1 | 7 | 2 | 0.29 | Brain | CGC 53:271 |
| 11.1-11.2 | D22S10 | 5 | 1 | 0.2 | Brain | CGC 53:271 |
| Unknown | D22S156 | 4 | 2 | 0.5 | Brain | CR 53:2386 |
| Unknown | D22S156 | 4 | 1 | 0.25 | Brain | CR 53:2386 |
| 13.3 | D22S171 | 2 | 0 | 0 | Brain | CGC 66:117 |
| 11.2 | D22S20 | 2 | 0 | 0 | Brain | CGC 66:117 |
| Unknown | D22S23 | 8 | 3 | 0.38 | Brain | CR 50:6783 |
| Unknown | D22S24 | 1 | 0 | 0 | Brain | CR 50:6783 |
| Unknown | D22S258 | 18 | 2 | 0.11 | Brain | CR 54:1397 |
| Unknown | D22S258 | 16 | 1 | 0.06 | Brain | CR 54:1397 |
| Unknown | D22S28 | 4 | 3 | 0.75 | Brain | CR 50:6783 |
| Unknown | D22S29 | 3 | 2 | 0.67 | Brain | CR 50:6783 |
| Unknown | D22S32 | 2 | 0 | 0 | Brain | CGC 66:117 |
| Unknown | D22S32 | 14 | 1 | 0.07 | Brain | CR 49:6572 |
| Unknown | D22S32 | 14 | 1 | 0.07 | Brain | CR 50:5784 |
| 13.1 | D22S80 | 4 | 0 | 0 | Brain | CGC 66:117 |
| Unknown | D22S9 | 8 | 2 | 0.25 | Brain | CGC 53:271 |
| Unknown | D22S9 | 1 | 0 | 0 | Brain | CGC 66:117 |
| Unknown | IGLV | 2 | 0 | 0 | Brain | CGC 66:117 |
| Unknown | IGLV | 1 | 0 | 0 | Brain | CR 50:6783 |
| 13 | IL2RB | 18 | 4 | 0.22 | Brain | CR 54:1397 |
| 13 | IL2RB | 15 | 0 | 0 | Brain | CR 54:1397 |
| 11.1-11.2 | LAMBDA1C | 4 | 1 | 0.25 | Brain | CGC 53:271 |
| 12.3 | MB | 5 | 0 | 0 | Brain | CGC 66:117 |
| 12.3 | MB | 1 | 1 | 1 | Brain | CGC 53:271 |
| 12.3-13.1 | PDGFB | 1 | 1 | 1 | Brain | CGC 53:271 |
| 11 | Unknown | 26 | 10 | 0.38 | Breast | JNCI 84:506 |
| Unknown | D22S10 | 16 | 4 | 0.25 | Breast | GCC 2:191 |
| Unknown | D22S113 | 9 | 1 | 0.11 | Breast | CR 50:7184 |
| Unknown | D22S9 | 24 | 4 | 0.17 | Breast | GCC 2:191 |
| 12.3 | MB | 42 | 8 | 0.19 | Breast | CR 53:4356 |
| 11.1-11.2 | D22S10 | 27 | 2 | 0.07 | Cervix | CR 54:4481 |
| Unknown | D22S113 | 8 | 1 | 0.12 | Cervix | GCC 9:119 |
| Unknown | D22S280 | 20 | 3 | 0.15 | Cervix | CR 56:197 |
| Unknown | D22S284 | 30 | 4 | 0.13 | Cervix | CR 56:197 |
| 11.2-12 | D22S1 | 11 | 1 | 0.09 | Colon | N 331:273 |
| 11.2-12 | D22S1 | 12 | 4 | 0.33 | Colon | IJC 53:382 |
| 11.1-11.2 | D22S10 | 12 | 0 | 0 | Colon | S 241:961 |
| 11.1-11.2 | D22S10 | 13 | 7 | 0.54 | Colon | IJC 53:382 |
| Unknown | D22S10 | 29 | 11 | 0.38 | Colon | CR 50:7166 |

Chromosome 22 - q Arm

| | | | | | | |
|-----------|---------------------------------|----|----|------|------------|--------------|
| Unknown | D22S9 | 20 | 10 | 0.5 | Colon | CR 50:7166 |
| Unknown | D22S9 | 3 | 1 | 0.33 | Colon | O 9:991 |
| Unknown | D22S9 | 17 | 3 | 0.18 | Colon | N 331:273 |
| Unknown | IGLC | 30 | 15 | 0.5 | Colon | CR 50:7166 |
| Unknown | IGLC | 17 | 3 | 0.18 | Colon | N 331:273 |
| Unknown | IGLC | 10 | 0 | 0 | Colon | S 241:961 |
| Unknown | IGLV | 4 | 0 | 0 | Colon | S 241:961 |
| Unknown | IGLV | 27 | 9 | 0.33 | Colon | CR 50:7166 |
| Unknown | IGLV | 30 | 6 | 0.2 | Colon | N 331:273 |
| 12.3-13.1 | PDGFB | 10 | 0 | 0 | Colon | S 241:961 |
| Unknown | SIS | 4 | 1 | 0.25 | Colon | N 331:273 |
| Unknown | D22S264 | 16 | 0 | 0 | Endocrine | GCC 13:9 |
| Unknown | D22S351 | 14 | 1 | 0.05 | Endocrine | CR 56:599 |
| 11.2-12 | D22S1 | 21 | 2 | 0.1 | Esophageal | CR 54:2996 |
| Unknown | D22S32 | 13 | 1 | 0.08 | Esophageal | GCC 10:777 |
| Unknown | D22S79 | 18 | 3 | 0.17 | Esophageal | CR 51:2113 |
| Unknown | D22S283 | 25 | 2 | 0.08 | Head&Neck | CR 54:4756 |
| Unknown | D22S283 | 22 | 2 | 0.09 | Head&Neck | CR 54:4756 |
| 13 | IL2RB | 24 | 7 | 0.29 | Head&Neck | CR 54:1152 |
| Unknown | D22S113 | 10 | 2 | 0.2 | Kidney | CR 51:820 |
| 12 | D22S268 | 39 | 1 | 0.03 | Kidney | BJC 69:230 |
| Unknown | D22S280-D22S282 | 22 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D22S280-D22S282 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D22S283 | 6 | 0 | 0 | Kidney | PNAS 92:2854 |
| Unknown | D22S283 | 16 | 0 | 0 | Kidney | PNAS 92:2854 |
| 11.2-12 | D22S1 | 10 | 0 | 0 | Liver | JJCR 81:108 |
| Unknown | D22S113 | 4 | 0 | 0 | Liver | CR 51:89 |
| Unknown | IGLC | 28 | 9 | 0.32 | Liver | JJCR 84:893 |
| Unknown | IGLC | 7 | 0 | 0 | Liver | CCG 48:72 |
| 11.2-12 | D22S1 | 7 | 2 | 0.29 | Lung | CR 54:5643 |
| 11.2-12 | D22S1 | 22 | 11 | 0.5 | Lung | CR 54:5643 |
| 11.2-12 | D22S1 | 3 | 2 | 0.67 | Lung | CR 54:5643 |
| Unknown | D22S113 | 16 | 3 | 0.19 | Lung | CR 52:2478 |
| Unknown | D22S283 | 35 | 2 | 0.06 | Melanoma | CR 56:589 |
| 11.1-11.2 | D22S10 | 13 | 3 | 0.23 | Ovary | IJC 54:546 |
| Unknown | D22S113 | 10 | 2 | 0.2 | Ovary | CR 51:5118 |
| Unknown | D22S156 | 10 | 3 | 0.3 | Ovary | BJC 69:429 |
| Unknown | D22S430-D22S282-D22S283-D22S274 | 32 | 23 | 0.72 | Ovary | BJC 70:905 |
| Unknown | D22S9 | 14 | 10 | 0.71 | Ovary | CR 53:2393 |
| Unknown | IL-2RB-CYP2D-D22S156 | 14 | 4 | 0.29 | Ovary | BJC 72:1330 |
| 12.3-13.1 | PDGFB | 5 | 1 | 0.2 | Ovary | CR 50:2724 |
| Unknown | SIS | 6 | 0 | 0 | Ovary | CR 49:1220 |
| 11.2-13.1 | TOPIP2 | 12 | 5 | 0.42 | Ovary | BJC 69:429 |
| Unknown | D22S113 | 4 | 0 | 0 | Pancreas | CR 54:2761 |
| Unknown | D22S156 | 26 | 20 | 0.77 | Pediatric | GCC 15:10 |

Chromosome 22 - q Arm

| | | | | | | |
|-----------|---------|------|-----|------|-----------|------------|
| Unknown | D22S257 | 20 | 10 | 0.5 | Pediatric | GCC 15:10 |
| Unknown | D22S258 | 23 | 18 | 0.78 | Pediatric | GCC 15:10 |
| Unknown | D22S264 | 26 | 9 | 0.35 | Pediatric | GCC 15:10 |
| Unknown | D22S273 | 21 | 14 | 0.67 | Pediatric | GCC 15:10 |
| Unknown | D22S273 | 26 | 16 | 0.62 | Pediatric | GCC 15:10 |
| Unknown | D22S274 | 14 | 10 | 0.71 | Pediatric | GCC 15:10 |
| Unknown | D22S275 | 17 | 13 | 0.76 | Pediatric | GCC 15:10 |
| Unknown | D22S280 | 25 | 17 | 0.68 | Pediatric | GCC 15:10 |
| Unknown | D22S281 | 20 | 12 | 0.6 | Pediatric | GCC 15:10 |
| Unknown | D22S283 | 29 | 18 | 0.62 | Pediatric | GCC 15:10 |
| Unknown | D22S301 | 20 | 14 | 0.7 | Pediatric | GCC 15:10 |
| Unknown | D22S303 | 21 | 12 | 0.57 | Pediatric | GCC 15:10 |
| Unknown | D22S315 | 26 | 18 | 0.69 | Pediatric | GCC 15:10 |
| Unknown | IGLV | 10 | 0 | 0 | Pediatric | CR 50:3279 |
| 12.3-13.1 | PDGFB | 7 | 1 | 0.14 | Prostate | G 11:530 |
| 11.2-12 | D22S1 | 21 | 8 | 0.38 | Sarcoma | CR 32:2419 |
| Unknown | D22S9 | 6 | 2 | 0.33 | Sarcoma | CGC 53:45 |
| 11.2-12 | D22S1 | 17 | 0 | 0 | Stomach | CR 48:2988 |
| Unknown | IGLC | 7 | 2 | 0.29 | Stomach | CR 52:3099 |
| 11.1-11.2 | D22S10 | 26 | 6 | 0.23 | Testis | O 9:2245 |
| 12.3-13.1 | PDGFB | 3 | 0 | 0 | Testis | CCG 52:72 |
| 12.3-13.1 | PDGFB | 2 | 0 | 0 | Testis | CCG 52:72 |
| 12.3-13.1 | PDGFB | 1 | 0 | 0 | Testis | CCG 52:72 |
| Unknown | D22S113 | 16 | 3 | 0.19 | Uterus | GCC 9:119 |
| 11.2-13.1 | TOPIP2 | 15 | 1 | 0.07 | Uterus | CR 54:4294 |
| SUM | | 1594 | 472 | 0.3 | | |

| Chromosome | Arm | LOH Freq. |
|------------|-----|-----------|
| 1 | p | 0.26 |
| 1 | q | 0.15 |
| 2 | p | 0.15 |
| 2 | q | 0.12 |
| 3 | p | 0.41 |
| 3 | q | 0.18 |
| 4 | p | 0.13 |
| 4 | q | 0.22 |
| 5 | p | 0.19 |
| 5 | q | 0.27 |
| 6 | p | 0.24 |
| 6 | q | 0.25 |
| 7 | p | 0.12 |
| 7 | q | 0.22 |
| 8 | p | 0.33 |
| 8 | q | 0.14 |
| 9 | p | 0.38 |
| 9 | q | 0.47 |
| 10 | p | 0.18 |
| 10 | q | 0.23 |
| 11 | p | 0.23 |
| 11 | q | 0.26 |
| 12 | p | 0.15 |
| 12 | q | 0.13 |
| 13 | q | 0.29 |
| 14 | p | 0.08 |
| 14 | q | 0.22 |
| 15 | p | 0.11 |
| 15 | q | 0.17 |
| 16 | p | 0.17 |
| 16 | q | 0.36 |
| 17 | p | 0.44 |
| 17 | q | 0.31 |
| 18 | p | 0.12 |
| 18 | q | 0.29 |
| 19 | p | 0.13 |
| 19 | q | 0.3 |
| 20 | p | 0.11 |
| 20 | q | 0.07 |
| 21 | q | 0.13 |
| 22 | q | 0.3 |

Fig. 5
1) Cyclins

Validation: Deletion of CDC23 (Anaphase Promoting), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---------------------------------|-------------------------|------------|---------------------|
| 9 | CDC-25A | | 1 | 3p21 |
| 10 | CDC-25C | | 1 | 5q31 |
| 524 | Wee1 | | 3 | 1p15.3-p15.1 |
| 1043 | CDC16Hs | | 2 | 13 |
| 1278 | Cyclin D1 | | 4 | 11q13 |
| 1280 | Cyclin D3 | | 2 | 6p21 |
| 1298 | Cyclin H Assembly Factor | | 1 | 4 |
| 1445 | Cyclin-Dependent Protein Kinase | | 2 | 12 |
| 1450 | RAN binding protein 1 | | 1 | 22 |
| 1523 | 14-3-3 PROTEIN TAU | | 1 | 10 |

1) Cyclin dependent kinases/phosphatases

Validation: Deletion of CDC28 (Cyclin Dependent Protein Kinase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1051 | CDC28 protein kinase 1 | | 2 | 17 |
| 1052 | CDC28 protein kinase 2 | | 1 | 9 |
| 1111 | Protein phosphatase 1, catalytic subunit, alpha isoform | | 4 | 11 |
| 1388 | M-PHASE INDUCER PHOSPHATASE 2 | | 1 | 20 |
| 1401 | M-phase phosphoprotein, mpp6 | | 5 | 7 |

1) Cell Division Structural Proteins

Validation: Deletion of CBF2 (Kinetochore Protein), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 20 | MCM7 (Minichromosome Maintenance) | | 3 | 7q21.3-q22.1 |
| 1246 | Chromatin assembly factor-I p60 subunit | | 2 | 21 |
| 1273 | Chromosome segregation gene homolog CAS | | 1 | 20 |
| 1347 | High-mobility group (nonhistone chromosomal) protein 1 | | 5 | 13q12 |
| 1487 | Chromatin structural protein homolog (SUPT5H) | | 3 | 7 |
| 1607 | Centromere protein B (80kD) | | 1 | 20p13 |

2) Uniporters

Validation: Deletion of SAT2(Osmotolerance), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|----------------------|
| 1253 | ATPase, Ca++ transporting, plasma membrane 2 | | 5 | 3p26-p25 X63575 |
| 1255 | ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide | | 4 | 12p13-qter X03559 |
| 1286 | Putative Chloride Channel | | 1 | 13q14.3-q21.1 X83378 |
| 1337 | Copper Transport Protein HAH1 | | 1 | 5 U70660 |
| 1407 | Nuclear chloride ion channel protein (NCC27) | | 4 | 20 U93205 |
| 1463 | Sodium channel, voltage-gated, type I, beta polypeptide | | 1 | 19q13.1 L16242 |
| 1505 | Transient receptor potential channel 1 | | 1 | 3 X89066 |
| 1521 | Voltage-dependent anion channel 2 | | 4 | L06328 |

2) Antiporters

Validation: Proven essential in mammalian cells by tritium suicide selection experiments.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1471 | Solute carrier family 9 (sodium/hydrogen exchanger) | | 1 | 1p36.1-p35 M81768 |
| 1250 | ATPase, Na+/K+ transporting, beta 1 polypeptide | | 1 | 1q22-q25 X03747 |
| 1251 | ATPase, Na+/K+ transporting, beta 2 polypeptide | | 2 | 17p M81181 |
| 1605 | Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1) | | 2 | 7q35-q36 U62531 |

3) Acyltransferase

Validation: Essential for metabolic processes such as biosynthetic reactions and energy metabolism. The *S. cerevisiae* histone acetyltransferase PAT1 and the N-alpha acetyltransferase which acetylates the N-termini of proteins are essential for growth.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1227 | Acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase) | | 2 | 3p23-p22 X12966 |
| 1387 | Lysophosphatidic acid acyltransferase-alpha | | 7 | 6 U56417 |

3) Amino Acid Biogenesis

Validation: Deletion of PRO1(Glutamate 5-Kinase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1330 | Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) | | 1 | 10q24.1-q25.1 |
| 1331 | Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) | | 2 | 16q21 |
| 1447 | Pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase) | | 1 | 10q24.3 |
| | | | | X94453 |

3) Amino Acid Transport

Validation: There are ten essential amino acids in man, which must be transported across the plasma membrane for use in protein synthesis.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1581 | Solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1 | | 2 | 2p16.3 |
| | | | | L11696 |

3) Addition, removal, or modification of phosphate groups

Validation: Deletion of CMD1(Calmodulin), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1269 | Calcineurin A catalytic subunit | | 2 | 8 |
| 1270 | Calcineurin B | | 1 | 10q21-q22 |
| 1351 | CALRETICULIN PRECURSOR | | 1 | 10q21-q22 |
| 1432 | SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, BETA ISOFORM | | 2 | 10 |
| 1476 | Snk interacting protein 2-28 | | 1 | |
| | | | | U83236 |

3) GDP Dissociation Inhibitors

Validation: Deletion of GDI1(GDP dissociation Factor), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--------------------------------------|-------------------------|------------|---------------------|
| 1448 | RAB GDP DISSOCIATION INHIBITOR ALPHA | | 2 | 14q23-q24 |
| | | | | D13988 |

3) Lactate Transport

Validation: Genes required to maintain organic compounds at levels required for cell growth or survival.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|----------------------|
| 1583 | Solute carrier family 16 (monocarboxylic acid transporters), member 1 | | 2 | 1p13.2-p12 L31801 |

3) Polyamine Biosynthesis

Validation: Inhibition of polyamine biosynthesis has antiproliferative effects as demonstrated by inhibitors of polyamine metabolism.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---------------------------|-------------------------|------------|---------------------|
| 1587 | Ornithine decarboxylase 1 | | 2 | 2p25 M16650 |

3) Protein Glycosylation

Validation: Deletion of DPM1(Dolichol-phosphate mannosyltransferase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1328 | Glutamine-fructose-6-phosphate transaminase | | 1 | 2p13 M90516 |
| 1339 | Heparan Heparan Heparan Heparan N-deacetylase/N-sulfotransferase-2 | | 2 | 10 U36601 |
| 1434 | UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase | | 3 | 18 U41514 |

3) Protein Kinase C

Validation: Deletion of PKC1(Protein Kinase C), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|----------------------------------|-------------------------|------------|---------------------|
| 1440 | Protein kinase C, beta 1 | | 4 | 16p11.2 X06318 |
| 1443 | Protein kinase C-theta | | 1 | 10p15 L01087 |
| 1444 | Protein kinase C substrate 80K-H | | 1 | 7 J03075 |

3) Protein Post-modification

Validation: Deletion of BET2(Geranylgeranyltransferase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1081 | geranylgeranyl transferase type II beta-subunit | | 2 | 1 X98001 |

3) Sugar Biosynthesis and Processing

Validation: Deletion of PGI1(Glucose-6-phosphate Isomerase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|-----------------------|
| 14 | PIP 5 Kinase beta | | 2 | 9q13 X92493 |
| 1229 | Aconitase 2, mitochondrial | | 1 | 22q11.21-q13.3 U80040 |
| 1249 | ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR | | 2 | 18 D14710 |
| 1257 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 | | 3 | 18 X60221 |
| 1258 | ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) | | 5 | 21q22.1-q22.2 X83218 |
| 1302 | Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) | | 5 | 11 AF001437 |
| 1303 | Dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) | | 5 | 7q31-q32 J03490 |
| 1346 | Hexokinase 1 | | 3 | 10q22 M75126 |
| 1366 | Isocitrate dehydrogenase 2 (NADP+), mitochondrial | | 2 | 15q26.1 X69433 |
| 1395 | NADH dehydrogenase | | 1 | 2p16 X81900 |
| 1421 | NADH:ubiquinone oxidoreductase subunit B13 | | 4 | 18p11.31-p11.2 U53468 |
| 1422 | NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) | | 1 | 18p11.31-p11.2 U65579 |
| 1424 | NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR | | 3 | 2 X61100 |
| 1427 | Pyruvate dehydrogenase (lipoamide) beta | | 9 | 3p13-q23 M34479 |
| 1430 | Phosphofructokinase | | 1 | 21q22.3 M10036 |
| 1451 | UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KD PROTEIN PRECURSOR | | 3 | 1,3 M36647 |
| 1464 | Succinate dehydrogenase, iron sulphur (Ip) subunit | | 3 | 1p22.1-qter D10245 |
| 1465 | Succinate dehydrogenase 2, flavoprotein (Fp) subunit | | 10 | 5p15 D30648 |
| 1576 | Pyruvate kinase, liver | | 2 | 1q21 D10326 |
| 1577 | Oxoglutarate dehydrogenase (lipoamide) | | 6 | 7p14-p13 D10523 |
| 1579 | Acyl-Coenzyme A dehydrogenase, very | | 3 | 17p11.2-p11.13 D43682 |

| | | | | |
|------|---|---|------------|--------|
| | long chain | | | |
| 1584 | Dihydrolipoamide S-succinyltransferase | 5 | 14q24.3 | L37418 |
| 1588 | Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain | 1 | 1p31 | M16827 |
| 1590 | Pyruvate kinase, muscle | 4 | 15q22 | M23725 |
| 1596 | Phosphoglucomutase 1 | 5 | 1p31 | M83088 |
| 1603 | Phosphofructokinase, muscle | 4 | 12q13.3 | U24183 |
| 1611 | Enolase 3, (beta, muscle) | 1 | 17pter-p12 | X16504 |

3) Sugar Transport

Validation: Genes required to maintain organic compounds at levels required for cell growth or survival.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1594 | Solute carrier family 2 (facilitated glucose transporter), member 5 | 3 | 1p31 | M55531 |
| 1598 | Solute carrier family 5 (sodium/glucose cotransporter), member 2 | 1 | 16 | M95549 |

4) Protein Degradation

Validation: Deletion of CDC48(Ubiquitin proteolysis), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1027 | 26S PROTEASE REGULATORY SUBUNIT 4 | 3 | 14 | L02426 |
| 1037 | CALPAIN 1, LARGE | 1 | 11 | X04366 |
| 1098 | Human mRNA for KIAA0123 gene, partial cds | 6 | 9,19 | D50913 |
| 1114 | Proteasome (prosome, macropain) subunit, beta type, 6 | 7 | 9,19 | D29012 |
| 1115 | Human mRNA for proteasome subunit z, complete cds | 4 | 9 | D38048 |
| 1116 | PROTEASOME COMPONENT C13 PRECURSOR | 2 | 9 | U17496 |
| 1117 | Human mRNA for proteasome subunit HsC7-I, complete cds | 6 | 1 | D26599 |
| 1118 | Human mRNA for proteasome subunit p112, complete cds | 2 | 2 | D44466 |
| 1119 | Human mRNA for proteasome subunit p27, complete cds | 1 | 2 | AB003177 |
| 1289 | ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT | 2 | 19 | Z50853 |

4) Protein Folding

Validation: Deletion of HSP10(Chaperonin), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|----|------|-------------------------|------------|---------------------|
|----|------|-------------------------|------------|---------------------|

| | | | | |
|------|---|---|-----|--------|
| 1287 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR | 1 | 10 | M80254 |
| 1305 | DNAJ PROTEIN HOMOLOG 2 | 1 | 9,2 | D13388 |
| 1358 | DNAJ PROTEIN HOMOLOG HSJ1 | 2 | 9,2 | X63368 |

4) Ribosomal Subunit

Validation: Deletion of GRC5(Ribosome), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1127 | H.sapiens mRNA for ribosomal protein L11 | 3 | 9,2 | X79234 |
| 1128 | Ribosomal protein L17 | 2 | 17,4 | X52839 |
| 1130 | 60S RIBOSOMAL PROTEIN L18A | 5 | 3 | X80822 |
| 1131 | Ribosomal protein L19 | 1 | 17q11 | X63527 |
| 1133 | 60S RIBOSOMAL PROTEIN L23A | 2 | 17,18 | U43701 |
| 1135 | Human ribosomal protein L27a mRNA, complete cds | 3 | 6,11 | U14968 |
| 1136 | Human ribosomal protein L28 mRNA, complete cds | 11 | 19 | U14969 |
| 1137 | Ribosomal protein L32 | 4 | 20 | X03342 |
| 1138 | Human ribosomal protein L35 mRNA, complete cds | 3 | 20 | U12465 |
| 1139 | Ribosomal protein L35a | 1 | 3q29-qter | X52966 |
| 1140 | Human mRNA for ribosomal protein L39, complete cds | 2 | 3q29-qter | U57846 |
| 1141 | Ribosomal protein L4 | 4 | 3,6 | L20868 |
| 1142 | Ribosomal protein L6 | 1 | 12 | X69391 |
| 1143 | Ribosomal protein L7 | 1 | 12 | L16558 |
| 5 | Ribosomal protein L7A | 1 | 19q33-q34 | M36072 |
| 1144 | Ribosomal protein L8 | 5 | 12 | Z28407 |
| 1145 | Ribosomal protein L9 | 2 | 12 | U09953 |
| 1146 | Ribosomal protein, large, P1 | 5 | 15,22 | M17886 |
| 1147 | Human ribosomal protein S10 mRNA, complete cds | 1 | 20 | U14972 |
| 1148 | Ribosomal protein S11 | 1 | 19q | X06617 |
| 1149 | 40S RIBOSOMAL PROTEIN S15 | 2 | 19q | J02984 |
| 1150 | 40S RIBOSOMAL PROTEIN S15A | 2 | 19q | X84407 |
| 1151 | Ribosomal protein S16 | 5 | 19 | M60854 |
| 1152 | Ribosomal protein S17 | 5 | 11pter-p13 | M13932 |
| 1154 | 40S RIBOSOMAL PROTEIN S23 | 2 | 5 | D14530 |
| 1155 | Ribosomal protein S25 | 2 | 11q23.3 | M64716 |
| 1157 | Ribosomal protein S28 | 2 | 19 | U58682 |
| 1158 | 40S RIBOSOMAL PROTEIN S29 | 1 | 19 | L31610 |
| 1159 | Ribosomal protein S5 | 2 | 19 | U14970 |
| 1160 | 40S RIBOSOMAL PROTEIN S7 | 3 | 19 | M77233 |
| 1161 | Ribosomal protein S9 | 3 | 19 | U14971 |
| 1223 | Ribosomal protein L7a | 6 | 9q34 | X52136 |

4) T-Complex

Validation: Deletion of CCT2(T-Complex), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|------------------------------------|-------------------------|------------|---------------------|
| 1489 | T-COMPLEX PROTEIN 1, ALPHA SUBUNIT | 1 | 6 | S70154 |

| | | | | |
|------|--------------------------------------|---|---|--------|
| 1490 | T-COMPLEX PROTEIN 1, EPSILON SUBUNIT | 3 | 5 | D43950 |
| 1491 | T-COMPLEX PROTEIN 1, GAMMA SUBUNIT | 2 | 1 | X74801 |

4) Translation Elongation

Validation: Deletion of CDC33(eIF4e), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence | |
|------|--|-------------------------|------------|---------------------|--------|
| 1063 | Eukaryotic translation elongation factor 1 delta | | 3 | 7 | Z21507 |
| 1073 | Eukaryotic translation initiation factor 4A (eIF-4A) isoform 2 | | 1 | 18p11.2 | D30655 |
| 1095 | Human mRNA for KIAA0031 gene, complete cds | | 3 | 17,2 | D21163 |
| 1099 | Human mRNA for KIAA0219 gene, partial cds | | 3 | 12 | D86973 |

4) Translation Factor

Validation: Deletion of CDC33(eIF4e), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence | |
|------|--|-------------------------|------------|---------------------|--------|
| 1049 | PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 | | 2 | 12 | X81625 |

4) Translation Initiation Factors

Validation: Deletion of CDC33(eIF4e), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence | |
|------|--|-------------------------|------------|---------------------|--------|
| 1068 | Human translation initiation factor eIF-3 p110 subunit gene | | 1 | 16 | U46025 |
| 1069 | EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34 | | 1 | 17 | D21853 |
| 1070 | Eukaryotic translation initiation factor 4C (eIF-4C) | | 3 | 1,X | L18960 |
| 1072 | Eukaryotic translation initiation factor 2A | | 2 | 14 | J02645 |
| 1074 | Eukaryotic translation initiation factor 4E | | 3 | 14 | M15353 |
| 1312 | Translation initiation factor 3 (eIF-3) p36 subunit | | 1 | 12 | U39067 |

4) tRNA Synthetases

Validation: Deletion of ALA1(Alanyl-tRNA synthetase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|------------------------------|-------------------------|------------|---------------------|
| 1031 | Alanyl-tRNA synthetase | | 2 | 16q22 D32050 |
| 1040 | Cysteinyl-tRNA synthetase | | 1 | 11p15.5 L06845 |
| 1079 | Glycyl-tRNA synthetase | | 2 | 7p15 U09510 |
| 1090 | Isoleucine-tRNA synthetase | | 2 | 9q21 D28473 |
| 1102 | ASPARAGINE SYNTHETASE | | 3 | M27396 |
| 1121 | Arginyl-tRNA synthetase | | 3 | 5pter-q11 S80343 |
| 1198 | Threonyl-tRNA synthetase | | 1 | 5p13-cen M63180 |
| 1218 | VALYL-TRNA SYNTHETASE | | 4 | 9 X59303 |
| 1221 | TRYPTOPHANYL-TRNA SYNTHETASE | | 1 | 14 M61715 |

4) Ubiquitin and Ubiquitin Associated

Validation: Deletion of UFD1(Ubiquitin Fusion), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1309 | Ubiquitin carrier protein (E2-EPF) | | 2 | 17 M91670 |
| 1315 | Cyclin-selective ubiquitin carrier protein | | 2 | 17 U73379 |
| 1362 | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 3 | | 2 | 14 D80012 |
| 1363 | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T | | 1 | 12 X91349 |
| 1420 | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 14 | | 4 | 13 M68864 |
| 1431 | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L1 | | 2 | 4 X04741 |
| 1511 | Ubiquitin A-52 residue ribosomal protein fusion product 1 | | 1 | 19p13.1-p12 S79522 |
| 1514 | Ubiquitin-conjugating enzyme E2I | | 6 | 16p13.3 U45328 |
| 1515 | Ubiquitin fusion-degradation protein (UFD1L) | | 4 | 18 U64444 |

5) DNA Helicases

Validation: Deletion of DNA2(DNA Helicase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1050 | Human CHL1 potential helicase (CHLR1), complete cds | | 3 | 18 U33833 |
| 1057 | ATP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT | | 1 | 2 M30938 |
| 1123 | RecQ protein-like (DNA helicase Q1-like) | | 2 | 12p12-p11 L36140 |
| 1397 | 218kD Mi-2 protein | | 1 | 12 X86691 |

5) DNA Polymerase

Validation: Deletion of POL2(DNA pol epsilon), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1059 | Human DNA polymerase delta small subunit mRNA, complete cds | | 3 | 12 U21090 |
| 1105 | DNA polymerase alpha subunit | | 1 | X,11 L24559 |

5) DNA Replication

Validation: Deletion of CDC45(Chromosomal DNA Replication), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1048 | DNA REPLICATION LICENSING FACTOR CDC47 HOMOLOG | | 1 | 4 D55716 |
| 1094 | Human mRNA for KIAA0030 gene, partial cds | | 2 | 3 X67334 |
| 1124 | Replication factor C (activator 1) 1 (145kD) | | 2 | 4p14-p13 L14922 |
| 1208 | DNA topoisomerase I | | 2 | 20q12-q13.1 J03250 |
| 22 | Topoisomerase II | | 2 | 17q21-q22 J04088 |
| 1222 | Minichromosome maintenance deficient (<i>S. cerevisiae</i>) 3 | | 1 | 17q21-q22 D38073 |
| 1461 | Replication protein A2 (32kD) | | 2 | 1p35 J05249 |

5) Histone

Validation: Deletion of CSE4(Similar Histone H3), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---------------|-------------------------|------------|---------------------|
| 1335 | Histone H1(0) | | 3 | 22 X03473 |
| 1336 | Histone H1x | | 3 | 22 D64142 |
| 1341 | HISTONE H1D | | 5 | 6 X57129 |
| 1342 | HISTONE H2A.1 | | 4 | 6 U90551 |
| 1343 | Histone H2A.2 | | 1 | 6 L19779 |
| 1344 | Histone H2B.1 | | 1 | 1 M60756 |
| 1345 | H4 histone | | 1 | 1 X60486 |

5) Polyadenylation and 3' Cleavage

Validation: Deletion of FIP1(Polyadenylation Factor), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|----|------|-------------------------|------------|---------------------|
|----|------|-------------------------|------------|---------------------|

| | | | | |
|------|--|---|----|--------|
| 1053 | Human cleavage and polyadenylation specificity factor mRNA, complete cds | 1 | 11 | U37012 |
| 1349 | HNRNP METHYLTRANSFERASE | 4 | 14 | D66904 |
| 1426 | Poly(A)-binding protein-like 1 | 2 | 14 | Y00345 |

5) Purine/Pyrimidine Biosynthesis

Validation: Deletion of CDC8(Thymidylate Kinase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1235 | ADENYLOSUCCINATE LYASE | 1 | 1 | X65867 |
| 1268 | CAD PROTEIN | 1 | 2 | D78586 |
| 1293 | CTP synthetase | 2 | 1p34.1 | X52142 |
| 1326 | Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase | 4 | 21q22.1 | X54199 |
| 1437 | Phosphoribosyl pyrophosphate amidotransferase | 2 | 4q12 | U00238 |
| 1510 | Thymidylate synthase | 2 | 18p11.32 | X02308 |
| 1517 | Uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) | 2 | 3q13 | J03626 |
| 1518 | Uridine Phosphorylase | 1 | 7 | X90858 |

5) Ribonucleotide Reductase

Validation: Deletion of RNR1(Ribonucleotide Reductase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1452 | RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1 CHAIN | 4 | 11 | X59543 |

5) RNA Helicase

Validation: Deletion of BRR2(RNA Helicase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1100 | Human mRNA for KIAA0224 gene, complete cds | 4 | 16 | D86977 |
| 1163 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A) | 1 | 1 | L13848 |
| 1484 | PUTATIVE ATP-DEPENDENT RNA HELICASE STE13 | 3 | 19 | U90426 |

5) RNA Polymerase II Components

Validation: Deletion of RPA135(RNA pol Subunit), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1026 | Homo sapiens (clone mf.18) RNA polymerase II mRNA, complete cds | | 3 | 19 L37127 |
| 1088 | Human RNA polymerase II subunit (hsRFB10) mRNA, complete cds | | 7 | 19 U37690 |
| 1109 | RNA polymerase II, polypeptide C (33kD) | | 3 | 16q13-qq21 J05448 |
| 1110 | Polymerase (RNA) II (DNA directed) polypeptide A (220kD) | | 1 | 17p13.1 X63564 |
| 1165 | DNA-DIRECTED RNA POLYMERASE II 23 KD POLYPEPTIDE | | 9 | 17p13.1 J04965 |
| 1360 | RNA polymerase II subunit hsRFB7 | | 1 | 11 U20659 |

5) RNA Polymerase III

Validation: Deletion of RPA135(RNA pol Subunit), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1170 | Human RNA polymerase III subunit (RPC62) mRNA, complete cds | | 1 | 11 U93867 |

5) RNA Splicing/Processing

Validation: Deletion of CUS1(U2 snRNP protein), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|-----------------------|
| 1171 | Human spliceosome associated protein (SAP 145) mRNA, complete cds | 0 | 1 | 2 U41371 |
| 1172 | Human splicesomal protein (SAP 61) mRNA, complete cds | | 3 | 2 U08815 |
| 1176 | H.sapiens mRNA for splicing factor SF3a120 | | 1 | 22 X85237 |
| 1177 | Splicing factor, arginine/serine-rich 2 | | 2 | 4,17 M90104 |
| 1181 | Human splicing factor SRP30c mRNA, complete cds | | 1 | 6 U30825 |
| 1183 | PRE-MRNA SPLICING FACTOR SRP75 | | 2 | 1 L14076 |
| 1216 | SPLICING FACTOR U2AF 65 KD SUBUNIT | | 1 | 1 X64044 |
| 1224 | Human (clone E5.1) RNA-binding protein mRNA, complete cds | | 4 | 1 L37368 |
| 1322 | Fibrillarin | | 1 | 1 X56597 |
| 1354 | Heterogeneous nuclear ribonucleoprotein K | | 1 | 9q21.32-q21.33 S74678 |

| | | | | |
|------|---|---|----------------|--------|
| 1455 | U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A | 3 | 9q21.32-q21.33 | X06347 |
| 1460 | U1 small nuclear RNP-specific C | 2 | 15 | X12517 |
| 1473 | SnRNP core protein Sm D3 | 2 | 22 | U15009 |
| 1474 | SnRNP core protein Sm D2 | 5 | 22 | U15008 |
| 1477 | U1 snRNP 70K protein | 3 | 19q13.3 | M22636 |
| 1478 | Small nuclear ribonucleoprotein polypeptides B and B1 | 3 | 20 | J04564 |
| 1480 | Small nuclear ribonucleoprotein polypeptide N | 5 | 15q12 | U41303 |

5) TATA-Binding Proteins

Validation: Deletion of TAF145(TAFII Complex), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|----------------------|------------|------------------|
| 1193 | H.sapiens mRNA for transcription factor TFIID subunit TAFII28 | | 1 | 6 X83928 |
| 1196 | Human TFIID subunit TAFII55 (TAFII55) mRNA, complete cds | | 1 | 5 U18062 |
| 1199 | TATA box binding protein | | 2 | 6q27 M55654 |
| 1361 | TBP-associated factor (hTAFII130) | | 1 | 20 U75308 |

5) Transcription Elongation Factors

Validation: Deletion of RPO21(RNA pol Subunit), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--------------------------------------|----------------------|------------|------------------|
| 1077 | TRANSCRIPTION ELONGATION FACTOR S-II | | 4 | 8 M81601 |
| 4 | TRANSCRIPTION ELONGATION FACTOR B3 | | 5 | 5q31 L34587 |
| 32 | Elongin TCEB1 | | 3 | 1p36.1 L47345 |

5) Transcription Factors

Validation: Deletion of BBP1(BFR1p binding), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|----------------------|------------|------------------|
| 33 | SUPT6H | | 3 | 17q11.2 U46691 |
| 1202 | Human TFIIA gamma subunit mRNA, complete cds | | 1 | 15 U14193 |
| 1205 | General transcription factor TFIIE beta subunit, 34 kD | | 1 | 8p21-p12 X63469 |
| 1206 | TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT | | 1 | 8p21-p12 X16901 |
| 1247 | CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1 | | 1 | 19p13.3 X55544 |
| 1248 | CAMP-dependent transcription factor | | 3 | 2 M86842 |

| | | | | |
|------|--|---|---------------|--------|
| | ATF-4 (CREB2) | | | |
| 1274 | Transcription Factor (CBFB) | 1 | 2 | L20298 |
| 1292 | CRM1 protein | 3 | 2 | Y08614 |
| 1368 | Transcription Factor IL-4 Stat | 1 | 21q21-q22.1 | U16031 |
| 1373 | SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA | 1 | 21q21-q22.1 | M97935 |
| 1411 | Nuclear Factor I-B2 (NFIB2) | 1 | 19 | U85193 |
| 1483 | Transcription Factor Stat5b | 1 | 17 | U48730 |
| 1496 | Transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) | 2 | 15q21 | M83233 |
| 1497 | Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | 8 | 19p13.3 | M31523 |
| 1498 | Transcription factor 6-like 1 (mitochondrial transcription factor 1-like) | 1 | 7p | M62810 |
| 1500 | TRANSCRIPTION FACTOR P65 | 3 | 11 | L19067 |
| 1501 | Transcription factor COUP 2 (a.k.a. ARP1) | 2 | 15q26.1-q26.2 | X91504 |

6) Clathrin

Validation: Deletion of RET1(Alpha-Cop), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|-------------------------------------|-------------------------|------------|---------------------|
| 1242 | CLATHRIN COAT ASSEMBLY PROTEIN AP47 | 2 | 8 | D38293 |
| 1243 | CLATHRIN COAT ASSEMBLY PROTEIN AP50 | 6 | 3 | U36188 |
| 1282 | cell surface protein | 5 | 22 | X83545 |
| 1290 | Clathrin, light polypeptide (Lcb) | 1 | 4q2-q3 | M20470 |
| 1291 | Clathrin heavy chain | 4 | 17q11-qter | U41763 |

6) Cytoskeleton

Validation: Deletion of MHP1(Microtubule Interacting), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1 | Actin, gamma Subunit Sh3p17(Myosin IC Heavy Chain) | 8 | 17p11-qter | X04098 |
| 1032 | Actin depolymerizing factor [human, fetal brain, mRNA, 1452 nt] | 4 | 1 21 | U61166 |
| 1038 | Capping protein (actin filament), gelsolin-like | 3 | 2cen-q24 | M94345 |
| 1039 | Human capping protein alpha mRNA, partial cds | 2 | 7 | U03851 |
| 1056 | Desmin | 1 | 2q35 | J03191 |
| 1080 | Gelsolin (amyloidosis, Finnish type) | 1 | 9q34 | X04412 |
| 1092 | Keratin 19 | 5 | | Y00503 |
| 1093 | KERATIN, TYPE II CYTOSKELETAL 6D | 13 | 5,12 | J00269 |
| 1267 | BETA-CENTRACTIN | 1 | 2 | X82207 |
| 1284 | Cofilin 1 (non-muscle) | 5 | 11q13 | X95404 |
| 1383 | LAMIN A | 1 | 20 | M13451 |
| 1385 | Lamin B receptor | 1 | 1q42.1 | L25931 |

| | | | | |
|------|---|---|--------|--------|
| 1386 | MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM | 1 | 12,17 | M22920 |
| 1404 | MYOSIN HEAVY CHAIN 95F | 1 | 4p16.3 | U90236 |
| 1405 | MYOSIN HEAVY CHAIN IB | 1 | 13 | D63476 |
| 1406 | Myosin-IC | 1 | 13 | U14391 |
| 1486 | SUPPRESSOR OF TUBULIN STU2 | 1 | 11 | X92474 |
| 1495 | MICROTUBULE-ASSOCIATED PROTEIN TAU | 1 | 17 | J03778 |
| 1507 | Tubulin, gamma polypeptide | 1 | 17 | M61764 |
| 1508 | TUBULIN ALPHA-4 CHAIN | 1 | 17 | X06956 |
| 1520 | Myosin VIIA (USH1B) | 2 | 17 | U39226 |

6) ER Protein

Validation: Deletion of BET1(v-SNARE), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---------------------------------------|-------------------------|-------------|---------------------|
| 1272 | Calnexin | | 1 | 5q35 |
| 1317 | ER LUMEN PROTEIN RETAINING RECEPTOR 2 | 1 | 19 | M88458 |
| 1614 | Ribophorin I | 4 | 3q | Y00281 |
| 1615 | Ribophorin II | 1 | 20q12-q13.1 | Y00282 |

6) Integrin

Validation: Deletion of MYO2(Myosin Heavy Chain), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--------------------------|-------------------------|------------|---------------------|
| 1378 | Integrin alpha-3 subunit | | 1 | 5q23-q31 |

6) Karyopherin

Validation: Deletion of KAP121(Karyopherin), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---------------------|-------------------------|------------|---------------------|
| 1091 | karyopherin alpha 3 | | 3 | 13 |
| 1214 | transportin (TRN) | | 1 | 13 |

6) Lysosomal Proteins

Validation: Essential for sequestering and degrading aged or defective organelles and polymers that can interfere with cell survival, proliferation as seen by human diseases such as Tay-Sachs disease.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1265 | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD | | 2 | 22pter-q11.2 X76228 |

6) MITOCHONDRIAL IMPORT

Validation: Genes required to maintain inorganic ions at levels compatible with cell growth or survival.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1578 | MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 | | 8 | 1 D13641 |

6) Nuclear Pore Complex

Validation: Deletion of GSP1(Nuclear Pore Trafficking), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 28 | Nuclear Pore Complex NUP214 | | 3 | 9 D14689 |
| 29 | Nucleoporin 98 | | 3 | 11p15 U41815 |
| 1266 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C | | 4 | 20 L38696 |
| 1350 | Heterogeneous nuclear ribonucleoprotein A1 | | 4 | 12q13.1 X79536 |
| 1355 | Nuclear pore complex protein hnup153 | | 3 | 6 Z25535 |
| 1425 | NUCLEAR PORE GLYCOPROTEIN P62 | | 1 | 11 X58521 |
| 1449 | Export protein Rae1 | | 5 | 20 U84720 |
| 1454 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 | | 3 | 12 M29063 |
| 1524 | 140 KD NUCLEOLAR PHOSPHOPROTEIN | | 5 | 10 D21262 |

6) Protein Transport

Validation: Deletion of BET3(v-SNARE associated), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 8 | Integral Transmembrane Protein | | 3 | 11q23-24 L38961 |
| 1467 | Sec23A isoform | | 2 | 14 X97064 |
| 1608 | Signal recognition particle receptor ('docking protein') | | 8 | 11q23-q24 X06272 |
| 1613 | TIM17 preprotein translocase | | 2 | 1 X97544 |

6) Syntaxin

Validation: Deletion of SED5(Syntaxin), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|-------------|-------------------------|------------|---------------------|
| 1186 | syntaxin 1A | | 1 | 21q22.1 |
| 1188 | syntaxin 3 | | 1 | 11 |
| 1189 | Syntaxin 5A | | 2 | 11 |
| 1190 | syntaxin 7 | | 1 | 6 |

6) Vacuolar Protein

Validation: Deletion of PPA1(Vacuolar H-ATPase), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1261 | Vacuolar H+ ATPase proton channel subunit | | 2 | 6 |

6) Vesicle Proteins

Validation: Deletion of SAR1(COP II), a *S. cerevisiae* gene in the same biochemical family, is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1025 | Human (chromosome 3p25) membrane protein mRNA | | 3 | 3,18 |
| 24 | COATOMER BETA SUBUNIT | | 1 | 3 |
| 1055 | COATOMER DELTA SUBUNIT | | 8 | 11 |
| 1082 | Human GP36b glycoprotein mRNA, complete cds | | 3 | 5 |
| 1173 | SEC14 (<i>S. cerevisiae</i>)-like | | 7 | 17q25.1-q25.2 |
| 1174 | Human homologue of yeast sec7 mRNA, complete cds | | 2 | 17q25.1-q25.2 |
| 1184 | Human chromosome 17q21 mRNA clone LF113 | | 1 | 17 |
| 1217 | H.sapiens mRNA for vacuolar-type H(+)-ATPase 115 kDa subunit | | 2 | 17 |

99) Direct Essential Yeast Homolog

Validation: Deletion of the *S. cerevisiae* homologue of this gene is lethal.

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1238 | Aldolase A | | 2 | 16q22-q24 |
| 1239 | Aldolase B, fructose-bisphosphate | | 2 | 9q22 |
| 1241 | S-adenosylmethionine decarboxylase 1 | | 1 | 6q21-q22 |
| 1271 | Calmodulin 1 (phosphorylase kinase, delta) | | 1 | 14q24-q31 |
| 1300 | DED81 | | 1 | 18 |

| | | | | |
|------|---|----|-----------------|----------|
| 1301 | Deoxyhypusine synthase | 3 | 19p13.11-p13.12 | L39068 |
| 1306 | Dolichol monophosphate mannose synthase (DPM1) | 2 | 20 | AF007875 |
| 1318 | ESS1 PROTEIN | 1 | 19 | U49070 |
| 1332 | Glucose phosphate isomerase | 1 | 19q13.1 | K03515 |
| 1333 | Guanylate kinase (GUK1) | 3 | 19q13.1 | L76200 |
| 1359 | Heat shock 60 kD protein 1 (chaperonin) | 1 | 9 | M34664 |
| 1367 | PERIODIC TRYPTOPHAN PROTEIN 1 | 1 | 12 | L07758 |
| 1372 | IPP isomerase | 1 | 10 | X17025 |
| 1396 | N-acetylglucosaminyltransferase I | 4 | 5q31.2-q31.3 | M55621 |
| 1399 | Mannose phosphate isomerase | 3 | 15q22-qter | X76057 |
| 1414 | Nipl | 1 | 5 | U15172 |
| 1415 | GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE | 2 | 17 | M86707 |
| 1433 | PHOSPHATIDYLINOSITOL 4-KINASE ALPHA | 10 | 17 | L36151 |
| 1446 | PERIODIC TRYPTOPHAN PROTEIN 2 | 2 | 8 | U53346 |
| 1519 | Uridine diphosphoglucose pyrophosphorylase | 1 | 2 | U27460 |

Fig. 6

Target Variances by Field Table for Conditionally Essential Genes

Conditionally Essential Biosynthetic Enzymes

Validation: Conditionally Essential

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1536 | 5-methyltetrahydrofolate-homocysteine methyltransferase | | 3 | U75743 |
| 1539 | Glutamate-ammonia ligase (glutamine synthase) | | 5 | 1q31 X59834 |

Proteins that Repair Radiation Induced DNA Damage

Validation: Conditionally Essential

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|--|-------------------------|------------|---------------------|
| 1541 | Fanconi anemia complementation group C | | 1 | 9q22.3 X66894 |

Proteins of DNA Repair

Validation: Conditionally Essential

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|----------------------|
| 1528 | DNA excision repair protein ERCC5 | | 4 | 13q33 D16305 |
| 1530 | HHR23A protein | | 3 | 9 D21235 |
| 1532 | DNA EXCISION REPAIR PROTEIN ERCC-1 | | 2 | 19q13.2-q13.3 M13194 |
| 1533 | DNA repair helicase ERCC3 | | 1 | 2q21 M31899 |
| 1537 | URACIL-DNA GLYCOSYLASE 1 PRECURSOR | | 2 | 8 X15653 |
| 1526 | Damage-specific DNA binding protein 1 (127 kD) | | 2 | 11, 15 AJ002955 |

Proteins that repair chemically induced DNA damage

Validation: Conditionally Essential

| ID | Name | Variances Identified | Chromosome | Genbank Sequence |
|------|---|-------------------------|------------|---------------------|
| 1534 | O-6-methylguanine-DNA methyltransferase | | 4 | 10q26 M60761 |

Fig. 7

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|---|-----------------|-----------------|----------------|
| 1.01 | 472 | CGGCCATGTA [C/T] GTGGCCATCC | 71 (36) | 1 (1) | Silent |
| .02 | 250 | ACGAGGCCCA [G/A] AGCAAGCGTG | 71 (36) | 1 (1) | Silent |
| .03 | 1003 | CGGGCATTGC [C/T] GACAGGATGC | 66 (35) | 6 (5) | Silent |
| .04 | 801 | ACGAGCTGCC [C/T] GATGGCCAGG | 71 (36) | 1 (1) | Silent |
| .05 | 1201 | AATGCTTCTA [A/G] ACGGACTCAG | 71 (36) | 1 (1) | Silent |
| .06 | 991 | CCACCATGTA [C/T] CCGGGCATTG | 17 (17) | 56 (35) | Silent |
| .07 | 1099 | TGTGGATCGG [T/C] GGCTCCATCC | 71 (36) | 1 (1) | Silent |
| .08 | 499 | GTGCTGTCCCT [C/G] TACGCCTCT | 65 (65) | 7 (7) | Silent |
| 4.01 | 2168 | CCGCCAGTAG [C/T] ATCAGCTTTA | 61 (34) | 11 (9) | 3'UT |
| .02 | 388 | TGGAAAGCCA [C/T] GGGAGCCGA | 62 (29) | 10 (7) | Thr->Met |
| .03 | 491 | AGAGGAGAGA [T/C] GAGAGAAAGA | 68 (36) | 4 (4) | Silent |
| .04 | 1171 | AAAACTAATT [T/C] GGATAGAAAG | 68 (36) | 4 (4) | Leu->Ala |
| .05 | 336 | TCGGGATGCC [C/T] TGCAGAAGGA | 71 (36) | 1 (1) | Silent |
| 5.01 | 421 | ACGTCCCAAC [G/A] AAGAGACCAC | 66 (36) | 6 (6) | Silent |
| 8.01 | 1570 | CTCCGTCCA [T/C] TGTACTATCTG | 70 (36) | 2 (2) | Silent |
| .02 | 778 | TCCACGTCCT [C/G] GTGCTGATGC | 71 (36) | 1 (1) | Silent |
| .03 | 158 | GGACACACTT [T/C] TGAAGCTTCT | 71 (36) | 1 (1) | Silent |
| 9.01 | 1929 | CCATGCACCA [C/A] GAGGACTTTA | 71 (36) | 1 (1) | His->Gln |
| 10.01 | 1099 | AACCGTGT CAGGGAACACCA | 69 (36) | 3 (3) | Gly->Arg |
| 14.01 | 911 | CAATTCAATC [G/A] CCGCCCTAAA | 69 (36) | 3 (3) | Arg->His |
| .02 | 1174 | CAACAGTAA [G/A] TGAAATGGT | 71 (36) | 1 (1) | |
| 20.01 | 1627 | CCCAGCACAT [C/T] ACCTATGTGC | 44 (30) | 28 (21) | Silent |
| .02 | 2041 | GCCGAAGTGT [C/G] CGGTTCTCTG | 71 (36) | 1 (1) | Asp->Glu |
| .03 | 1393 | cagccatcca [c/t] gaggtcatgg | 71 (36) | 1 (1) | Silent |
| 22.01 | 4008 | CAACAAAAAC [A/C] AAATTCACAA | 71 (36) | 1 (1) | Silent |
| .02 | 4446 | AGCCATCCAC [T/G] TCTGATGATT | 71 (36) | 1 (1) | Silent |
| 24.01 | 1101 | GCCACTGGCA [G/A] TAAAGGATAT | 71 (36) | 1 (1) | Val->Ile |
| 28.01 | 5009 | TGCCACGCCC [G/C] TGTTTGGGCA | 70 (36) | 2 (2) | Val->Leu |
| .02 | 2023 | AGAAATCACC [C/T] AGGATAACCC | 71 (36) | 1 (1) | Silent |
| .03 | 2041 | CCCCTCCAGC [G/A] GCAAAGCCAG | 71 (36) | 1 (1) | Silent |
| 29.01 | 1768 | CCCTGCCACT [A/C] GAGTCCGGCC | 67 (36) | 5 (5) | Silent |
| .02 | 2781 | AGGAGCATCC [G/A] TCTAAAATA | 70 (36) | 2 (2) | Silent |
| .03 | | 2 bp deletion | | | 3'UT |
| 32.01 | 1171 | AAAACTAATT [T/C] GGATAGAAAG | 70 (36) | 2 (2) | Leu->Ala |
| .02 | 388 | TGGAAAGCCA [C/T] GGGAGCCGA | 59 (33) | 13 (10) | Pro->Met |
| .03 | 2168 | CGGCCAGTAGCATCAGCTTTA | 60 (34) | 12 (10) | Silent |
| 33.01 | 2397 | GGCTAGATGG [T/C] CTGGCCAAAA | 47 (33) | 25 (12) | Silent |
| .02 | 3708 | AGGTGCGGGT [C/T] GATGTCAACC | 63 (35) | 9 (8) | Silent |
| .03 | 3795 | GGACCCACCT [C/A] CTGAAGATCC | 62 (35) | 10 (9) | Silent |
| 524.01 | 1598 | CACAAGTTGA [G/A] GAGGGCGATA | 68 (36) | 4 (4) | Silent |
| .02 | 2548 | CTTATATTTC [T] ¹⁰ GATGTCAACC | 71 (36) | 1 (1) | 3'UT |
| .03 | 3158 | AAAATTGTCT [GTTT] GTTTTCTCAT | 50 (34) | 22 (20) | 3'UT |
| 525.01 | 255 | CTGCGGTTCT [C/T] GAGGGCGATA | 54 (34) | 18 (16) | Silent |
| .02 | 346 | CGTGCGGGT [C/T] TTCACCATCC | 71 (36) | 1 (1) | Leu->Phe |
| .03 | 523 | CCCCATCCTC [A/G] TCCCGTGCCA | 63 (36) | 9 (9) | Ile->Val |
| 1025.01 | 1051 | CAACTAACCA [G/A] ACAACTGGGA | 24 (20) | 48 (44) | 3'UT |

| | | | | | |
|---------|------|------------------------------|---------|---------|------------|
| .11 | 418 | GGCCCTTTTG [C/T] AGCCCAAGGC | 6 (5) | 5 (3) | N/D |
| .12 | 640 | CAACTAACCA [G/A] ACAACTGGGA | 15 (7) | 7 (6) | N/D |
| 1026.2 | 47 | GTCTGGACGC [G/A] ACGGCGGCGG | 2 (2) | 3 (2) | 5' UT |
| .9 | 262 | CCCACCCCTT [G/A] GAGCACAAGA | 28 (13) | 4 (1) | Silent |
| .19 | 602 | ATAAAGTATAGCGG [A/G] AGAGAN | 5 (5) | 11 (8) | 3' UT |
| 1027.2 | 405 | TGGAAGAGAT [T/C] ATTGATGACA | 2 (2) | 2 (2) | Silent |
| .6 | 942 | GGACAAAAAG [A/G] TATGACTCCA | 8 (8) | 4 (4) | Silent |
| .16 | 1361 | CAGGAAGGCA [C/A] CCTTGAGGGG | 13 (11) | 3 (3) | Thr -> Asn |
| 1031.31 | 2990 | CCTTCGCCCA [G/A] CTGCGCCTCG | 9 (7) | 2 (2) | Silent |
| .32 | 2991 | CTTCGCCAG [C/G] TCGCCTCGG | 4 (4) | 4 (4) | Leu -> Val |
| 1032.1 | 3 | AGTCGCCG [G/A] GGAGGACGGTCT | 5 (4) | 3 (3) | 5' UT |
| .2 | 4 | GTCCGCCG [G/A] GAGGACGGTCTGC | 5 (5) | 3 (2) | 5' UT |
| .3 | 69 | CCGCCGCGGC [G/A] AAGATGGCCT | 5 (5) | 2 (2) | 5' UT |
| .10 | 312 | AAAAAGATTG [T/C] CGCTATGCTT | 8 (8) | 3 (3) | Silent |
| 1037.20 | 2919 | TGGTTATGGG [G/C] GTGCCAGAGG | 15 (13) | 2 (2) | 3' UT |
| 1038.5 | 723 | CAGGTCCTGG [G/C] CCCAAGCCT | 7 (7) | 3 (3) | Silent |
| .10 | 862 | ACTCCAGCCC [C/A] TTTGCCCTTG | 5 (5) | 13 (10) | Silent |
| .13 | 1053 | CCTCAGGGCC [G/A] TGAGAGTCCC | 13 (10) | 8 (7) | Arg -> His |
| 1039.19 | 1665 | ACCATGTCTC [A/G] GTTTATTTT | 2 (2) | 6 (5) | 3' UT |
| .23 | 1748 | TATTTAGTA [G/A] AAAATCACTT | 3 (3) | 2 (2) | 3' UT |
| 1040.7 | 2056 | GCTGAAGAAG [T/C] CTTCGAGGCT | 20 (16) | 2 (2) | 3' UT |
| 1043.1 | 351 | ACTTGAAGGA [T/C] GAAAGTGGCT | 2 (2) | 3 (3) | Silent |
| .2 | 372 | TCAAAGATCC [C/T] TCCAGCGACT | 2 (2) | 3 (3) | Silent |
| 1048.3 | 341 | GCTACGCGAA [G/A] CTCTTGCTG | 2 (2) | 2 (2) | Silent |
| 1049.10 | 2648 | CCTGAAACCC [T/A] GAAGCTGATG | 5 (4) | 3 (1) | 3' UT |
| .12 | 2768 | CAGTGGTAGC [G/A] ATGAAAAAA | 8 (6) | 2 (1) | 3' UT |
| 1050.11 | 2381 | CAGGAAGAAG [A/G] TATTCAGGA | 4 (2) | 2 (2) | Ile -> Val |
| .13 | 2750 | TTTGGCCAGC [G/A] TAGTGCTCCT | 2 (2) | 2 (1) | Val -> Ile |
| .14 | 3034 | GAGTCCAGAG [T/C] GCTGCCAGGA | 2 (2) | 2 (1) | 3' UT |
| 1051.10 | 260 | AGCTGGCAAG [C/T] TACTTTTCAG | 15 (10) | 3 (1) | 3' UT |
| .18 | 409 | TTTGCTTCTT [G/A] AGTAGAGCCA | 17 (12) | 3 (1) | 3' UT |
| 1052.7 | 428 | TGTACAAATC [T/C] TTCATCCATA | 7 (6) | 2 (2) | 3' UT |
| 1053.24 | 4113 | AGGAGAAGAC [C/T] TACCGGCGGC | 8 (7) | 8 (8) | Silent |
| 1055.17 | 3122 | CAGCGTCAGC [C/A] AGCTCAGCCT | 4 (4) | 4 (4) | 3' UT |
| .23 | 3450 | TGAGAAGGGC [T/C] TGGACAAGA | 26 (12) | 3 (3) | 3' UT |
| .25 | 3568 | TCAAAAACC [T/C] TTTTCTG | 26 (12) | 2 (2) | 3' UT |
| .01 | 2061 | AGGCTGGTCG [C/T] GAACTCCTGA | 61 (34) | 11 (9) | 3' UT |
| .02 | 2419 | TTAAAGATA [C/A] GCATGTCTTC | 59 (33) | 13 (10) | 3' UT |
| .03 | 3047 | TAAGTCTTT [G/T] AGTGTCTATCA | 71 (36) | 1 (1) | 3' UT |
| .04 | 2960 | TATTACTCAC [G/A] TATACCCCAT | 71 (36) | 1 (1) | 3' UT |
| .05 | 3450 | TGAGAAGGGC [T/C] TGGACAAGA | 60 (33) | 12 (9) | 3' UT |
| .06 | 3296 | CTGCAAAGAG [T/C] GTACTGTGCT | 60 (33) | 12 (9) | 3' UT |
| 1056.12 | 407 | CAAGAGCACC [G/C] GTGGGCCCC | 13 (9) | 2 (2) | Val -> Arg |
| 1057.20 | 3067 | TAACTTTTCG [G/A] TCTTTCCCAT | 7 (5) | 3 (3) | 3' UT |
| 1059.11 | 1130 | AACGTGAGTG [A/G] CATTTTCCGA | 5 (5) | 2 (2) | Asp -> Ala |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .19 | 1327 | AATCATCCGA (G/A) GTCCTGAGGA | 19 (14) | 3 (3) | Val -> Ser |
| .27 | 1474 | GGGAGGCCCTG (G/A) GGCTGGGCC | 15 (11) | 2 (2) | Gly -> Arg |
| 1063.21 | 705 | CGGACATGGC (C/T) CAGCTGGAGG | 8 (7) | 8 (7) | Silent |
| .22 | 721 | GGAGGCCCTGT (G/T) TGCCTCTAT | 16 (14) | 2 (2) | Val -> Leu |
| .38 | 949 | GCGTGCGTGA (G/A) GGCCCTGCCA | 2 (2) | 2 (2) | 3' UT |
| 1068.30 | 2756 | GCGCCGCGGT (G/C) GCTACGCCCA | 21 (15) | 2 (2) | Ala -> Arg |
| 1069.10 | 1199 | GGGCGCCAGC (C/G) GAGTGCTTAT | 17 (13) | 2 (2) | Arg -> Glu |
| 1070.3 | 303 | AAGAGGATGG (G/T) CAGGAGTATG | 3 (2) | 6 (6) | Gly -> Val |
| .7 | 615 | ACATTGGAGA (T/C) GATGATGAAG | 6 (6) | 2 (1) | Silent |
| .12 | 1092 | GAAGTCTGCA (G/T) TTGAAGAAAA | 5 (5) | 3 (3) | 3' UT |
| 1072.20 | 1309 | TCACGAGATT (T/C) GCCAGGGGCA | 15 (10) | 2 (2) | 3' UT |
| .21 | 1310 | CACGAGATTT (G/T) CCAGGGGCAT | 4 (3) | 5 (5) | 3' UT |
| 1073.2 | 65 | GGCCCAGAGG (G/A) AATGGACCCC | 2 (1) | 2 (2) | Silent |
| 1074.18 | 1428 | TTGTGTGATT (T/C) CCTAAACATA | 5 (4) | 2 (2) | 3' UT |
| .21 | 1650 | TTGTCTTTTA (G/A) ACAACTAGAT | 6 (6) | 3 (3) | 3' UT |
| .22 | 1652 | GTCTTTTAGA (C/A) AACTAGATTT | 5 (5) | 3 (3) | 3' UT |
| 1077.19 | 1275 | TATAATAATT (G/T) TATGGTACCT | 3 (2) | 3 (3) | 3' UT |
| .22 | 1585 | ATGTACATAA (T/A) TTTGAGGTAG | 7 (5) | 3 (1) | 3' UT |
| .30 | 2336 | TCAGGCACCC (A/G) TAGAAGACC | 4 (3) | 10 (9) | 3' UT |
| .34 | 2460 | GAATTGGCCC (G/A) CTGGTACCAA | 5 (4) | 16 (14) | 3' UT |
| 1079.11 | 2035 | CTGCTGTAGT (T/C) GCTCCATTCA | 19 (14) | 2 (1) | Silent |
| .18 | 2347 | GCAACATCAC (A/G) TGGGCTGATG | 25 (17) | 2 (2) | Silent |
| 1080.24 | 2367 | TGCCTGAGGA (A/C) GGGCAGGGCC | 1 (1) | 5 (4) | 3' UT |
| 1081.17 | 805 | GATTGATAGA (G/A) AGAAACTGCG | 13 (8) | 2 (1) | Ser -> Lys |
| .36 | 1178 | ATGCATATTGTAAATAAA (A/G) A | 2 (2) | 10 (9) | 3' UT |
| 1082.19 | 767 | TTGGGGGCTT (C/T) CGCCGGCACC | 7 (5) | 2 (2) | Ser -> Phe |
| .27 | 924 | ACGTGGACGA (C/A) CCCACGGGGA | 3 (3) | 3 (3) | Asp -> Glu |
| .40 | 1333 | GTCTACAGAT (G/T) GGCTGTGGCC | 4 (4) | 5 (5) | 3' UT |
| 1088.11 | 112 | CCGAGGGGGA (C/T) GCGCTGGATG | 23 (16) | 7 (5) | Silent |
| .12 | 144 | AAGCGCTACT (G/C) CTGCCGCCGG | 24 (18) | 5 (4) | Cys -> Ser |
| .13 | 145 | AGCGCTACTG (C/G) TGCGGCCGGA | 21 (16) | 5 (4) | Cys -> Trp |
| .20 | 226 | GACCACGCTG (A/G) AACCCACCCA | 23 (16) | 18 (11) | 3' UT |
| .21 | 238 | ACCCACCCAC (C/A) CGCTGTGCTG | 31 (19) | 3 (3) | 3' UT |
| .24 | 270 | TGAGCGTCTT (A/G) CCCCGAATTC | 29 (18) | 9 (6) | 3' UT |
| .27 | 338 | GTGTGTATCC (C/G) ATACCCCACT | 23 (15) | 2 (2) | 3' UT |
| 1090.18 | 4153 | GTGTAAAATA (T/C) GCTGCTTGGA | 13 (12) | 2 (2) | 3' UT |
| .21 | 4215 | CTCACAGTAA (T/C) CTTCACTT | 21 (16) | 2 (1) | 3' UT |
| 1091.3 | 793 | AGGATCCCCC (A/G) CCGCCTATGG | 2 (1) | 5 (2) | Silent |
| .9 | 962 | CTTTCTTGTG (C/T) CCCTTCTGAG | 4 (3) | 5 (2) | Pro -> Ser |
| .14 | 2078 | AAGAGGTGCA (A/G) TGTGATCTGA | 6 (5) | 11 (8) | 3' UT |
| 1092.5 | 342 | CCTGGAGGCG (G/C) CCAACGGCGA | 16 (8) | 4 (1) | Ala -> Pro |
| .10 | 401 | GGCCTGGGCC (C/T) TCCCGCGACT | 9 (6) | 11 (5) | Silent |
| .11 | 503 | AGATCGACAA (C/T) GCCCGTCTGG | 11 (6) | 6 (5) | Silent |
| .22 | 1034 | TTGGAGCCCA (G/C) CTGGCGCATA | 4 (4) | 3 (2) | Gln -> His |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .23 | 1035 | TGGAGCCCGAG [C/G] TGGCGCATAT | 3 (3) | 3 (2) | Leu -> Val |
| 1093.2 | 258 | CTCTCACAGA [C/T] GAGATCAACT | 3 (2) | 2 (1) | Silent |
| .3 | 330 | CAGACACATC [T/C] GTGGTGCTGT | 3 (2) | 3 (2) | Silent |
| .4 | 339 | CTGTGGTGCT [G/A] TCCATGGACA | 3 (2) | 3 (2) | Silent |
| .6 | 420 | TTGCTCAGAG [A/G] AGCCGGGCTG | 3 (2) | 3 (2) | Silent |
| .22 | 954 | GCGTTGGAGG [T/C] GGCTTCAGTT | 7 (2) | 3 (1) | Val -> Ala |
| .23 | 960 | GAGGTGGCTT [C/T] AGTTCCAGCA | 7 (2) | 3 (1) | Silent |
| .24 | 972 | GTTCCAGCAG [T/C] GGCAGAGCCA | 7 (2) | 3 (1) | Silent |
| .27 | 983 | GGCAGAGCCA [T/C] TGGGGGTGGC | 7 (2) | 3 (1) | Ile -> Thr |
| .28 | 1065 | GGAAGAGCTA [T/C] AAGCACTAAA | 9 (3) | 3 (1) | Silent |
| .44 | 1198 | TAGAGCTGGG [G/T] ATGAATGCTT | 13 (2) | 3 (1) | 3' UT |
| .45 | 1202 | GCTGGGGATG [A/G] ATGCTTAGTG | 13 (2) | 4 (1) | 3' UT |
| .49 | 1579 | TGTGCTCTTC [A/G] CTCTTTGCAA | 14 (3) | 5 (2) | 3' UT |
| .50 | 1582 | GCTCTTCACT [C/G] TTTGCAATTG | 13 (3) | 6 (3) | 3' UT |
| 1094.24 | 3103 | TGCTTTTGCT [C/G] GCTTTGGCCA | 15 (9) | 4 (2) | 3' UT |
| .25 | 3104 | GCTTTTGCTC [G/C] CTTTGGCCAG | 2 (2) | 4 (2) | 3' UT |
| 1095.17 | 2885 | CGTAGGAAGG [G/C] CCTCAGTGAA | 18 (11) | 2 (2) | Silent |
| .25 | 2994 | GTGGACTCCT [G/T] GGAGCTCCTG | 14 (10) | 3 (3) | 3' UT |
| .31 | 3246 | GGGGATGAAA [C/A] CCCAAGGGGC | 10 (7) | 12 (11) | 3' UT |
| 1098.10 | 1486 | GGCAGTGGCC [G/C] CCCTGGGTGA | 8 (7) | 3 (3) | Ala -> Pro |
| .13 | 1522 | CACGTATGAG [G/C] ACATCCAGAC | 2 (1) | 12 (10) | Asp -> His |
| .21 | 1740 | TGCATTCTTT [T/C] GGAACCTCAAT | 11 (6) | 2 (2) | 3' UT |
| .25 | 1850 | GGAGGGCGGT [C/T] GGTGCTTCCC | 21 (13) | 2 (2) | 3' UT |
| .29 | 1942 | TGACCTATCA [A/G] AGCCTCCCGG | 16 (11) | 6 (5) | 3' UT |
| .35 | 2029 | CCAAGGAGCG [C/A] GCTCCACGCG | 13 (10) | 2 (2) | 3' UT |
| 1099.36 | 7590 | TGGTTTGAGA [G/C] CTGGCGCTAC | 12 (11) | 6 (4) | 3' UT |
| .37 | 7591 | GGTTTGAGAG [C/G] TGGCGCTACC | 9 (8) | 6 (4) | 3' UT |
| .44 | 7705 | ATGGATCTGA [C/T] CCCTGTCAGA | 13 (12) | 9 (8) | 3' UT |
| .01 | 215 | ATTCTCTAGT [C/T] CTTTCATGATG | 63 (36) | 9 (9) | Ile->Val |
| .02 | | Nucleotide repeat | 66 (35) | 6 (5) | 3' UT |
| 1100.16 | 3865 | ATTGGGTCTCT [C/G] AGCCTTCTGG | 4 (3) | 4 (3) | 3' UT |
| .17 | 3904 | GGACAAAGCC [T/C] TTTCATCTGA | 2 (2) | 4 (3) | 3' UT |
| .19 | 3994 | GGTGGAGTTC [T/C] TCCATGCAGG | 6 (6) | 6 (5) | 3' UT |
| .22 | 4046 | TATCCGAGGT [G/T] CTGCCGGGGC | 6 (6) | 5 (5) | 3' UT |
| 1102.29 | 1967 | TAACCTGGGT [T/G] TGAAAAAAT | 2 (1) | 25 (20) | 3' UT |
| .30 | 1982 | AAAAATAAAA [T/G] TCCTAAATTT | 2 (1) | 24 (20) | 3' UT |
| .31 | 1991 | AAAAATAAAATTCCTAAAT [T/C] T | 2 (1) | 21 (17) | 3' UT |
| 1105.15 | 2038 | GGGCCTGCCT [G/C] TGAGTGGTGC | 3 (3) | 6 (6) | 3' UT |
| 1109.4 | 884 | AGCTTGCCCTG [C/T] TTCAGCAAAA | 4 (4) | 2 (1) | 3' UT |
| 1110.11 | 6466 | CTGATGCAGA [T/C] TCTTGTCTTG | 5 (5) | 5 (5) | 3' UT |
| 1111.8 | 794 | AAGACGGCTA [T/C] GAGTTCCTTG | 2 (1) | 7 (6) | Silent |
| .15 | 1087 | CTGCCATGCT [G/T] GGGGGGGGTC | 8 (5) | 4 (4) | 3' UT |
| .16 | 1110 | CCCGACCCCT [A/C] AGGCCACCT | 3 (1) | 18 (17) | 3' UT |
| .17 | 1146 | GAGCCTTGGT [G/T] TATTTTCTT | 22 (18) | 4 (4) | 3' UT |
| 1114.18 | 540 | ATGCTACCTA [C/T] CGGGAAGGCA | 29 (16) | 2 (2) | Silent |
| .20 | 585 | TCAGTGCCAA [T/A] GCTCTCGCTT | 22 (15) | 6 (4) | Asn -> Lys |
| .21 | 586 | CACGCGCAAT [G/T] CTCTCGCTTT | 16 (12) | 6 (4) | Ala -> Ser |
| .27 | 704 | CCCAAAATCG [C/T] CGTTGCCACT | 20 (14) | 3 (3) | Ala -> Val |
| .01 | 177 | GAACAACCAC [T/C] GGGTCCTACA | 70 (36) | 2 (2) | Silent |
| .02 | 328 | ACTGAATGAG [C/G] CTCCACTGGT | 71 (36) | 1 (1) | Pro->Ala |

| | | | | | |
|--------|-----|-----------------------------|---------|---------|--------|
| .03 | 328 | GGCCGGAGGC (A/G) TTCACTCCAG | 30 (20) | 42 (32) | Silent |
| 1115.2 | 77 | ACTGCCGCAG (G/A) AATGCCGTCT | 13 (9) | 4 (1) | Silent |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .5 | 130 | CTTCCAAAGG [T/C] CCGGAAAAGT | 8 (7) | 14 (4) | Val -> Ala |
| .15 | 643 | TTCAACGACC [T/C] GGGCTCCGGA | 11 (8) | 2 (1) | Leu -> Pro |
| .16 | 732 | CAAGAAGGGG [A/C] CCAGGCTTGG | 12 (7) | 4 (2) | Thr -> Pro |
| 1116.2 | 121 | CGGACCGTCC [T/A] GACTACAGTT | 2 (1) | 4 (4) | Silent |
| .3 | 173 | CCGGGGAATG [A/C] AGCCACAGA | 2 (1) | 5 (5) | Lys -> Gln |
| 1117.1 | 15 | CCTGCAGCCC [T/C] GGCCTTCCGC | 10 (7) | 4 (3) | 5' UT |
| .2 | 16 | CTGCAGCCCT [G/T] GCCTTCCGCC | 10 (7) | 4 (3) | 5' UT |
| .5 | 19 | CAGCCCTGGC [C/T] TTCCGCCACC | 10 (7) | 2 (2) | 5' UT |
| .19 | 401 | TGGCAGCCTT [G/T] GCCAAGGCC | 12 (7) | 8 (4) | Leu -> Phe |
| .01 | 1287 | GCCATGCACT [C/G] ACCAACGCCA | 65 (36) | 7 (7) | Ser->Val |
| .02 | 3385 | TTGCCTGGAC [G/A] TTGCCTGCG | 70 (36) | 2 (2) | 3' UT |
| 1118.5 | 1681 | GACATGGTTG [G/A] TTATGCACAA | 6 (5) | 2 (1) | Val -> Asp |
| .28 | 2945 | ATGATTAAGG [A/G] CCAGAGGATC | 7 (6) | 7 (5) | 3' UT |
| 1119.11 | 1075 | TCACAAATTA [G/A] GCCACGGCCC | 3 (3) | 3 (3) | 3' UT |
| 1121.17 | 1524 | CATCCGTTGC [A/G] TATGGCTGCA | 3 (3) | 2 (2) | Silent |
| .23 | 1669 | TGCACGTCCT [G/C] CCAATATTGA | 6 (6) | 3 (3) | Ala -> Pro |
| .27 | 1902 | GACGACTGG [G/A] AAAATATTGA | 2 (2) | 20 (17) | Gly -> Glu |
| 1123.9 | 2485 | CCTGATATGA [A/C] TGTACTAAA | 5 (5) | 4 (4) | Asn -> Thr |
| .17 | 2807 | TTGACATAAC [T/C] ATCTTTTGA | 4 (3) | 3 (3) | 3' UT |
| 1124.2 | 119 | TCTTATCGGA [G/A] CTTGTATGTG | 2 (1) | 3 (3) | 5' UT |
| .7 | 3616 | TACTCCATAC [G/T] CACTTCAAGC | 2 (1) | 5 (3) | Ala -> Ser |
| 1127.2 | 4 | TGCAAAA [G/A] CGCAGGATCAAGG | 13 (8) | 2 (1) | Ala -> Thr |
| .15 | 75 | TCAACATCTG [T/C] GTTGGGGAGA | 22 (14) | 2 (1) | Silent |
| .34 | 339 | AGGAACACAT [T/C] GATCTGGGTA | 2 (2) | 31 (16) | Silent |
| 1128.9 | 483 | AAATAAAAAAAAA [A/C] AAAACCC | 4 (3) | 4 (3) | 3' UT |
| .10 | 484 | AAATAAAAAAAAA [A/T] AAACCC | 4 (3) | 4 (3) | 3' UT |
| 1130.7 | 248 | CCCCCTGCGG [G/T] TGAAGAACTT | 25 (12) | 9 (4) | Val -> Leu |
| .11 | 320 | GGAATACCGG [G/T] ACCTGACCAC | 26 (12) | 2 (1) | Asp -> Tyr |
| .13 | 364 | ACCGAGACAT [G/T] GGTGCCCGGC | 15 (10) | 3 (2) | Met -> Ile |
| .16 | 377 | TGCCCGGCAC [C/G] GCGCCCGAGC | 16 (8) | 4 (3) | Arg -> Ala |
| .19 | 421 | TGGAGGAGAT [C/T] GCGGTGAGCA | 12 (7) | 2 (1) | Silent |
| 1131.12 | 502 | TGGCTGACCA [G/A] GCTGAGGCC | 18 (13) | 2 (2) | Silent |
| 1133.20 | 279 | CTGAGTCTGC [C/T] ATGAAGAAGA | 41 (18) | 2 (1) | Silent |
| .35 | 517 | CCTAATTCTG [A/G] ATATATATAT | 19 (12) | 4 (2) | 3' UT |
| 1135.22 | 301 | AAAACAAGAC [T/G] GGGGCTGCTC | 38 (20) | 8 (4) | Silent |
| .23 | 343 | CGGGCTACTA [C/T] AAAGTTCTGG | 40 (18) | 4 (2) | Silent |
| .32 | 438 | AAGAGTGTG [G/A] GGGGGCTGT | 32 (18) | 2 (2) | Gly -> Ser |
| 1136.1 | 13 | CGCCGCTGCG [G/A] AGGGAGCCGC | 9 (9) | 10 (6) | 5' UT |
| .16 | 190 | GGAGCCGGCA [G/A] CCGACGGCAA | 31 (21) | 5 (4) | Ala -> Thr |
| .18 | 197 | GCAGCCGACG [G/C] CAAAGGTGTC | 32 (23) | 5 (5) | Silent |
| .19 | 198 | CAGCCGACGG [C/A] AAAGGTGTCG | 21 (16) | 8 (5) | Ala -> Glu |
| .23 | 243 | GCCAGCGGAA [G/C] CTGCCACCT | 31 (20) | 5 (5) | Lys -> Asn |
| .24 | 244 | CCAGCGGAAG [C/G] CTGCCACCTC | 31 (20) | 5 (5) | Pro -> Ala |
| .25 | 245 | CAGCGGAAGC [C/T] TGCCACCTCC | 31 (22) | 6 (3) | Pro -> Leu |
| .29 | 283 | CAACAAGAAT [G/C] CTCGCCAC | 26 (18) | 5 (5) | Ala -> Pro |
| .30 | 284 | AACAAGAATG [C/G] TCGGCCACG | 26 (18) | 5 (5) | Ala -> Val |
| .32 | 286 | CAAGAATGCT [C/T] GCGCCACGCT | 31 (22) | 2 (2) | Arg -> Cys |
| .41 | 387 | TCCTGCGCAC [G/C] CAGAAGCCTG | 2 (2) | 19 (14) | Silent |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1137.1 | 3 | CTTCCTTC [G/T] AGGAGGTGGCAG | 2 (2) | 3 (2) | 5' UT |
| .15 | 331 | GTGCCGAGAT [C/T] GCTCACAATG | 22 (12) | 4 (2) | Silent |
| .23 | 419 | CAATGCCAGG [C/G] TGC GCAGTGA | 13 (9) | 3 (2) | Leu -> Val |
| .25 | 488 | TAAAAACTGC [C/A] ATCTGGCATC | 8 (8) | 4 (4) | 3' UT |
| 1138.8 | 78 | AGGAGGAGCT [G/T] CTGAAACAGC | 30 (17) | 2 (2) | Silent |
| .14 | 127 | GCTGCGCGTC [G/A] CCAAAGTGAC | 31 (15) | 2 (2) | Ala -> Thr |
| .24 | 354 | AGCAGCAGCG [G/T] AAGGAGCGGC | 28 (16) | 2 (2) | Silent |
| 1139.21 | 334 | TTCCGAAGCA [A/G] TCTTCTGTCT | 33 (20) | 3 (1) | Asn -> Ser |
| 1140.3 | 17 | CCGCTGCTCG [C/A] CATGTCTTCT | 22 (15) | 3 (2) | 5' UT |
| .20 | 341 | AATATGTAAG [G/A] CCTTCTTTT | 32 (16) | 2 (2) | 3' UT |
| 1141.5 | 201 | ATCAGACTAG [A/T] GCTGAGTCTT | 2 (1) | 11 (5) | Arg -> Ser |
| .7 | 346 | GCGCCGTGG [C/A] ATCGTAGAGT | 4 (3) | 3 (2) | His -> Asn |
| .18 | 1071 | GGATAAGGCA [G/A] CTGCTGCAGC | 5 (4) | 6 (3) | Silent |
| .21 | 1376 | TGTTATACAGGCAGTGA [G/A] AAA | 14 (10) | 5 (4) | 3' UT |
| 1142.13 | 556 | CTTGTGACTG [A/G] CCTCTGGTCC | 8 (7) | 3 (3) | Asp -> Ala |
| 1143.17 | 470 | ATCTACAAGC [G/T] TGGTTATGGC | 32 (20) | 2 (2) | Arg -> Leu |
| 1144.1 | 211 | GCCGCGGCGC [G/C] CCCCTGCGCA | 7 (5) | 4 (4) | Silent |
| .5 | 286 | CCGCCGAGGG [C/A] ATTCACACGG | 11 (9) | 5 (4) | Ala -> Glu |
| .6 | 287 | CGCCGAGGGC [A/T] TTCACACGGG | 15 (13) | 4 (3) | Ile -> Phe |
| .17 | 494 | TGTGAAGCTG [C/T] CCTCCGGCTC | 9 (8) | 2 (2) | Pro -> Ser |
| .26 | 700 | ACCAGCACAT [C/T] GGCAAGCCCT | 24 (18) | 2 (2) | Silent |
| 1145.18 | 395 | GTGAAAAATA [C/T] ATCCGCAGGG | 21 (14) | 7 (7) | Silent |
| .20 | 405 | CATCCGCAGG [G/T] TTCGGATGAG | 27 (20) | 2 (2) | Val -> Phe |
| 1146.16 | 276 | TGTTTGCAAA [G/T] GCCCTGGCCA | 16 (12) | 3 (3) | Lys -> Asn |
| .18 | 285 | AGGCCCTGGC [C/A] AACGTCAACA | 13 (10) | 5 (5) | Silent |
| .22 | 340 | ACCTGCTCCA [G/C] CAGCTGGTGC | 16 (12) | 3 (3) | Ala -> Pro |
| .23 | 341 | CCTGCTCCAG [C/G] AGCTGGTGTCT | 15 (12) | 3 (3) | Ala -> Glu |
| .25 | 343 | TGCTCCAGCA [G/A] CTGGTGCTGC | 17 (12) | 2 (2) | Ala -> Thr |
| 1147.22 | 324 | GAGACTGGCA [G/A] GCCTCGGCCCT | 7 (5) | 3 (3) | Arg -> Lys |
| 1148.29 | 390 | TCGGTGACAT [C/T] GTCACAGTGG | 33 (17) | 3 (2) | Silent |
| 1149.14 | 174 | GAACCGGGGC [C/G] TGCGGCGGAA | 14 (12) | 3 (2) | Leu -> Val |
| .22 | 414 | CGTAAAGCAT [G/T] GCCGGCCCCG | 23 (20) | 4 (3) | Ala -> Cys |
| 1150.20 | 257 | CTCAAAGACC [T/C] GGAAAAATGG | 42 (19) | 2 (1) | Leu -> Pro |
| .34 | 435 | CCTCATGGAC [T/A] AAAAAAAAAA | 7 (6) | 4 (3) | 3' UT |
| 1151.13 | 312 | TCCAAAGCCC [T/C] GGTGGCCTAT | 33 (16) | 6 (1) | Leu -> Pro |
| .14 | 313 | CCAAAGCCCT [G/T] GTGGCCTATT | 33 (16) | 6 (1) | Silent |
| .16 | 346 | TGGATGAGGC [T/C] TCCAAGAAGG | 34 (16) | 2 (1) | Silent |
| .22 | 439 | AGTTTGGAGG [C/T] CCTGGTGCCC | 20 (14) | 6 (4) | Ala -> Val |
| .25 | 517 | TAATAAACAG [T/A] TTTTGAGGGA | 23 (15) | 3 (1) | 3' UT |
| 1152.15 | 131 | GCGCGTGTGC [G/A] AGGAGATCGC | 34 (18) | 3 (2) | Ser -> Lys |
| .19 | 160 | CCAGCAAAAA [G/C] CTCGCAACA | 31 (18) | 6 (4) | Lys -> Asn |
| .20 | 161 | CAGCAAAAAG [C/G] TCCGCAACAA | 29 (16) | 5 (3) | Leu -> Val |
| .24 | 184 | TAGCAGGTTA [C/T] GTCACGCATC | 20 (9) | 22 (15) | Silent |
| .31 | 379 | CCAACCTTCA [G/A] GTCACCTCAGC | 36 (23) | 2 (2) | Silent |
| 1154.8 | 119 | GGGCACAGCC [C/T] TAAAGGCCAA | 17 (9) | 3 (2) | Silent |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|--------------|-------|-----------------------------------|--------------------|--------------------|-------------------|
| .39 | 477 | TAGTAATAAA [T/C] TTTCATATGC | 21 (15) | 2 (2) | 3' UT |
| 1155.6 | 64 | TATTCTCCGA [G/C] CTCGCAATG | 29 (19) | 3 (3) | 5' UT |
| .7 | 65 | ATTCTCCGAG [C/G] TTCGCAATGC | 25 (17) | 3 (3) | 5' UT |
| 1157.3 | 75 | TGGGCAGGAC [C/G] GGTTCTCAGG | 18 (11) | 3 (3) | Silent |
| .12 | 290 | GTCTGTCA [A/G] TCTGCTCCTT | 28 (12) | 11 (7) | 3' UT |
| 1158.4 | 55 | CGAAAATTTCG [G/A] CCAGGGTTCT | 36 (20) | 2 (1) | Ala -> Asp |
| 1159.2 | 68 | AGCACCAGCG [G/T] TGGCAGAGAC | 24 (14) | 2 (1) | Val -> Leu |
| .7 | 199 | ACAGTGCAGG [G/A] CGGTATGCCG | 16 (10) | 5 (3) | Gly -> Glu |
| 1160.10 | 124 | TCAGGGAGCT [G/A] AATATTACGG | 28 (18) | 2 (1) | Glu -> Lys |
| .15 | 166 | GTGGTGGTCG [G/A] AAAGCTATCA | 28 (17) | 2 (2) | Glu -> Lys |
| .17 | 229 | TCCAAGTCCG [C/G] CTAGTACGCG | 2 (2) | 29 (19) | Pro -> Ala |
| 1161.8 | 263 | AAGGCAACGC [C/T] CTGCTGCGGC | 30 (16) | 2 (2) | Silent |
| .9 | 264 | AGGCAACGCC [C/T] TGCTGCGGCG | 22 (14) | 9 (9) | Silent |
| .11 | 283 | CGGCTGGTCC [G/C] ATTGGGGGTG | 13 (9) | 4 (4) | Arg -> Pro |
| 1163.8 | 1522 | GTACTTCCTC [G/T] TCCTCATGCC | 2 (2) | 5 (1) | Arg -> Leu |
| 1165.1 | 97 | CCACGACCGT [G/C] GCTATCTGGT | 3 (3) | 2 (2) | Ala -> Arg |
| .4 | 180 | GTGAGGGGCG [G/T] CCGCGGCGCA | 4 (3) | 4 (2) | Silent |
| .7 | 273 | CCAAGGTGGG [C/A] ATCAAGACCA | 10 (7) | 4 (3) | Ala -> Glu |
| .8 | 274 | CAAGGTGGG [A/T] TCAAGACCAT | 20 (12) | 3 (2) | Ile -> Phe |
| .13 | 429 | AGCAGGAGCT [G/C] CTCATCAACA | 8 (7) | 5 (4) | Silent |
| .14 | 430 | GCAGGAGCTG [C/T] TCATCAACAT | 5 (5) | 8 (5) | Leu -> Phe |
| .29 | 901 | CCCCCAGAGG [G/A] AGGTCACCTG | 13 (10) | 4 (3) | 3' UT |
| .35 | 1007 | GCTTCCTCCT [G/T] GGCCCTCAAT | 6 (5) | 4 (4) | 3' UT |
| .38 | 1189 | GATGTTTTGA [C/G] GAAATAAATT | 2 (2) | 7 (6) | 3' UT |
| 1170.2 | 410 | ATTGCGAATC [G/C] TTAGATATCC | 2 (2) | 2 (2) | Val -> Leu |
| 1171.27 | 2823 | AAGAGATGAA [A/T] AAAAAAAAAA | 8 (6) | 4 (4) | 3' UT |
| 1172.15 | 1519 | CTCTAGTGTT [G/C] AGGGATGTAG | 7 (7) | 2 (1) | 3' UT |
| .19 | 1784 | CAGGTCTTAA [T/C] GCCTCCATAC | 3 (3) | 2 (2) | 3' UT |
| .25 | 2423 | GAGAGACTGG [T/A] GGGTCTGTCT | 7 (6) | 5 (4) | 3' UT |
| 1173.12 | 4730 | AGTAGGTAGG [G/T] CTAGTAGGTA | 6 (6) | 2 (1) | 3' UT |
| .01 | 981 | GCAGCCCCAG [T/C] GCACCTGAGC | 24 (18) | 48 (30) | Silent |
| .02 | 1041 | ACATCAAGAG [A/G] TACCTGGGCG | 71 (36) | 1 (1) | Silent |
| .03 | 2400 | AGCTGAGTGC [C/T] GCCACCACCT | 71 (36) | 1 (1) | Silent |
| .04 | | 4 bp deletion | | | |
| .05 | 2567 | CTAGATAGCA [A/G] ATAGCTCTCA | 71 (36) | 1 (1) | 3' UT |
| .06 | 2888 | CCCAAGCTGC [C/T] TCATGGCCCCG | 63 (36) | 9 (9) | 3' UT |
| 1174.24 | 3200 | TGTTGACAGG [G/C] TTTTAAAGAA | 10 (8) | 2 (2) | 3' UT |
| .27 | 3302 | TCTGCCCAAGC [A/C] AAAAAAAAAA | 5 (3) | 3 (2) | 3' UT |
| 1176.13 | 2571 | GAGGCTTTGC [C/T] TTGCCTGCAT | 6 (4) | 3 (3) | 3' UT |
| 1177.18 | 1684 | CTCTTCCCCC [T/C] AAAAAATGGTA | 13 (10) | 3 (3) | 3' UT |
| .21 | 1864 | GTTAGCTTTA [A/G] AAAAAAAAAA | 5 (5) | 3 (3) | 3' UT |
| 1181.8 | 678 | TACCAAAGCA [G/A] GGTTTCCCCA | 10 (7) | 2 (2) | Arg -> Lys |
| 1183.18 | 1719 | CTTCCTGCTC [G/A] ACTGAAAAAA | 14 (9) | 2 (1) | 3' UT |
| .21 | 1799 | TGGCTTTCAG [G/C] CCTGGCCTTT | 15 (10) | 5 (4) | 3' UT |

| | | | | | |
|---------|------|------------------------------|---------|--------|-------|
| 1184.14 | 2292 | GCCTAAATGT [G/T] TGAAGTGC GA | 30 (18) | 2 (2) | 3' UT |
| ----- | | | | | |
| 1186.7 | 1337 | GGGAGAGGTG [A/G] CCCTGAGGGA | 2 (1) | 4 (3) | 3' UT |
| ----- | | | | | |
| 1188.7 | 1601 | AGTCATCTGA [G/A] GTTATGCTTT | 4 (3) | 2 (1) | 3' UT |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1189.13 | 1270 | CGGAAAGGAA [G/A] CGTTGGCAGC | 11 (9) | 3 (2) | 3' UT |
| .16 | 1341 | AGCCCCAGGG [A/G] CCAATTTTCC | 14 (12) | 2 (1) | 3' UT |
| 1190.5 | 1010 | GGGGTTGGGC [G/T] GGTTCCTTTG | 2 (2) | 3 (3) | 3' UT |
| 1193.1 | 79 | CTCTCCCCTC [C/G] AATCCTATCC | 5 (5) | 2 (2) | 5' UT |
| 1196.23 | 2123 | TATGTTTTCC [T/C] ATGCAATAGT | 19 (14) | 2 (2) | 3' UT |
| 1198.29 | 2395 | TGGCAAAGTC [T/C] GAAATAGGTC | 20 (15) | 4 (2) | 3' UT |
| 1199.3 | 1012 | AGATTCAGAA [C/T] ATGGTGGGGA | 3 (2) | 2 (2) | Silent |
| .13 | 1460 | TGAGAACACC [G/C] CGCAGCGTGA | 8 (7) | 2 (2) | 3' UT |
| 1202.7 | 671 | ACCATAACTT [T/C] TTTTAAAGGA | 13 (7) | 11 (6) | 3' UT |
| 1205.1 | 942 | GGAGAAAATT [G/A] AAGAATATCT | 13 (6) | 2 (1) | Glu -> Lys |
| 1206.3 | 740 | ACATCACAAA [A/G] CAACCTGTGG | 3 (3) | 2 (1) | Silent |
| 1208.3 | 1984 | TATTCCGTAC [G/A] TACAATGCCT | 2 (1) | 2 (2) | Silent |
| .15 | 3163 | AATTTTTTTT [T/C] TTTTAAATTA | 2 (1) | 15 (6) | 3' UT |
| 1214.9 | 1566 | GCATCCTGGA [C/T] AGCAACAAGA | 5 (3) | 2 (2) | Silent |
| 1216.8 | 202 | AGCGGAGCGC [C/G] TCCCGGACAC | 5 (4) | 3 (2) | Silent |
| 1217.3 | 2545 | GCCTCTCGGC [C/T] TTTCTCCACG | 5 (3) | 2 (1) | Silent |
| .5 | 2688 | GCCGTGTGCC [C/A] ATGCTACCCT | 12 (6) | 3 (3) | 3' UT |
| 1218.10 | 2757 | GCAGGCTGCC [C/T] TTTAGAGAGG | 4 (2) | 2 (1) | Silent |
| .01 | 1100 | GATGTCAGTG [G/C] CCCCATGCCC | 71 (36) | 1 (1) | Gly->Ser |
| .02 | 1287 | GCCATGCACT [C/G] ACCAACGCCA | 71 (36) | 1 (1) | Silent |
| .03 | 3385 | TTGCCTGGAC [G/A] TTGGCCTGCG | 71 (36) | 1 (1) | Silent |
| 1221.20 | 1893 | TGGAGCCTTC [G/T] GCTGGAAGTC | 9 (7) | 3 (2) | 3' UT |
| 1222.30 | 2797 | CACAAACCCA [A/G] TTGTAATAAA | 14 (11) | 2 (1) | 3' UT |
| 1223.3 | 2813 | AAGCAGGAGG [C/T] TAAGAAAGTG | 13 (10) | 2 (1) | N/D |
| .9 | 3662 | GGACCGCAGT [C/T] CAGCATTGT | 2 (2) | 2 (1) | N/D |
| .10 | 3727 | TAAACTGAAG [T/A] GTGTTTTTCC | 4 (4) | 3 (2) | N/D |
| .15 | 3855 | ACGTCCCAAC [G/A] AAGAGACCAC | 24 (19) | 2 (2) | N/D |
| .16 | 4110 | CACCTTGGTG [G/A] AGAACAAAGAA | 20 (17) | 2 (2) | N/D |
| .20 | 4155 | CGACGTGGAT [C/T] CCATCGAGGT | 21 (17) | 2 (2) | N/D |
| 1224.13 | 1739 | GCAGAGCCAC [C/A] AGGGAAAAGT | 2 (2) | 2 (2) | 3' UT |
| .17 | 1936 | CCTCTTCTAA [T/C] CTCAAGGTC | 3 (2) | 8 (7) | 3' UT |
| .21 | 2061 | GCGAGTGAGT [G/T] GAGAGCCAGC | 15 (11) | 17 (13) | 3' UT |
| .22 | 2079 | AGCTCTGCGG [A/G] GTCATCACGC | 15 (11) | 17 (13) | 3' UT |
| 1227.9 | 1107 | AGAAGGTGAA [C/A] CCCCTGGGGG | 9 (6) | 4 (3) | Asn -> Lys |
| .16 | 1207 | TGGGAAGAGG [G/C] CATACGAGT | 20 (14) | 2 (2) | Ala -> Pro |
| 1229.18 | 1919 | ACTCCGTGCG [C/T] AATGCCGTCA | 4 (3) | 2 (1) | Silent |
| 1235.11 | 1194 | TAGCCGCCAG [G/A] ATTGCCATGA | 18 (12) | 2 (2) | Asp -> Asn |
| 1238.14 | 1133 | AGAACCTGAA [G/A] GCTGCGCAGG | 6 (4) | 2 (2) | Silent |
| .17 | 1298 | AACAACCTCA [G/A] GCCCTGCCCC | 8 (6) | 2 (1) | 3' UT |
| 1239.13 | 1289 | ACTTTTCCTC [T/C] AATCCTGGAA | 11 (5) | 7 (4) | 3' UT |

.14 1292 TTTCCTCTAA (T/C) CCTGGAAATT 16 (7) 2' (-2) 3'-UT

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1241.13 | 1802 | AATTAAAGTTTTTCTTC [C/T] ATG | 10 (7) | 2 (2) | 3' UT |
| 1242.18 | 3296 | TCCTGTGACA [T/C] GTGCAGCAGG | 13 (11) | 2 (2) | 3' UT |
| .20 | 3328 | AGCGGGCATC [G/T] CTGCCGCCAT | 7 (7) | 3 (3) | 3' UT |
| 1243.5 | 134 | GAACGCAGTG [G/A] ATGCCTTTCG | 4 (4) | 3 (3) | Asp -> Asn |
| .6 | 184 | TGCGCAGCCC [C/G] GTCACCAACA | 7 (7) | 3 (2) | Silent |
| .7 | 185 | GCGCAGCCCC [G/T] TCACCAACAT | 7 (7) | 4 (2) | Val -> Phe |
| .24 | 1528 | CGGTGGAGCA [G/A] CCCCTGGGCT | 10 (8) | 3 (2) | 3' UT |
| .31 | 1789 | TACACGTGTT [G/A] CTTGCTCCAG | 14 (9) | 2 (2) | 3' UT |
| .32 | 1790 | ACACGTGTTG [C/A] TTCGTCCAGT | 16 (9) | 8 (7) | 3' UT |
| 1246.6 | 1512 | ATCCCGGAGG [G/T] TCACTCTGAA | 2 (2) | 2 (1) | Val -> Phe |
| .9 | 1958 | ACGTTTAAAC [A/G] TAGTAAATCC | 3 (3) | 6 (6) | 3' UT |
| 1247.6 | 517 | GCGGACAGTA [C/T] ATTGCCATTG | 2 (2) | 2 (2) | Silent |
| 1248.4 | 164 | TGATGTCCCC [C/T] TCGACCCGT | 4 (3) | 2 (2) | Silent |
| .5 | 172 | CCCTTCGACC [C/A] GTCGGGTTTG | 2 (1) | 3 (3) | Pro -> Gln |
| .11 | 815 | AGCACAGCCC [C/T] TCTACCAGGG | 13 (7) | 2 (2) | Silent |
| 1249.1 | 50 | ACCGCCTGCG [G/A] AGTAAC TGCA | 4 (3) | 2 (2) | 5' UT |
| .26 | 1800 | TTGTAAGG [G/T] TTACTCTCAT | 26 (16) | 2 (1) | 3' UT |
| 1250.1 | 353 | GCCCCGCCAG [G/A] ATTAACACAG | 3 (2) | 2 (2) | Silent |
| 1251.11 | 1070 | CCGCCAACGG [C/A] AACATCGACC | 2 (1) | 4 (2) | Ala -> Glu |
| .18 | 1974 | CTGGGAAATG [C/A] GGGACTGGAA | 2 (1) | 2 (2) | 3' UT |
| 1253.7 | 673 | GCCAGGTGGT [G/C] CAGATCCCTG | 2 (2) | 2 (1) | Silent |
| .11 | 1620 | GCCTATGTCG [G/A] CGACGTCCAC | 2 (2) | 2 (1) | Ala -> Asp |
| .13 | 1672 | ACACCAAGAC [C/T] ATGGAGCTGC | 2 (2) | 2 (1) | Silent |
| .16 | 3427 | TCGACCACGC [G/A] GAGCGGGAGC | 2 (2) | 2 (1) | Silent |
| .21 | 3848 | GACCCCGCTG [C/T] CACCCGCTTT | 2 (2) | 2 (1) | 3' UT |
| 1255.11 | 895 | TCAAATGAAT [C/G] AACCACCTGG | 2 (2) | 2 (1) | Gln -> Glu |
| .23 | 1729 | TCATTTTCT [A/G] TATAGGCTGC | 2 (2) | 17 (8) | 3' UT |
| .24 | 1731 | ATTTTCTAT [A/G] TAGGCTGCAC | 2 (2) | 17 (8) | 3' UT |
| .27 | 1801 | TTTCCAATAAATC [G/A] GAATTC | 3 (2) | 3 (3) | 3' UT |
| 1257.11 | 674 | AACAAGAACA [C/T] ATGATAAATT | 9 (6) | 2 (1) | Silent |
| .19 | 954 | GTGAGAGAAC [G/C] AAATCTCTAT | 21 (14) | 3 (2) | 3' UT |
| .20 | 955 | TGAGAGAACG [A/C] AATCTCTATC | 19 (14) | 3 (2) | 3' UT |
| 1258.11 | 329 | ATCACAGCAA [A/G] AGAGAGGTTT | 22 (9) | 4 (1) | Lys -> Arg |
| .15 | 357 | TCCTACCAA [C/T] CTGATCAATT | 24 (10) | 6 (3) | Silent |
| .17 | 422 | TCTGCCCTTT [C/T] TACCATGATG | 25 (11) | 2 (1) | Ser -> Phe |
| .20 | 533 | AGCTTCCTAA [G/A] TCAAGGCCAA | 27 (13) | 2 (1) | Ser -> Asn |
| .32 | 745 | GCTTCCAGAA [C/G] AGATCAAAAA | 17 (10) | 2 (1) | 3' UT |
| 1261.6 | 425 | CTGGCATCAT [C/T] GCCATCTACG | 9 (3) | 2 (1) | Silent |
| .20 | 908 | CGCCCCCTCCA [G/A] GCCCCCGGCG | 8 (3) | 3 (3) | 3' UT |
| 1265.1 | 46 | ACTCGAGCCT [G/A] CTGTTACCCG | 3 (2) | 2 (1) | 5' UT |
| .19 | 1023 | GGAGGGGGCA [A/G] ATGGTGGTTG | 2 (1) | 20 (7) | 3' UT |
| 1266.1 | 343 | CGCTGCGGAC [G/A] AAAAGGCCAA | 2 (2) | 3 (2) | Glu -> Lys |
| .7 | 661 | AGCAGGTGAA [G/A] GGCATCGCTG | 7 (6) | 4 (3) | 3' UT |
| .9 | 671 | GGGCATCGCT [G/T] CCCCAGGCCT | 10 (9) | 4 (3) | 3' UT |
| .16 | 865 | GTAGAGCACA [G/A] GGGTTTCCCC | 25 (12) | 2 (2) | 3' UT |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1267.11 | 1776 | GGCTAGAGGA [T/C] GCACGGTGGC | 2 (2) | 7 (5) | 3' UT |
| 1268.10 | 6529 | TTCATCCTCA [C/T] TCCCCACATC | 10 (6) | 2 (2) | Thr -> Ile |
| 1269.19 | 1893 | CAACTTCAAC [C/G] TGGAGGTGCA | 12 (4) | 3 (3) | 3' UT |
| .20 | 1941 | TAAAAAGGTG [A/G] CTGTTTATA | 12 (4) | 4 (4) | 3' UT |
| 1270.11 | 331 | TTGTCCTCAG [T/C] ACCTCTCCGT | 11 (9) | 2 (2) | 5' UT |
| 1271.14 | 949 | GGGTGTATTA [T/C] CCAGTACTC | 18 (11) | 5 (1) | 3' UT |
| 1272.10 | 2678 | TGTTAAGGAA [C/T] GCTAGCAGGG | 3 (1) | 3 (1) | 3' UT |
| 1273.13 | 3127 | AAAGGAAGTT [T/C] TCCTTTTGAA | 7 (2) | 10 (3) | 3' UT |
| 1274.16 | 2696 | ATATTTTTC [A/G] TAATCTATAT | 7 (6) | 3 (2) | 3' UT |
| 1278.7 | 864 | AGTGTGACCC [G/A] GACTGCCTCC | 3 (1) | 2 (2) | Silent |
| .32 | 3897 | CCAGAACACG [G/C] CTCACGCTTA | 5 (3) | 3 (3) | 3' UT |
| .33 | 3898 | CAGAACACGG [C/G] TCACGCTTAC | 4 (3) | 4 (4) | 3' UT |
| .34 | 4013 | TGTTGTGTGT [A/G] TCGAGAGGCC | 10 (7) | 3 (2) | 3' UT |
| 1280.5 | 1648 | TTAAGAGGAC [G/A] TAATGGGGTTC | 14 (8) | 4 (3) | 3' UT |
| .15 | 1957 | TAAAGATGATTGTGG [G/A] AATTC | 2 (2) | 9 (8) | 3' UT |
| 1282.1 | 2155 | TTTGGTGGGC [C/T] TACTTGGTGC | 7 (3) | 6 (1) | 3' UT |
| .2 | 2283 | GTGTGGCGTA [G/C] GCAGTGGGTC | 13 (1) | 2 (2) | 3' UT |
| .9 | 2799 | TTACATCACC [G/A] CCACTACTGC | 6 (3) | 2 (2) | 3' UT |
| .10 | 2824 | CAGTGCCCG [T/C] GGCGCATGC | 4 (1) | 3 (3) | 3' UT |
| .15 | 2937 | TGGTTTGTGTT [G/C] CCTGACACAG | 11 (4) | 3 (1) | 3' UT |
| 1284.1 | 249 | CTGTCGACGA [T/C] CCCTACGCCA | 7 (7) | 4 (3) | Silent |
| .6 | 522 | GGGGCAGTGC [G/C] GTCATCTCCC | 5 (1) | 5 (4) | Silent |
| .7 | 523 | GGGCAGTGGC [G/T] TCATCTCCCT | 7 (4) | 4 (1) | Val -> Phe |
| .10 | 608 | GCCCTTGGGG [G/T] TTGCAGGCTG | 8 (7) | 2 (1) | 3' UT |
| .20 | 651 | GGGCTGGGGG [G/A] ATCCCAGCAG | 8 (8) | 2 (2) | 3' UT |
| 1286.20 | 5366 | GGCCATTGCC [G/A] CAGTCGCAGC | 12 (11) | 2 (2) | 3' UT |
| 1287.10 | 864 | AGGGATGTTAGACGGAATT [C/G] C | 2 (2) | 4 (3) | 3' UT |
| 1289.15 | 885 | ATCATGTGGA [G/A] GGGCCAGAGG | 13 (9) | 2 (1) | 3' UT |
| .22 | 1006 | GGCATTCCAG [C/G] TGAGACACTG | 21 (10) | 5 (2) | 3' UT |
| 1290.7 | 929 | CCCTCACCCC [A/G] TCACGCCTCG | 3 (1) | 2 (2) | 3' UT |
| 1291.5 | 1060 | TCAACAAAA [G/A] GGACAGGTAC | 2 (1) | 2 (1) | Silent |
| .8 | 2168 | TAAGTACCAC [G/A] AGCAGCTGGG | 2 (1) | 2 (1) | Ser -> Lys |
| .12 | 4517 | GCTGACAGAG [G/A] AGGAGGACTA | 5 (2) | 2 (1) | Ser -> Lys |
| .13 | 5114 | CCAGCCTCCA [G/A] TGTACAACTT | 4 (1) | 2 (1) | 3' UT |
| 1292.11 | 3547 | AGGCAAATTC [A/G] ATTTGAACAT | 7 (3) | 5 (3) | 3' UT |
| .20 | 3888 | TGTGTGTGTG [T/G] GCTGTGCTT | 11 (9) | 3 (3) | 3' UT |
| .21 | 3889 | GTGTGTGTGT [G/T] CTGTCGCTTG | 11 (9) | 4 (3) | 3' UT |
| 1293.10 | 2480 | CATGCCTGTG [C/G] GTGCGCTTCC | 2 (2) | 3 (2) | 3' UT |
| .11 | 2481 | ATGCCTGTGC [G/C] TGCCTTCCT | 4 (4) | 2 (1) | 3' UT |
| 1298.20 | 960 | TTCAGTGGGC [T/C] TTTCTGGCAG | 12 (8) | 2 (1) | Leu -> Pro |
| 1300.7 | 566 | AAGTGACCT [T/G] GAATTCCTTG | 2 (2) | 4 (2) | N/D |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1301.12 | 668 | CGCCCGGCTG [G/C] GCAAGGAGAT | 9 (5) | 3 (1) | Ala -> Arg |
| .30 | 1058 | CAAGGTCTAT [G/C] CTGACGCCTC | 16 (7) | 3 (2) | Ala -> Pro |
| .31 | 1059 | AAGGTCTATG [C/G] TGACGCCTCC | 13 (6) | 3 (2) | Ala -> Val |
| 1302.7 | 759 | ACAGGCCACA [T/G] CTGGACCATC | 2 (2) | 5 (5) | Ser -> Ala |
| .8 | 806 | TATCAACTCC [C/T] GGACAACCCA | 2 (2) | 4 (4) | Silent |
| .10 | 866 | TTCGAAGAGT [T/C] ATTGCCAAGA | 4 (4) | 2 (2) | Silent |
| .17 | 2000 | GAATTTAATA [G/T] GTACAGAAGT | 5 (5) | 4 (4) | 3' UT |
| .19 | 2158 | ACTTCTAAAG [C/A] AAGAGGATAA | 8 (7) | 9 (9) | 3' UT |
| 1303.5 | 1226 | TGCTGTGCAC [A/G] TTGACTACAA | 6 (5) | 2 (2) | Ile -> Val |
| .15 | 1624 | GATTATATAT [T/A] TTTTCTCTG | 7 (5) | 3 (3) | 3' UT |
| .21 | 1813 | GTGCACTAAT [A/G] TGTAAGACAA | 9 (6) | 3 (3) | 3' UT |
| .22 | 1920 | TTAAATAGCT [C/T] TTTTCTCTGA | 2 (1) | 14 (8) | 3' UT |
| .23 | 2079 | TCTATAAACC [A/G] AACTGATGTA | 2 (1) | 16 (9) | 3' UT |
| 1305.12 | 1434 | AATAAACTATAGTAGTGTT [T/A] T | 8 (8) | 5 (4) | 3' UT |
| 1306.14 | 407 | TTTGATATTG [C/T] CTCTGGAACCT | 2 (2) | 4 (4) | Ala -> Val |
| .21 | 1021 | TTTTTTTGCA [A/T] AAAACTAAAT | 2 (2) | 4 (3) | 3' UT |
| 1309.4 | 466 | GCGGGCCGCC [T/C] GCTCTGGAG | 5 (5) | 2 (1) | Leu -> Pro |
| .5 | 494 | AGGAGTATGC [G/A] GCTCGGGCCC | 4 (3) | 3 (3) | Silent |
| 1312.10 | 492 | ACCCCTGGGG [G/A] AGTGCATCAT | 7 (6) | 3 (3) | Ser -> Lys |
| 1315.13 | 339 | AAGTTCCTCA [C/A] GCCCTGCTAT | 13 (10) | 2 (2) | Thr -> Lys |
| .22 | 766 | TCCTTTTTTA [A/G] AAAAAA | 8 (7) | 3 (3) | 3' UT |
| 1317.4 | 1083 | GATAGATTAT [G/A] TATTCTTCCA | 3 (3) | 4 (3) | N/D |
| 1318.2 | 183 | GGGAGCCTGC [C/A] AGGGTCCGCT | 12 (11) | 3 (3) | Silent |
| 1322.12 | 876 | TGACTCCACA [G/A] CCTCAGCCGA | 23 (14) | 5 (5) | Ala -> Thr |
| 1326.5 | 139 | GGCCTGGAAA [C/T] TTGCACAGTC | 5 (5) | 3 (1) | Leu -> Phe |
| .12 | 1339 | TAGGAAAGAC [G/A] TCGGCTTTCCG | 5 (2) | 3 (3) | Val -> Ile |
| .17 | 2214 | TCCCCAGGGT [T/C] TTCTCATGGT | 2 (2) | 5 (3) | Silent |
| .19 | 2333 | ATTCTGAGGG [A/G] TATCCAGCAG | 4 (4) | 4 (2) | Asp -> Val |
| 1328.5 | 2968 | CCTAAAAGTG [T/G] TTTTATTTC | 6 (4) | 4 (4) | 3' UT |
| 1330.13 | 1526 | TTGATCATGA [G/A] ACATAGGTAT | 6 (3) | 2 (1) | 3' UT |
| 1331.15 | 1666 | ACAAGCACAC [C/G] TTAGAGGCTT | 2 (2) | 10 (4) | 3' UT |
| .24 | 2009 | CTGCTGATGC [C/T] GTACCCCTCAC | 13 (7) | 2 (2) | 3' UT |
| 1332.5 | 618 | AGCTGAACCC [G/C] GAGTCTCTCC | 2 (1) | 2 (1) | Silent |
| 1333.4 | 89 | GAGCACAGCG [G/A] CATCTTTGGC | 7 (5) | 2 (2) | Ala -> Asp |
| .10 | 279 | CGGTGCAGGC [C/A] ATGAACCGCA | 5 (5) | 6 (5) | Silent |
| .24 | 756 | TGACCCCGA [C/A] CCAGCCTCGC | 6 (6) | 7 (6) | 3' UT |
| 1335.1 | 331 | AGGGCTGGCC [C/T] TTGGAAGGCG | 4 (4) | 2 (2) | 5' UT |
| .13 | 872 | AGCCAAGCCG [G/T] TCAAGGCATC | 7 (6) | 2 (1) | Val -> Phe |
| .28 | 2268 | GGAAAAGGGA [G/A] AACTGAGCG | 6 (6) | 2 (2) | 3' UT |
| 1336.6 | 851 | GCCGCGAGGC [C/G] TGGTCTGAGC | 5 (5) | 11 (5) | 3' UT |
| .7 | 889 | GGTCTCTCA [G/A] TCTTTCCCT | 21 (10) | 2 (2) | 3' UT |
| .15 | 990 | TTGGCAACGG [C/T] CGTCTCATG | 17 (11) | 2 (1) | 3' UT |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1337.12 | 420 | GCAGTCATGC [C/G] GGGTGATCGT | 32 (15) | 3 (2) | 3' UT |
| 1339.17 | 2972 | TATTAGTCCA [A/G] TGAGATTTCC | 12 (9) | 7 (4) | 3' UT |
| .20 | 3146 | GTCGGACAGT [G/T] GCTCATAGAG | 6 (6) | 5 (4) | 3' UT |
| 1341.3 | 630 | CTCGTAAGGC [G/T] TCCGGTCCCC | 4 (4) | 6 (3) | Silent |
| .4 | 633 | GTAAGGCGTC [C/T] GGTCCCCCGG | 10 (9) | 4 (2) | Silent |
| .17 | 896 | AAAAAGGCGG [G/C] CGGAACCAA | 22 (14) | 2 (1) | Silent |
| .29 | 1107 | AGGCTGTGAA [G/A] CCCAAGGCCG | 13 (8) | 2 (1) | Silent |
| .32 | 1195 | AAACCCAAA [G/A] GCTCTTTCA | 7 (5) | 5 (3) | 3' UT |
| 1342.5 | 142 | GCGCCAAAGC [G/A] AAATCCCCT | 11 (9) | 3 (2) | Silent |
| .7 | 227 | CGCAGAGCGG [G/T] TTGGGGCAGG | 4 (4) | 5 (4) | Val -> Phe |
| .8 | 271 | TGTTAGAGTA [C/T] CTGACCGCCG | 11 (11) | 4 (2) | Silent |
| .10 | 314 | CGCGGCTCGC [G/A] ACAACAAGAA | 8 (8) | 2 (2) | Asp -> Asn |
| 1343.17 | 514 | GAACTCAAAA [G/A] GCTCTTTCA | 7 (7) | 4 (4) | 3' UT |
| 1344.2 | 149 | GAGCGCATCG [C/G] GGGAGAGGCT | 2 (2) | 2 (2) | Ala -> Gly |
| 1345.3 | 360 | GGCGCGGTGG [G/C] GTCAAGCGCA | 3 (3) | 3 (1) | Gly -> Ala |
| 1346.1 | 2269 | CAGACTGGTG [A/G] ACGAATATTC | 2 (2) | 2 (2) | Asn -> Asp |
| .2 | 2407 | CTCTGAGACG [A/C] TGAAGACCCG | 2 (2) | 3 (3) | Met -> Leu |
| .10 | 3265 | TGCCGGGCTT [C/T] CCTCCGGGG | 3 (3) | 2 (2) | 3' UT |
| 1347.3 | 107 | GAAGCCGAGA [C/G] GGAAAATGTC | 12 (8) | 4 (3) | Arg -> Gly |
| .5 | 109 | AGCCGAGACG [G/A] AAAATGTCAT | 2 (2) | 3 (3) | Silent |
| .6 | 111 | CCGAGACGGA [A/G] AATGTCATCA | 16 (12) | 2 (1) | Lys -> Arg |
| .37 | 994 | GGTTCTTGTT [T/G] GGGCACAGCA | 16 (11) | 3 (3) | 3' UT |
| .38 | 996 | TTCTTGTTTG [G/T] GCACAGCACA | 17 (11) | 4 (4) | 3' UT |
| 1349.4 | 351 | ATCGGGATCG [T/A] GTGTTCCAGT | 4 (1) | 9 (5) | Val -> Ser |
| .9 | 1136 | GCCCTGCACG [A/G] GCCCAGGGGC | 19 (13) | 3 (3) | 3' UT |
| .10 | 1137 | CCCTGCACGA [G/A] CCCAGGGGCT | 10 (6) | 11 (7) | 3' UT |
| .11 | 1150 | CAGGGGCTGA [G/A] CGTTCCTAGG | 20 (12) | 2 (2) | 3' UT |
| 1350.4 | 188 | CCAAGCGCTC [T/C] AGGGGCTTTG | 4 (4) | 12 (7) | Silent |
| .5 | 275 | ATGGAAGAGT [T/C] GTGGAACCAA | 15 (10) | 2 (1) | Silent |
| .10 | 473 | GGGGCTTTGC [C/T] TTTGTAACCT | 9 (8) | 3 (2) | Silent |
| .12 | 770 | ATGGATTGG [C/T] AATGATGGAA | 5 (5) | 2 (2) | Ala -> Val |
| 1351.25 | 1695 | GTGTGGAGAA [G/A] CCACAGGCCT | 10 (7) | 10 (8) | 3' UT |
| 1354.23 | 2233 | CAACAATTTT [C/T] TATGTTAGTT | 7 (6) | 3 (1) | 3' UT |
| 1355.7 | 4296 | AGCCTTCAGG [C/T] TCGGGGGGCT | 2 (2) | 2 (1) | Ala -> Val |
| .8 | 4778 | GCGCTGATAA [C/G] GTTCATGGAA | 3 (3) | 3 (3) | 3' UT |
| .10 | 4785 | TAACGTTTCAT [G/A] GAACGCGTTG | 5 (5) | 2 (1) | 3' UT |
| 1358.8 | 2515 | CAGGGCGAGT [G/C] GCATGCTCTGC | 7 (7) | 2 (2) | 3' UT |
| .17 | 2629 | CTTGGCATGT [G/A] ATGGCAGCTC | 20 (17) | 2 (2) | 3' UT |
| 1359.3 | 297 | ATAAATACAA [G/A] AACATTGGAG | 3 (2) | 2 (2) | Silent |
| 1360.12 | 548 | TGTAAGCTGA [G/C] CCTGGTGGCC | 8 (6) | 2 (1) | 3' UT |
| 1361.10 | 4077 | CTGTCTTTCC [A/G] TTTTTCATG | 14 (9) | 2 (1) | 3' UT |
| 1362.9 | 1832 | CCGCCAGGCG [G/A] ATTTTGTTC | 2 (2) | 2 (2) | Silent |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .11 | 2248 | CCTATCGGCT [C/G] TTTGCAGTGG | 3 (2) | 3 (3) | Leu -> Val |
| 1363.22 | 2874 | CCGGAATCCA [A/C] AGTGCTCTGC | 2 (2) | 7 (5) | 3' UT |
| 1366.3 | 615 | CGCCCATGGC [G/A] ACCAGTACAA | 7 (7) | 2 (2) | Asp -> Asn |
| .6 | 722 | TGTACAACCT [T/C] CCCGCAGGCG | 2 (2) | 8 (7) | Silent |
| 1367.18 | 1851 | AAAAAGTAATTCCTTAAA [C/A] AT | 4 (4) | 4 (3) | 3' UT |
| 1368.5 | 2964 | TCTGAGACAC [G/A] CCCCAACATG | 3 (3) | 2 (2) | 3' UT |
| 1372.1 | 276 | AGATGCTAAG [A/G] TTACCTTTCC | 4 (3) | 2 (2) | Ile -> Val |
| 1373.13 | 3855 | AATATAATAT [C/T] GACACAGTGC | 4 (4) | 2 (2) | 3' UT |
| 1378.12 | 4157 | TGCTGGGGCA [T/C] GCGGGGATCC | 2 (2) | 2 (1) | 3' UT |
| 1383.14 | 1832 | ATCACCACCA [C/T] GTGAGTGGTA | 12 (6) | 4 (3) | Silent |
| 1385.17 | 3454 | CAGTGCTAAT [G/A] TGTGCAAGCA | 7 (5) | 4 (3) | 3' UT |
| 1386.31 | 470 | GGGTGACGGG [C/G] CCATGGGGCG | 5 (5) | 3 (3) | 3' UT |
| 1387.5 | 1385 | TCGGTGCACT [T/C] TCCACTCTTG | 2 (2) | 2 (2) | 3' UT |
| .7 | 1678 | CAGGCTCATC [C/A] TGGGAGCTTT | 3 (3) | 5 (3) | 3' UT |
| .8 | 1900 | CAGCCCTGCT [G/A] ACCATCTCAC | 4 (4) | 2 (2) | 3' UT |
| .11 | 1967 | GCCCCCTGGG [G/A] AGTTGGGGAA | 17 (13) | 2 (2) | 3' UT |
| .15 | 2075 | ATTCTTCTCT [G/T] GTGGCATTAG | 18 (14) | 3 (3) | 3' UT |
| .17 | 2089 | GCATTAGCCA [C/T] TCCCTGCCTC | 22 (15) | 2 (2) | 3' UT |
| .22 | 2234 | AAGAGAGAGAGA [A/G] AAAAAAAA | 13 (10) | 6 (4) | 3' UT |
| 1388.17 | 2799 | CACAGAAGCA [G/C] CTAAACCAAG | 15 (11) | 4 (1) | 3' UT |
| 1395.4 | 327 | CAATGTGTTA [T/C] GTAGTGCTTA | 35 (17) | 2 (1) | 3' UT |
| 1396.10 | 1887 | GGCAGGAGCC [C/T] TCCTTCTATA | 3 (3) | 3 (1) | 3' UT |
| .12 | 1921 | CCCCAGTGGG [G/A] ACTGAGTTAT | 3 (3) | 5 (2) | 3' UT |
| .21 | 2403 | TGACCAGGAC [G/C] CCTCTGGCCC | 2 (2) | 3 (3) | 3' UT |
| .26 | 2579 | AAAGGCTGAA [T/A] TGTCTGAAAA | 10 (7) | 3 (1) | 3' UT |
| 1397.23 | 6232 | TATTCAGAGT [G/T] GGCTGGGCCC | 3 (3) | 2 (2) | 3' UT |
| 1399.2 | 177 | CCCCGAGGG [G/A] ATGCCAAGAT | 3 (3) | 2 (2) | Asp -> Asn |
| .10 | 1136 | AGGGGACAGT [A/G] ATAGCCAGCA | 3 (3) | 4 (4) | Silent |
| .16 | 1279 | CTGCTGTAAA [G/A] GCTGCAGCCT | 8 (8) | 2 (2) | 3' UT |
| 1401.3 | 71 | CCAAGAATCT [G/A] CTGCGCATGA | 2 (2) | 3 (3) | Silent |
| .17 | 874 | TTATGTTTAT [G/A] TTTATTATGT | 8 (6) | 6 (4) | 3' UT |
| .19 | 917 | TGGAATCAA [G/A] TGTCAATAAGA | 8 (7) | 5 (4) | 3' UT |
| .21 | 1081 | TCTACTTTCA [A/C] AAAAAAAAAA | 2 (2) | 7 (6) | 3' UT |
| .23 | 1083 | TACTTTCAAA [A/T] AAAAAAAAAA | 2 (2) | 3 (3) | 3' UT |
| 1404.12 | 3921 | TGTTGCACAC [T/C] AGCCTTACAG | 3 (3) | 2 (2) | 3' UT |
| 1405.15 | 4823 | GTCCACATGC [A/G] CTGGGCGTCT | 4 (4) | 12 (10) | 3' UT |
| 1406.5 | 4618 | TGCTTTCTAG [G/C] TCAGTCCCTG | 5 (3) | 6 (4) | 3' UT |
| 1407.5 | 405 | CCCAGGGGGG [G/C] AGCTCCCAT | 5 (4) | 2 (2) | Ser -> Gln |
| .9 | 713 | TCTCTCAGAG [G/A] AAGTTTTTGG | 10 (7) | 2 (1) | Silent |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .18 | 1053 | GGGCAGGGAA [T/C] CCTGGAGCAC | 21 (13) | 2 (2) | 3' UT |
| .21 | 1144 | GTGGGGTGGG [G/A] TGAGTAGGAC | 2 (2) | 25 (14) | 3' UT |
| 1411.4 | 2009 | GGCGTCAGAG [A/G] TGCTGGGTGA | 6 (4) | 7 (5) | 3' UT |
| 1414.13 | 930 | ACATACGAAC [C/T] GCCTCCTTCC | 16 (13) | 3 (2) | 3' UT |
| 1415.24 | 1362 | GTGCGATTCT [A/G] GATAAAGCCA | 7 (5) | 3 (3) | N/D |
| .26 | 1442 | GAGAATCCCT [G/A] GCAAAGGGAG | 10 (8) | 3 (3) | N/D |
| 1420.6 | 461 | CAGCGGGAGC [G/T] TGAAGAAAGA | 2 (2) | 2 (2) | Arg -> Leu |
| .8 | 685 | TGGTGGCAGT [G/T] TGGGCTCTCA | 12 (8) | 2 (1) | Val -> Leu |
| .9 | 689 | GGCAGTGTGG [G/C] CTCTCAGCCA | 15 (12) | 2 (2) | Silent |
| .16 | 853 | GCTGGCAGCT [G/T] TGAGGCTCTA | 25 (19) | 2 (2) | Val -> Leu |
| 1421.8 | 169 | AAGTATACAG [A/G] ACAGATTACA | 20 (14) | 2 (1) | Silent |
| .25 | 1166 | GTTAGTTTTC [T/C] GGCCCGTGGC | 4 (3) | 3 (2) | 3' UT |
| .26 | 1167 | TTAGTTTTCT [G/T] GGCCGTGGCC | 4 (3) | 11 (7) | 3' UT |
| .29 | 1275 | TCTGGCATAC [C/G] GATAGGCTTA | 6 (5) | 14 (11) | 3' UT |
| 1422.7 | 278 | CGGGGAACCG [G/C] CCACCATCAA | 4 (3) | 3 (3) | Ala -> Pro |
| 1424.3 | 1012 | GGGAGGATGC [T/G] CTCTCTCGCG | 2 (2) | 5 (3) | Silent |
| .4 | 1021 | CTCTCTCTCG [C/T] GTAGCTGGAA | 5 (3) | 2 (1) | Silent |
| .7 | 1295 | GTTTAATGCA [T/A] GGATTCGAAA | 2 (2) | 3 (2) | Trp -> Arg |
| 1425.3 | 274 | GCACTGGAGG [G/T] TTTAATTTTG | 2 (2) | 2 (2) | Gly -> Val |
| 1426.2 | 1364 | GATCACCAGA [T/C] ACCAGGGTGT | 9 (6) | 2 (1) | Tyr -> His |
| .17 | 2298 | TCTCCAGAGT [C/T] ACTCCGTTCT | 4 (4) | 3 (3) | Ser -> Leu |
| 1427.3 | 90 | CGCCGGCTGC [G/C] CTGCAGGTGA | 8 (6) | 3 (1) | Silent |
| .4 | 91 | GCCGGCTGCG [C/G] TGCAGGTGAC | 8 (6) | 3 (1) | Leu -> Val |
| .6 | 109 | GACAGTTCGT [G/A] ATGCTATAAA | 12 (6) | 2 (2) | Asp -> Asn |
| .11 | 438 | TCTTCAGGGG [A/G] CCCAATGGTG | 7 (2) | 2 (2) | Glu -> Gly |
| .23 | 1172 | CTATTCTATA [A/C] GGAAAACGAT | 10 (5) | 12 (7) | 3' UT |
| .24 | 1179 | TAAAGGAAAA [C/T] GATTTCTAAA | 21 (10) | 2 (2) | 3' UT |
| .31 | 1323 | CAAATTATAT [C/A] ACATTTTATC | 8 (3) | 13 (10) | 3' UT |
| .34 | 1376 | GCAGAGTCCT [G/C] ATGAAAGATG | 13 (7) | 5 (4) | 3' UT |
| .37 | 1433 | GCATATAATA [C/T] ACATTTACTG | 6 (2) | 9 (7) | 3' UT |
| 1430.3 | 682 | TCTTTGGGGA [G/A] TCAGATGAGC | 7 (6) | 2 (2) | Ser -> Glu |
| 1431.2 | 79 | GCCAGTGGCG [C/T] TTCGTGGACG | 7 (6) | 2 (2) | Silent |
| .6 | 296 | TCACGCAGTG [G/C] CCAATAATCA | 10 (7) | 7 (6) | Ala -> Pro |
| 1432.8 | 2640 | AAGTTGCTTA [G/A] AGAGCCACCA | 8 (7) | 2 (1) | 3' UT |
| .9 | 2695 | GTTTTAATGC [A/C] AAGGAAATTT | 12 (9) | 3 (3) | 3' UT |
| 1433.7 | 1695 | AGCCGGGCTG [C/T] TACCTGCCCA | 3 (3) | 2 (2) | Silent |
| .10 | 2052 | CCCCTGGGTG [C/T] GGGGTGATCG | 2 (2) | 2 (2) | Silent |
| .11 | 2160 | ATGAGTCCAC [T/C] CTGGCCTTCC | 2 (2) | 2 (2) | Silent |
| .23 | 2698 | GGACCTTCGA [G/A] GGCCTCTGCC | 4 (4) | 3 (3) | 3' UT |
| .28 | 2787 | GTGGAGGAGA [G/A] GCCTGTGGCC | 6 (6) | 2 (2) | 3' UT |
| .30 | 2844 | GGTGGCGCAG [C/G] CTTGGTAACG | 15 (13) | 8 (6) | 3' UT |
| .31 | 2848 | GCGCAGCCTT [G/A] GTAACGCCAT | 15 (13) | 8 (6) | 3' UT |
| .32 | 2857 | TGGTAACGCC [A/G] TGGACTGCAG | 16 (14) | 8 (6) | 3' UT |
| .33 | 2877 | GCGACAATCA [A/G] TGGATGGTGC | 16 (14) | 8 (6) | 3' UT |
| .34 | 2942 | CCCTACCTGT [C/T] TTATTTTATA | 17 (14) | 14 (9) | 3' UT |
| 1434.15 | 2041 | ACTGTACCTT [C/T] TATGGTTTGC | 2 (1) | 5 (4) | 3' UT |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .17 | 2127 | TGATTAGAAC [G/T] GGTAGCCAGT | 2 (1) | 5 (4) | 3' UT |
| .18 | 2154 | AATATTGATA [G/T] AAAAAATAAAA | 2 (1) | 5 (4) | 3' UT |
| 1437.16 | 2825 | AGTTTAAGAT [G/C] ACTTGACCCC | 5 (4) | 3 (2) | 3' UT |
| .19 | 3129 | CATGCGTAGC [C/T] TCTTGTCTTA | 7 (5) | 3 (2) | 3' UT |
| 1440.5 | 940 | AACCTCAGAA [G/A] GCCAGTGTG | 2 (1) | 3 (3) | Silent |
| .6 | 1327 | TGGCCCTGCC [T/C] GGGAGCCGC | 2 (1) | 2 (2) | Silent |
| .9 | 1906 | GACCTGAAGG [C/T] GAACGTGATA | 2 (1) | 2 (2) | Ala -> Val |
| .14 | 2282 | TCTTAGAGGC [C/T] TTTCTTGTAT | 2 (2) | 3 (3) | 3' UT |
| 1443.4 | 1943 | CTTCGTGCCA [G/A] AACCTGAGAA | 3 (2) | 2 (1) | Glu -> Lys |
| 1444.31 | 1905 | CCAACAGCCT [C/T] CAAAGATGGG | 3 (2) | 28 (20) | 3' UT |
| 1445.4 | 425 | CCAGGCTTGC [C/A] AGCCGAAACG | 8 (5) | 2 (2) | Pro -> Gln |
| .25 | 1281 | AACAAAGAAA [A/T] AAAAAAAAAA | 5 (4) | 4 (4) | 3' UT |
| 1446.3 | 1227 | AGGTGTGGAA [C/T] ACCCTCAGCG | 2 (1) | 2 (2) | Silent |
| .17 | 3090 | TTATTATAT [T/C] TTTAACATAA | 10 (7) | 2 (2) | 3' UT |
| 1447.8 | 2681 | GGCAATAGCA [A/G] TCTTGGCTGA | 3 (3) | 3 (2) | 3' UT |
| 1448.2 | 521 | AGAAGACCAC [A/G] ATGCGAGATG | 3 (2) | 3 (1) | Silent |
| .3 | 587 | GTCATGCTCT [T/C] GCACTTTACA | 4 (3) | 3 (1) | Silent |
| 1449.20 | 1261 | TGCGTAATGC [G/A] GCCGAAGAGC | 4 (3) | 21 (13) | Silent |
| .28 | 1447 | CTGAGAGCCC [C/G] AGGCGTCCGC | 21 (14) | 2 (1) | 3' UT |
| .31 | 1652 | TGCGAGATTG [A/C] ATAAAAAAAA | 8 (6) | 6 (4) | 3' UT |
| .32 | 1653 | TGCGAGATTGA [A/T] TAAAAAAAAA | 11 (7) | 3 (3) | 3' UT |
| .33 | 1654 | GCAGATTGAA [T/A] AAAAAAAAAA | 6 (6) | 4 (4) | 3' UT |
| 1450.2 | 156 | CCCCATGGCG [G/A] CCGCCAAGGA | 11 (9) | 2 (2) | Ala -> Thr |
| 1451.13 | 200 | GATGAGCGTG [A/T] TTCCTCTCGA | 3 (2) | 31 (20) | Asp -> Val |
| .14 | 201 | ATGAGCGTGA [T/A] TCCTCTCGAT | 3 (2) | 31 (20) | Asp -> Glu |
| .18 | 417 | AAGTTCACAT [C/G] AACCTCATGG | 2 (1) | 28 (18) | 3' UT |
| 1452.12 | 1659 | GTACCAGAGG [C/T] ATGCCATCA | 4 (4) | 2 (1) | Ala -> Val |
| .18 | 2410 | ATTTAAGGAC [G/A] AGACCAGCAG | 3 (3) | 9 (5) | Silent |
| .19 | 2419 | CGAGACCAGC [A/G] GCTAATCCAA | 9 (8) | 3 (1) | Silent |
| .23 | 2717 | GTTAATGATG [T/A] TAATGATTTT | 17 (13) | 5 (3) | 3' UT |
| 1454.3 | 338 | AGGGCTTTGC [C/T] TTCGTTCACT | 3 (2) | 6 (2) | Silent |
| .7 | 1211 | CATGCTCACT [G/T] TTCTCCCAT | 9 (6) | 2 (1) | 3' UT |
| .8 | 1391 | GTTTTTAAAAAAA [A/T] AAAAAA | 3 (2) | 3 (3) | 3' UT |
| 1455.6 | 294 | CCAGGCCTTT [G/T] TCATCTTCAA | 9 (8) | 2 (2) | Val -> Phe |
| .22 | 911 | CAGCTCGCGA [T/A] GCCCTGCAGG | 13 (12) | 3 (3) | Asp -> Glu |
| .23 | 912 | AGCTCGCGAT [G/T] CCCTGCAGGG | 8 (8) | 4 (4) | Ala -> Ser |
| 1460.1 | 6 | AATTC [C/G] CAGAGCAACATGCC | 5 (5) | 3 (3) | 5' UT |
| .30 | 547 | GTTCTGCTTC [A/C] CCAGGAGATC | 25 (17) | 5 (3) | 3' UT |
| 1461.5 | 154 | TCCCCGGGGG [G/C] CTTTGGATCG | 8 (7) | 2 (2) | Silent |
| .32 | 1463 | GTGTTACTGC [A/G] TTTTGTACAA | 14 (8) | 11 (8) | 3' UT |
| 1463.3 | 761 | CAGCGTGGGG [G/T] TGGCCACTCC | 2 (1) | 2 (2) | 3' UT |
| 1464.3 | 21 | GCCTGCAGGC [C/T] TCCCAGGAG | 6 (3) | 2 (2) | Silent |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .4 | 130 | GCAGACTTAT [A/G] AGGTTGACCT | 3 (1) | 11 (7) | Lys -> Ser |
| .5 | 132 | AGACTTATAA [G/A] GTTGACCTTA | 3 (1) | 10 (7) | Silent |
| 1465.4 | 897 | AGTTCCACCC [T/C] ACAGGCATAT | 2 (2) | 3 (3) | Silent |
| .5 | 1044 | TGTCTCGGTC [C/G] ATGACTCTGG | 4 (4) | 2 (2) | Silent |
| .12 | 1758 | GAGCAGAGGC [A/G] CGGAAGGAGT | 8 (8) | 3 (3) | Silent |
| .30 | 1892 | ACCCTGTCTT [A/T] TGTGGACGTT | 19 (17) | 6 (6) | Tyr -> Phe |
| .34 | 1938 | ATAGACCCGT [G/A] ATCGACAAAA | 16 (15) | 9 (9) | Silent |
| .37 | 1975 | CTGTGCCACC [G/A] TCCCGCCAGC | 21 (20) | 6 (6) | Val -> Ile |
| .38 | 1980 | CCACCGTCCC [G/C] CCAGCCATTC | 21 (20) | 5 (5) | Silent |
| .41 | 2014 | AGACAAGATG [T/C] GGTGATGACA | 22 (20) | 5 (5) | 3' UT |
| .42 | 2102 | TTCTGCACTC [T/C] GGGGAAGAAG | 23 (20) | 8 (7) | 3' UT |
| .45 | 2139 | GATTGGCACC [T/C] AGTGGCTGGG | 24 (20) | 7 (6) | 3' UT |
| 1467.9 | 2297 | CATGGAGGCA [G/A] CCAGGCCCGT | 4 (4) | 2 (2) | Ser -> Asn |
| .11 | 2353 | TAATAATATG [T/C] ATGCCTGGGG | 3 (3) | 2 (2) | Tyr -> His |
| 1471.4 | 3042 | CACCCAACCT [G/A] TCCTTACTCA | 2 (2) | 3 (1) | 3' UT |
| 1473.9 | 390 | GAAAAGCTGC [C/T] ATTCTCAAGG | 13 (11) | 5 (3) | Silent |
| .10 | 399 | CCATTCTCAA [G/A] GCCCAAGTGG | 11 (8) | 3 (3) | Silent |
| 1474.1 | 8 | TCT [G/A] AACGGAGAGCGTAGTGA | 13 (10) | 4 (3) | 5' UT |
| .2 | 9 | CT [A/T] ACGGAGAGCGTAGTGACC | 14 (11) | 3 (3) | 5' UT |
| .9 | 94 | GCGAGAGGAG [G/T] AGGAATTTAA | 27 (14) | 2 (1) | Ser -> *** |
| .24 | 370 | GCGGAACCCG [C/T] TCATCGCCGG | 21 (15) | 3 (2) | Leu -> Phe |
| .26 | 392 | AAGTAGGGGC [C/A] GCCTGTCTGT | 28 (14) | 2 (1) | 3' UT |
| 1476.6 | 230 | CACAAGTGCC [C/T] TTCGAGCAGA | 12 (9) | 2 (2) | Silent |
| 1477.20 | 1470 | ATTTGATGGA [G/C] GCTGCGCCGG | 31 (12) | 6 (4) | Ser -> Asp |
| .24 | 1480 | GGCTGCGCCG [G/C] AGTGAAGAGG | 34 (14) | 2 (2) | Ser -> Gln |
| .28 | 1647 | TTCTGTGTA [A/T] AAAAAAAAAA | 9 (6) | 3 (2) | 3' UT |
| 1478.19 | 838 | TATGGAAGTA [G/A] CTCGCGAGAG | 17 (11) | 2 (2) | Ala -> Thr |
| .29 | 1009 | TCCTCAGCTC [C/T] CTGCTGTTT | 26 (18) | 2 (1) | 3' UT |
| .30 | 1095 | AATAAACTCTTAAAGA [G/A] CCTT | 2 (2) | 24 (16) | 3' UT |
| 1480.17 | 913 | AAGAGGCACT [G/T] TAGCAGCTGC | 17 (13) | 2 (2) | Val -> Leu |
| .18 | 939 | TGCTGCGAC [T/C] GCCAGTATTG | 18 (13) | 2 (2) | Silent |
| .19 | 979 | CCCACCAGGA [C/A] GGGGCACTCC | 17 (12) | 4 (4) | Silent |
| .20 | 980 | CCACCAGGAC [G/C] GGGCACTCCG | 11 (10) | 4 (4) | Arg -> Pro |
| .29 | 1113 | TAGGCATGCC [G/C] CCTCCGGGAA | 20 (13) | 2 (2) | Silent |
| 1483.12 | 1969 | ACTTCTCCAT [C/T] CGGTCCCTAG | 2 (1) | 2 (2) | Silent |
| 1484.2 | 140 | ATTACGATGA [G/A] GAGGAAGAGC | 3 (2) | 12 (8) | Ser -> Glu |
| .7 | 288 | CTGTGGCTTG [G/A] AGCATCCTTC | 8 (7) | 2 (2) | Ser -> Lys |
| .11 | 674 | AGCACTTTGT [G/C] CTGGACGAGT | 3 (3) | 2 (2) | Silent |
| 1486.24 | 6427 | GCATTAACTA [A/T] AAAAAAAAAA | 5 (5) | 7 (5) | 3' UT |
| 1487.15 | 2896 | GCGCCAAGCC [C/A] AGCAGGCTAC | 3 (3) | 3 (1) | Pro -> Gln |
| .20 | 3303 | AGCCACGGGC [G/T] TCCTACTGAG | 8 (7) | 3 (3) | Val -> Phe |
| .22 | 3394 | CTGGGAAGC [T/C] CCTGGAAGCC | 11 (10) | 2 (2) | Leu -> Pro |
| 1489.14 | 1419 | ACTCAACTCA [C/A] GGTACAAGAC | 7 (5) | 3 (3) | 3' UT |
| 1490.6 | 443 | AGGCTGCTCG [T/C] GTTGCTATTG | 2 (2) | 2 (2) | Val -> Ala |
| .31 | 1710 | CTCGTGATGC [A/G] TCTACAGTTA | 11 (7) | 19 (12) | 3' UT |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .33 | 1824 | GTGGGGGTAC [C/T] ATCTCAACTG | 7 (4) | 13 (9) | 3' UT |
| 1491.21 | 1488 | GCATATGGGA [G/C] CCATTGGCTG | 11 (8) | 2 (2) | Ser -> Asp |
| .31 | 1826 | TGTAAGGTTT [C/T] CATTAGTTT | 28 (16) | 3 (1) | 3' UT |
| 1495.3 | 391 | CAAAAACCCC [G/A] CCGCTCCAA | 3 (2) | 3 (2) | Silent |
| 1496.5 | 3017 | AATAATAACC [A/G] AGACTTTTCA | 6 (4) | 2 (2) | 3' UT |
| .15 | 3932 | CTGCCTGGCC [C/T] TTTTCTTTC | 3 (1) | 6 (5) | 3' UT |
| 1497.13 | 1332 | GCCCCATGTC [G/A] CTGGGTGGGC | 3 (2) | 5 (5) | Silent |
| .14 | 1338 | TGTCGCTGGG [T/C] GGGCGGCACG | 3 (2) | 5 (5) | Val -> Ala |
| .16 | 1508 | GCCACGGCGG [C/T] CGCCAGCGAG | 8 (4) | 2 (2) | Ala -> Val |
| .20 | 1608 | CCCCCGGGC [C/G] CGGACCAGCC | 6 (4) | 5 (3) | Silent |
| .23 | 1713 | AGCGGCTGCG [G/T] GTCCGTGACA | 6 (3) | 3 (2) | Silent |
| .39 | 4022 | GGCTTCCCCT [G/A] CGCCCTGGGA | 3 (2) | 6 (5) | 3' UT |
| .43 | 4187 | AAACAGCAGT [T/C] CCTGGGAACC | 12 (10) | 2 (1) | 3' UT |
| .44 | 4254 | TTTCAAAAA [T/A] TTTTITAAA | 2 (2) | 11 (9) | 3' UT |
| 1498.5 | 167 | GGCGTGCTGA [G/C] TGCCCTGGGA | 8 (4) | 3 (3) | Ser -> Thr |
| 1500.16 | 2206 | GAAGGAAACA [G/A] TGCAACAGCA | 16 (13) | 2 (2) | 3' UT |
| .18 | 2310 | GTTGTAAAGA [G/T] TGGGGGAGAG | 25 (18) | 2 (1) | 3' UT |
| .23 | 2426 | TGCCAAGCTG [G/A] ACGGCACGAG | 10 (7) | 4 (4) | 3' UT |
| 1501.5 | 388 | GCGCTGTGCG [G/T] TGTCCCGTTC | 2 (2) | 2 (2) | Silent |
| .16 | 1238 | CCCCGGGAGG [G/A] AGCTGACTGA | 8 (8) | 2 (2) | 3' UT |
| 1505.9 | 3934 | TTAGTCATTC [T/C] AAAAAACACC | 6 (4) | 4 (4) | 3' UT |
| 1507.2 | 130 | CCCCGAGGCG [A/T] TCGTGGAGGA | 3 (3) | 3 (2) | Ile -> Phe |
| 1508.19 | 5111 | CATCGCCGAG [G/C] CCTGGGCCCCG | 12 (10) | 3 (2) | N/D |
| 1510.6 | 1066 | CAAAGGAGCT [T/C] GAAGGATATT | 2 (2) | 5 (5) | 3' UT |
| .8 | 1136 | TCTAAAAGAA [A/G] AAGGAAC TAG | 3 (2) | 2 (1) | 3' UT |
| 1511.10 | 222 | CTACAATATT [C/G] AAAAGGAGTC | 18 (11) | 2 (1) | Gln -> Glu |
| 1514.6 | 103 | CGGGGCTGCG [G/A] CCGCCCGAGG | 11 (5) | 4 (4) | 5' UT |
| .24 | 624 | GGCATCGTCA [G/A] AAGGAAGGGA | 13 (5) | 6 (5) | 3' UT |
| .35 | 879 | GCTGTAAAT [T/C] ATAACTTTT | 27 (12) | 2 (1) | 3' UT |
| .38 | 913 | TCCCCCAGGG [G/C] CGAGTTCCTC | 25 (11) | 3 (2) | 3' UT |
| .39 | 914 | CCCCCAGGGG [C/G] GAGTTCCTCG | 20 (11) | 3 (3) | 3' UT |
| .43 | 1069 | AGACCCAGG [G/T] CAGCATCTCG | 21 (9) | 5 (4) | 3' UT |
| 1515.6 | 175 | CATGCTAGCA [T/G] GGCCTAATGA | 3 (2) | 9 (8) | Trp -> Gly |
| .28 | 855 | CTGGAGAGCT [T/G] GGCTTCCGCG | 15 (11) | 4 (4) | Silent |
| .30 | 858 | GAGAGCTTGG [C/G] TTCCGCGCTT | 6 (6) | 7 (5) | Ala -> Gly |
| .38 | 1146 | ATAATAAAG [T/A] TTCATTGCA | 2 (2) | 23 (14) | 3' UT |
| 1517.9 | 742 | AATCATAATG [G/C] TTCTCCCTT | 6 (3) | 2 (2) | Val -> Ala |
| .16 | 1424 | AAGTTATTGG [C/T] AAACGAGGTT | 11 (7) | 3 (3) | Ala -> Val |
| 1518.8 | 947 | AGAGCTGAGC [G/A] AGTTCACCAC | 5 (4) | 2 (2) | Ser -> Lys |
| 1519.15 | 1209 | CCATCAAAG [C/T] TTTGAGAATT | 2 (2) | 6 (5) | Silent |
| 1520.12 | 6696 | CAGCCTCATC [G/A] ATCCCAAAC | 5 (2) | 3 (1) | Asp -> Asn |
| .13 | 6806 | TGCGCGGGAG [C/A] AAAC TGCTCT | 2 (1) | 3 (1) | Ser -> Arg |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1521.6 | 851 | AGACTCTGAG (G/C) CCTGGTGTGA | 7 (6) | 2 (2) | Arg -> Ser |
| .10 | 976 | TTGGGAATGG (A/G) TATCAGAAGA | 15 (8) | 4 (1) | 3' UT |
| .15 | 1165 | TCACCTATAC (A/G) TTATTTAAAT | 20 (8) | 4 (1) | 3' UT |
| .17 | 1236 | GAAACTGTG (C/A) AATTGTGTGC | 7 (4) | 3 (1) | 3' UT |
| 1523.7 | 417 | CACCACGGTG (C/T) TGGAAATTGTT | 9 (8) | 3 (3) | Silent |
| 1524.13 | 2996 | AAAATGACAT (T/G) AGTTTGA AAAA | 3 (2) | 3 (2) | 3' UT |
| .22 | 3384 | AACAGCTTTT (A/T) GGCCAAGCTG | 20 (9) | 4 (4) | 3' UT |
| .23 | 3385 | ACAGCTTTTA (G/A) GCCAAGCTGG | 16 (7) | 6 (5) | 3' UT |
| .25 | 3397 | CCAAGCTGGC (C/T) TGACGGTATG | 25 (11) | 4 (3) | 3' UT |
| .26 | 3398 | CAAGCTGGCC (T/G) GACGGTATGG | 25 (11) | 3 (2) | 3' UT |
| 1526.6 | 2476 | TGGAGGTGCA (T/C) AACCTACTTA | 2 (1) | 2 (1) | Silent |
| .7 | 2715 | GTGAAAGGGG (A/C) CGTGTACTCT | 2 (2) | 3 (1) | Asp -> Ala |
| 1528.6 | 770 | CCAAAAGGAA (G/A) TGAATCAGCA | 2 (2) | 2 (2) | Val -> Met |
| .10 | 2396 | GCAGTGCGCA (A/T) TCCTGGACCT | 1 (1) | 4 (4) | Val -> Phe |
| .26 | 3317 | TTCAAGTGAA (G/C) ATGCTGAAAG | 12 (8) | 7 (6) | Asp -> His |
| .32 | 3598 | TATAATTAGT (T/C) ATGACAGCCA | 19 (16) | 2 (1) | 3' UT |
| 1530.8 | 427 | ATCCGCCCCC (A/G) CGAGCTCCCC | 4 (3) | 2 (1) | Thr -> Ala |
| .13 | 894 | TGCTGAACGA (G/A) CCCCTGGGG | 8 (5) | 2 (1) | Ser -> Glu |
| .30 | 1579 | AGTCCTGAAA (G/A) GCCCAAGGCC | 4 (3) | 7 (6) | 3' UT |
| 1532.6 | 496 | TCGTGCGCAA (C/T) GTGCCCTGGG | 4 (2) | 6 (3) | Silent |
| .10 | 963 | CTGGCCTTAT (G/T) CCCAGGCCTG | 6 (4) | 2 (2) | Cys -> Phe |
| 1533.12 | 2092 | GTATCCAGG (A/G) CACACAGGAA | 3 (3) | 2 (2) | Asp -> Ala |
| 1534.4 | 264 | CCGTGCCGGC (A/T) CTTCAACATC | 2 (1) | 5 (4) | Silent |
| 1536.22 | 6641 | TTAGATATAT (A/G) TATTCAATTCT | 3 (3) | 4 (3) | 3' UT |
| .24 | 6779 | ATTTTATTG (G/A) GCCCAAAAAC | 2 (2) | 11 (8) | 3' UT |
| .28 | 7097 | AGTGGAATGT (T/A) TAAAAA AAAA | 4 (3) | 4 (3) | 3' UT |
| 1537.5 | 871 | AGGGCAGTGC (C/A) ATTGATAGGA | 7 (6) | 3 (3) | Silent |
| .10 | 1466 | GCAGGCATGC (C/A) AGTCTCTGCC | 7 (7) | 3 (3) | 3' UT |
| 1538.21 | 938 | CCTCCACCTT (T/C) GACGCTGGGG | 14 (7) | 3 (2) | Silent |
| 1539.1 | 67 | TCGCGGCCTA (G/C) CTTTACCCGC | 3 (3) | 2 (1) | 5' UT |
| .3 | 304 | TCGATGGCTC (T/C) AGTACTTTAC | 4 (4) | 4 (3) | Silent |
| .9 | 1075 | GTAGCGCCAG (A/C) CTACGCATTG | 2 (2) | 3 (2) | Arg -> Ser |
| .16 | 2048 | CAAGGAAGTG (G/A) TTCTTAGATG | 8 (7) | 4 (2) | 3' UT |
| .21 | 2718 | GCCTAACATAA (A/G) AAAAAA AAAA | 8 (8) | 3 (3) | 3' UT |
| 1541.1 | 4123 | TGGCGAGGGG (G/C) CTTGACGGCG | 2 (1) | 2 (2) | 3' UT |
| 1543.4 | 319 | GCACCGGAAG (G/A) AGGCGCTGAC | 6 (5) | 2 (2) | Ser -> Lys |
| 1544.3 | 534 | TTGAGCCCAA (C/G) TGCTTGGACG | 2 (2) | 7 (4) | Asn -> Lys |
| .4 | 543 | ACTGCTTGGG (C/T) GCCTTCCCAA | 4 (4) | 7 (4) | Silent |
| .8 | 643 | ACCTGTGTTT (T/A) CAAAGATGGC | 12 (8) | 3 (3) | Ser -> Thr |
| .12 | 728 | GCTGCCAGG (C/G) TGTGCAGCGC | 12 (11) | 4 (1) | 3' UT |
| .21 | 902 | AACATCCCCT (C/T) CCATCATTAC | 5 (4) | 4 (2) | 3' UT |
| .22 | 986 | CTGCCTGGCC (C/T) CTCGCCTGTG | 5 (4) | 2 (2) | 3' UT |
| 1545.4 | 1470 | CGGTGAGACC (G/A) TTGCCCGCTG | 2 (1) | 2 (2) | Val -> Ile |
| 1546.1 | 172 | CTCTGAAGAC (A/T) TGGAGATACT | 3 (1) | 3 (3) | Met -> Leu |

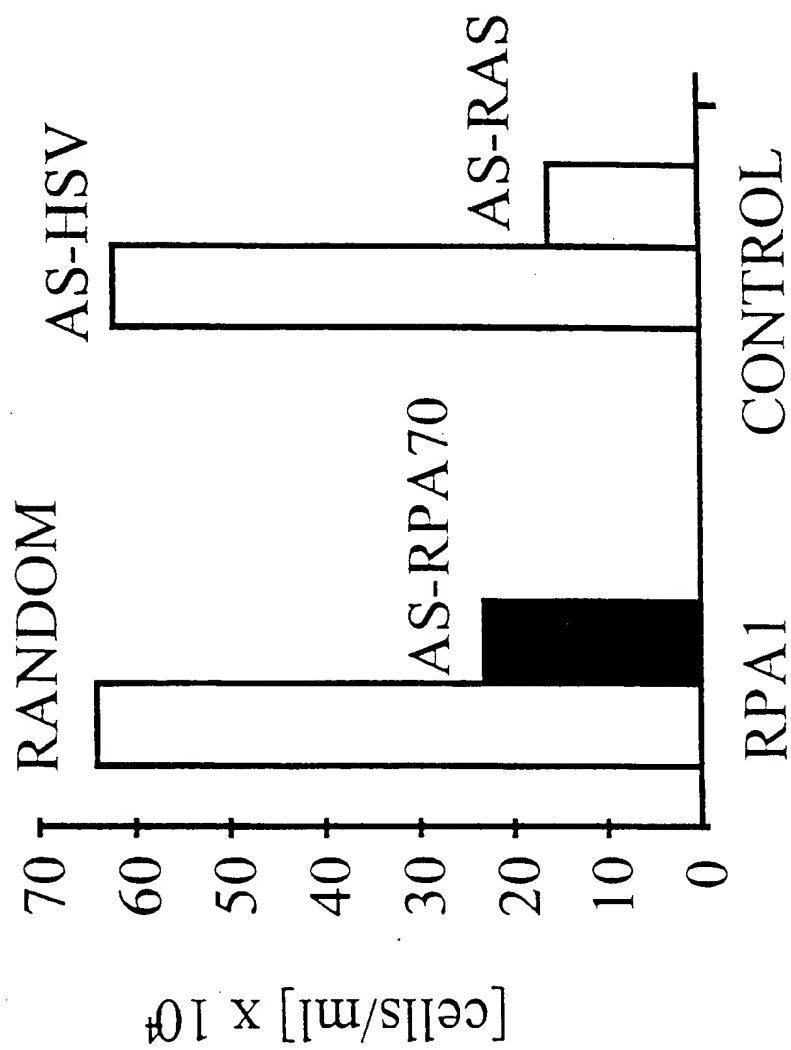
| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1547.17 | 976 | TGCTTTAAAG (G/A) GCCTGCCTGG | 13 (10) | 2 (2) | 3' UT |
| 1548.3 | 1209 | CATTATTGGC (C/T) TCATCAAACC | 3 (3) | 3 (1) | Leu -> Phe |
| .4 | 1286 | TGAAAGGTGT (A/G) AATAAGTTAC | 2 (2) | 3 (2) | Silent |
| .8 | 1904 | ATAACTAAGA (C/T) TTCTGTGCAT | 6 (3) | 5 (3) | 3' UT |
| 1550.7 | 797 | TGGACGCCTT (T/C) CCAAATCTGA | 2 (2) | 5 (2) | Silent |
| 1551.12 | 2215 | CGAGACCATC (T/C) TGGCCCCCTCC | 3 (1) | 10 (9) | 3' UT |
| .14 | 2242 | TGCCTGAGCC (T/C) AGGAGCTTGA | 3 (1) | 9 (8) | 3' UT |
| .15 | 2341 | ACTGGGTCTC (G/A) CTCCGAGTGG | 3 (1) | 9 (8) | 3' UT |
| .16 | 2372 | GGAGGGAGGG (T/A) CAGGGGAGG | 3 (1) | 9 (8) | 3' UT |
| 1554.12 | 834 | GGGACTTTAT (C/G) GATTGCTTCC | 6 (5) | 2 (1) | Ile -> Met |
| .14 | 999 | ACCCAGAGGT (C/G) ACAGCTAAAG | 8 (6) | 2 (1) | Silent |
| .23 | 1539 | ATCTGGCTGC (T/C) GATCTGCTAT | 5 (4) | 5 (4) | 3' UT |
| 1555.5 | 424 | TATGGATGCC (A/G) AGCACCACAA | 17 (8) | 3 (1) | Lys -> Ser |
| .9 | 515 | GCCAGCACCA (G/C) CCAGGAGCTG | 17 (7) | 3 (3) | Ser -> Thr |
| .30 | 1088 | TCCTCGGCTG (C/A) GTTCAGTCTT | 2 (2) | 8 (5) | 3' UT |
| 1556.7 | 2037 | TGATCTTTCG (C/T) CCTGGTATGC | 5 (5) | 5 (3) | 3' UT |
| 1560.7 | 2335 | GCATTCAAGA (C/T) GGATACAGAG | 5 (5) | 2 (1) | Thr -> Met |
| 1561.1 | 90 | CTGTGCTGCC (C/T) GGCTCCCCCA | 2 (2) | 2 (2) | Silent |
| .5 | 373 | CCCTGACATC (A/G) TGGAGTTCTG | 2 (1) | 2 (2) | Met -> Val |
| .22 | 1250 | TGTTTCCTTT (T/G) GGGCTCAAAG | 8 (7) | 4 (4) | 3' UT |
| .23 | 1251 | GTTTCCTTTT (G/T) GGCTCAAAGC | 7 (6) | 4 (4) | 3' UT |
| 1562.14 | 540 | ATTGTGCGAC (C/T) TCCTACACCT | 21 (9) | 2 (1) | Silent |
| .30 | 799 | AGCCATGAGT (G/T) GGGCTGGGCC | 14 (7) | 3 (3) | Gly -> Trp |
| 1563.10 | 3076 | ACTCCCCTTC (A/G) TGAACCAGA | 2 (1) | 2 (2) | Met -> Val |
| 1564.7 | 339 | CTTTGGAAAG (T/C) GTGAAAGCTG | 15 (10) | 2 (1) | Silent |
| 1566.2 | 53 | GCAGGCACAG (T/C) GTCACCTTCG | 2 (1) | 2 (2) | 5' UT |
| .4 | 175 | TCCTGGCGGC (G/A) CCTCGTGTGC | 3 (1) | 4 (4) | Arg -> His |
| .10 | 791 | GCATGAATCC (C/T) GGCCAGGCG | 3 (1) | 4 (4) | Silent |
| .23 | 1741 | TGCACTCTGT (G/C) CTCGCCCAA | 3 (2) | 3 (2) | Cys -> Ser |
| .24 | 1742 | GCACTCTGTG (C/G) TCCGCCCAAG | 3 (2) | 3 (2) | Cys -> Trp |
| 1567.2 | 1083 | GGAATACTGG (G/A) AGAATCTTCG | 5 (3) | 2 (1) | Ser -> Lys |
| 1571.4 | 1480 | AGAGAAAATT (G/A) GGGAAAAGGT | 4 (4) | 3 (2) | 3' UT |
| .14 | 2087 | TCTGTCTGGT (G/A) TGGTATGAAT | 5 (5) | 4 (2) | 3' UT |
| 1576.13 | 1777 | CGCCCCCTCC (C/T) CCTCTGGCCC | 3 (2) | 2 (2) | 3' UT |
| .16 | 2031 | AATTGTACATC (C/T) CTGCATCC | 3 (2) | 2 (2) | 3' UT |
| 1577.10 | 3022 | TGCCGGCCGG (A/G) ACCCAGCGGC | 2 (2) | 6 (5) | Asn -> Asp |
| .15 | 3229 | CACACCACCG (T/C) CCTCTCGCT | 2 (2) | 5 (4) | 3' UT |
| .33 | 3859 | GGTAGCCACC (G/A) CCGGGGCACT | 18 (13) | 4 (3) | 3' UT |
| .38 | 3980 | CTGATGCATC (G/A) TTTTCTTTGC | 18 (14) | 4 (3) | 3' UT |
| .47 | 4049 | GCCAGGCCAT (G/T) GCCAAGGGGC | 7 (6) | 3 (3) | 3' UT |
| .50 | 4055 | CCATGGCCAA (G/A) GGGCCAGCTG | 5 (5) | 5 (5) | 3' UT |
| 1578.5 | 178 | TACTTCGACC (G/A) CAAAAGACGA | 7 (7) | 2 (2) | Arg -> His |
| .12 | 451 | CTTCCACCAC (C/T) AGTGTTCCAG | 8 (6) | 3 (2) | Pro -> Leu |

| Target ID | Loc'n | Sequence around [polymorphism] | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| .13 | 468 | CCAGATGCTT [C/T] TGACTAAGCT | 8 (6) | 3 (2) | Silent |
| .15 | 501 | TCAGAGAATT [G/C] TAAGTGCTCA | 5 (5) | 2 (2) | Val -> Leu |
| .17 | 551 | AAACAAATGT [C/T] AACATAATAA | 5 (5) | 4 (3) | 3' UT |
| .19 | 630 | GGGCAAATAT [G/C] CTGTGTATGA | 7 (6) | 2 (2) | 3' UT |
| .20 | 683 | CTTTGTGTAG [A/G] TCCATTTGTC | 9 (7) | 2 (2) | 3' UT |
| .25 | 2725 | AGGTGAGAAC [A/G] AAAAAACCCC | 6 (5) | 3 (3) | 3' UT |
| 1579.15 | 1735 | GCTGCAGCGG [C/T] TGGCAGACGG | 17 (12) | 2 (2) | Silent |
| .19 | 1881 | GGATCCGAGA [G/A] GGCATGGCCG | 14 (12) | 5 (5) | Ser -> Glu |
| .26 | 2010 | GAATACTCCC [G/C] GCCAGGGCCT | 12 (10) | 17 (10) | 3' UT |
| 1581.2 | 1897 | CCGCTAAAT [G/A] AGAATAAGGT | 3 (3) | 5 (4) | Met -> Ile |
| .5 | 2232 | TGAATGTAAC [T/C] GCTTTAAGAA | 3 (3) | 5 (5) | 3' UT |
| 1583.7 | 1482 | AAGACACAGA [A/T] GGAGGGCCCA | 5 (5) | 3 (2) | Glu -> Asp |
| .11 | 1772 | GCTTTTAATA [G/C] TGTCATAAAG | 3 (3) | 2 (2) | 3' UT |
| 1584.18 | 576 | CGCCCTCACA [G/A] CCTCCTTCTG | 2 (2) | 2 (2) | Silent |
| .34 | 1098 | ATATGGATGG [C/T] GGTACCTTCA | 3 (3) | 2 (2) | Ala -> Val |
| .46 | 1708 | GAGAAACCCC [C/T] GGGGACCATG | 3 (3) | 2 (2) | 3' UT |
| .50 | 1848 | GAGGGATTGA [G/A] CACAGGCACA | 2 (2) | 6 (6) | 3' UT |
| .51 | 1857 | AGCACAGGCA [C/A] AGAGGTGCTG | 2 (2) | 6 (6) | 3' UT |
| 1587.11 | 1330 | GCCTGCGTGG [G/C] AACTCATGCA | 7 (2) | 11 (10) | Glu -> Gln |
| .12 | 1356 | TCCAGAACCC [C/T] GACTTCCCAC | 18 (14) | 2 (2) | Silent |
| 1588.26 | 1956 | TTGTACACAA [T/C] CTCATTTTCAT | 7 (6) | 4 (3) | 3' UT |
| 1590.2 | 172 | TGCACGCAGC [C/A] ATGGCTGACA | 6 (3) | 2 (2) | Silent |
| .7 | 547 | CGCTGGATAA [C/T] GCCTACATGG | 8 (4) | 2 (2) | Silent |
| .9 | 850 | TCATCCGCAA [G/A] GCATCTGATG | 4 (2) | 2 (2) | Silent |
| .33 | 2139 | AGCCGACTCT [G/T] GCCCTGGCCC | 14 (9) | 4 (4) | 3' UT |
| 1594.10 | 1730 | ACCCAGTGG [G/A] AACTGTGCAA | 6 (5) | 2 (2) | 3' UT |
| .13 | 1975 | GAAACTAACT [C/T] GGTGGCCCCA | 6 (5) | 9 (6) | 3' UT |
| .14 | 1985 | CGGTGGCCCC [A/G] ACAGGTCTTC | 6 (5) | 9 (6) | 3' UT |
| 1596.3 | 1773 | TGATGTGGTA [C/T] GTCCTCCAC | 10 (7) | 3 (2) | 3' UT |
| .6 | 1844 | GTATTCACCA [A/C] GCATTTTAGG | 10 (8) | 4 (3) | 3' UT |
| .11 | 1899 | GCATTACAA [G/A] GCACTGCCAA | 17 (12) | 3 (3) | 3' UT |
| .12 | 1900 | CATTTACAAG [G/T] CACTGCCAAA | 19 (12) | 2 (2) | 3' UT |
| .16 | 1949 | AGAGGACCTG [C/T] GGGCTTAGAT | 24 (16) | 2 (1) | 3' UT |
| 1598.3 | 2042 | ATGCCTAAGA [C/A] CAACTGCGTT | 2 (2) | 3 (1) | 3' UT |
| 1603.5 | 592 | TCTGTGGCAC [T/C] GATATGACCA | 2 (2) | 2 (2) | 5' UT |
| .16 | 2566 | TGAAACTGAG [G/C] CCCATCCTCA | 17 (12) | 2 (2) | Arg -> Ser |
| .18 | 2662 | CGGGGAAGC [T/G] GCCGTCTAAA | 13 (11) | 3 (3) | Silent |
| .28 | 2953 | TTAGAATTTT [C/T] CTAAAAATAA | 26 (18) | 2 (1) | 3' UT |
| 1605.14 | 2879 | AACACGGCCC [T/C] GCTGTGCTG | 2 (2) | 2 (1) | Leu -> Pro |
| .30 | 4011 | AATTTAAAGT [A/C] TTCTCCTCCC | 4 (2) | 6 (6) | 3' UT |
| 1607.13 | 2354 | CTTTCTCTGG [C/T] CCTGTCCATG | 9 (8) | 2 (2) | 3' UT |
| 1608.3 | 2120 | CAGCCGCCAT [T/C] TGCAAGGAAG | 2 (2) | 2 (2) | 3' UT |
| .11 | 2552 | CAAAAGATGA [G/T] TCCTTGCTTC | 16 (9) | 4 (3) | 3' UT |
| .17 | 2733 | TCCTAAGCAG [T/C] CCTGGCTTTT | 25 (11) | 3 (3) | 3' UT |
| .01 | 2091 | CTCCTTCCAA [C/T] CCCACTCCCC | 65 (36) | 7 (7) | 3' UT |
| .02 | 2120 | CAGCCGCCAT [T/C] TGCAAGGAAG | 25 (18) | 47 (40) | 3' UT |
| .04 | 2578 | GAAATAAAAG [T/G] AGCCAGCTG | 26 (19) | 46 (29) | 3' UT |
| .05 | 969 | AACCTAGTGC [G/A] ACCAAGGGAA | 69 (36) | 3 (3) | Silent |

| | | | | | |
|---------|------|-----------------------------|---------|--------|--------|
| .06 | 2174 | CCTCTCCCAG [C/T] GGCCTCCCC | 71 (36) | 1 (1) | Silent |
| .07 | 2129 | TTTGCAAGGA [A/G] GGCCTAATCA | 66 (36) | 6 (6) | Silent |
| ----- | | | | | |
| 1611.20 | 1388 | AACACTGGTGCCAACCAA [G/A] AC | 3 (3) | 3 (3) | 3' UT |

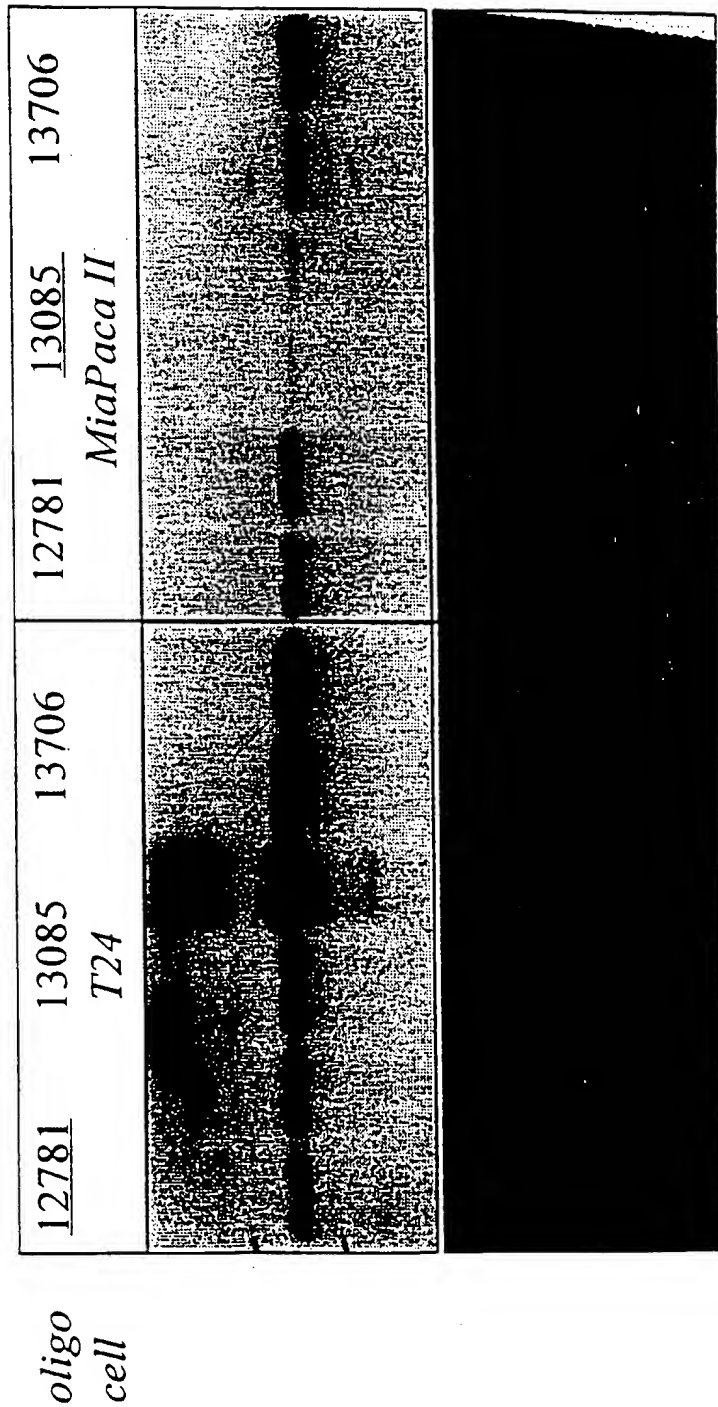
| Target ID | Loc'n | Sequence around (polymorphism) | # Varia 1 (Lib) | # Varia 2 (Lib) | Protein Change |
|-----------|-------|--------------------------------|-----------------|-----------------|----------------|
| 1613.2 | 350 | AGTGGCCATG (G/A) TTGGGTCAGC | 10 (7) | 3 (3) | Val -> Ile |
| .11 | 842 | TGATCATCAT (T/C) TCCTTGCGGA | 3 (3) | 6 (4) | 3' UT |
| 1614.5 | 1343 | CCTATCTGGA (T/C) ACATTGGGCC | 2 (2) | 3 (3) | Silent |
| .13 | 1841 | CGGCGGTGGA (G/A) GCTGAGCGCC | 10 (9) | 2 (2) | Ser -> Glu |
| .23 | 2158 | TTTTTTTTT (T/A) AAAAAAGAAA | 7 (7) | 8 (5) | 3' UT |
| .28 | 2261 | CTGAAGTCTA (G/A) GATATTTTTC | 5 (5) | 2 (2) | 3' UT |
| 1615.25 | 2113 | CCTGGCCATC (T/C) TGGGCAGTGT | 16 (11) | 7 (5) | Silent |

Fig. 9



Variance Specific Inhibition of mRNA levels by Oligonucleotides Against RPA1

Fig. 10



T24 Cells

Mia Paca II Cells

Oligo:

ISIS 13706

ISIS 12781

Varia 13085

Northern .

match

ISIS 13706

ISIS 12781

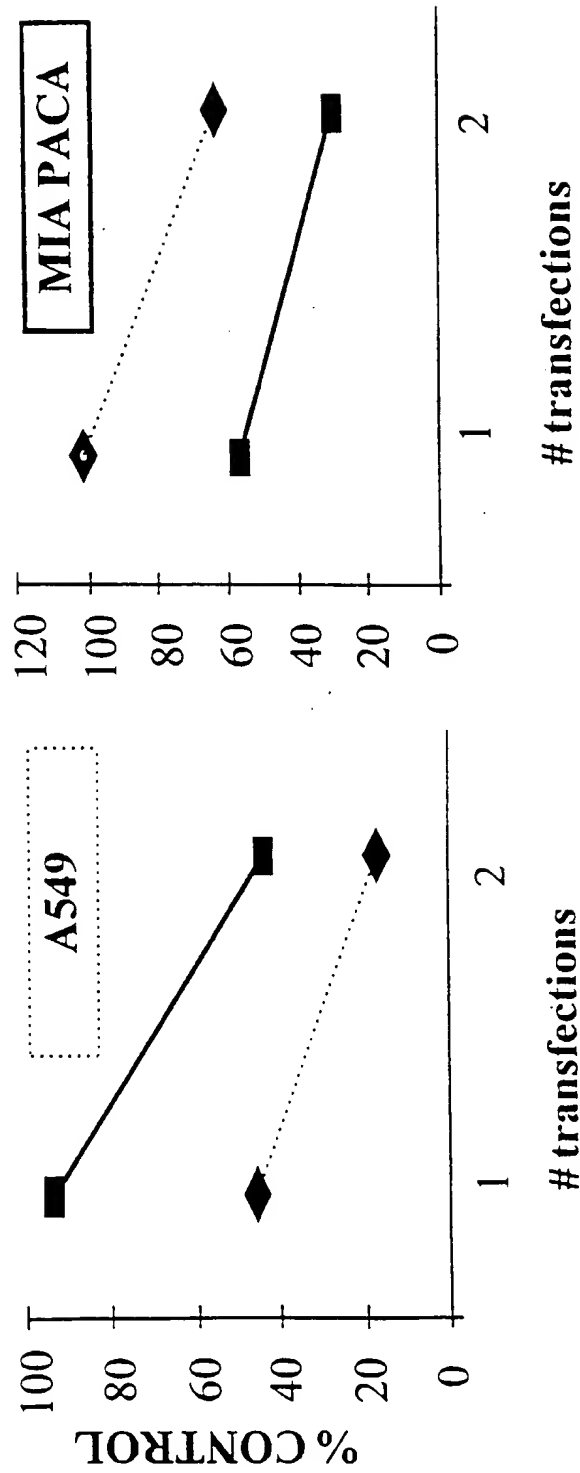
Varia 13085

match

RNA

$F_{15, 11}$

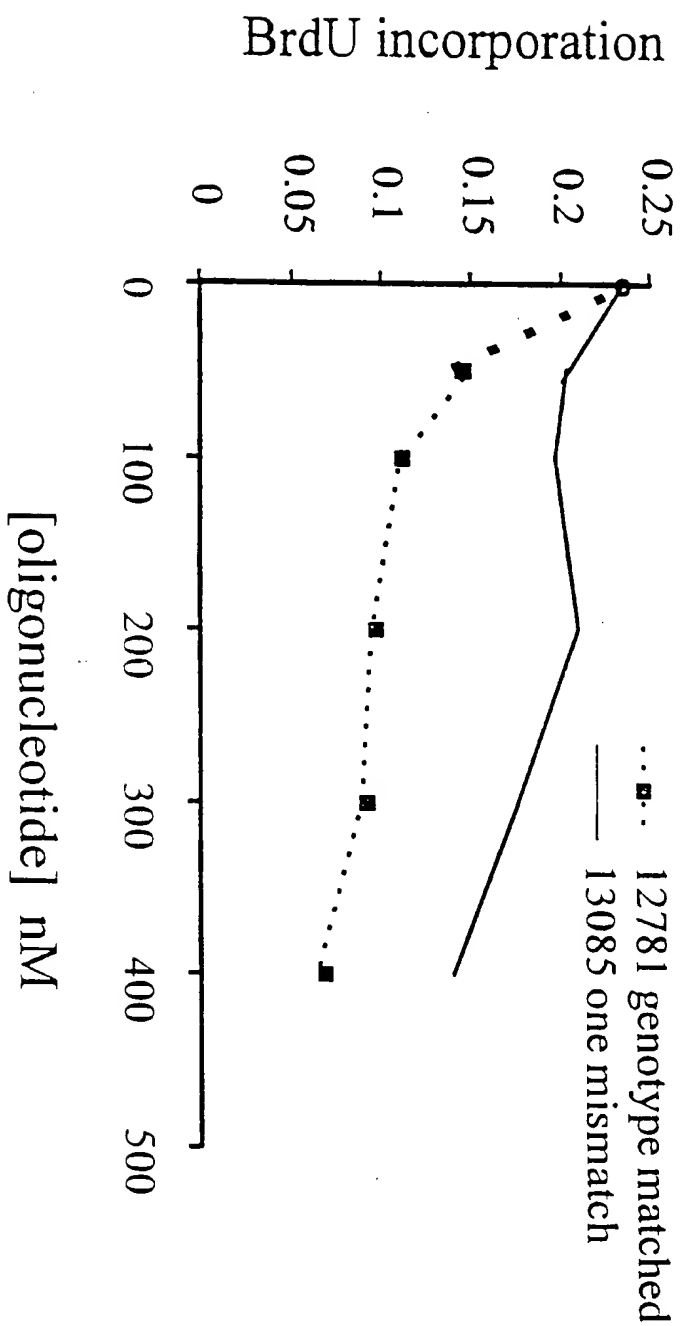
Fig. 12



12781
13085 —

Variance Specific Inhibition of A549 Cell Proliferation by Oligonucleotides Against RPA1

Fig. 13



Variance Specific Cell Killing of A549 Cells by Oligonucleotides Against RPA1

Fig. 14

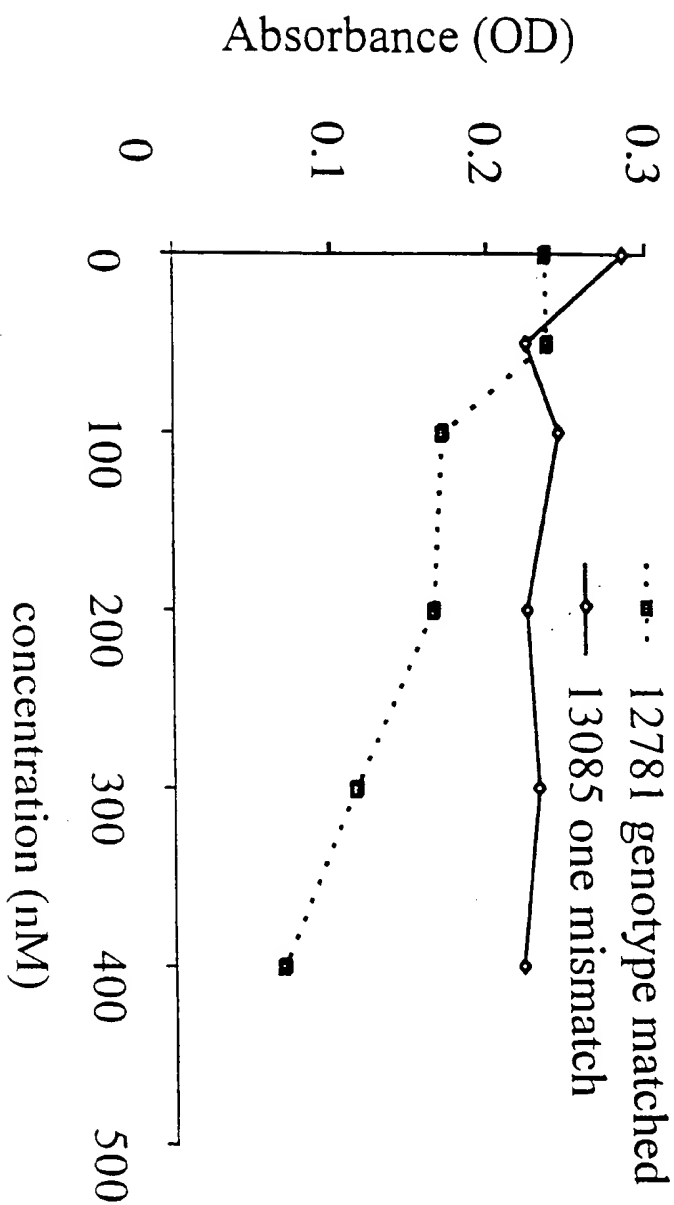
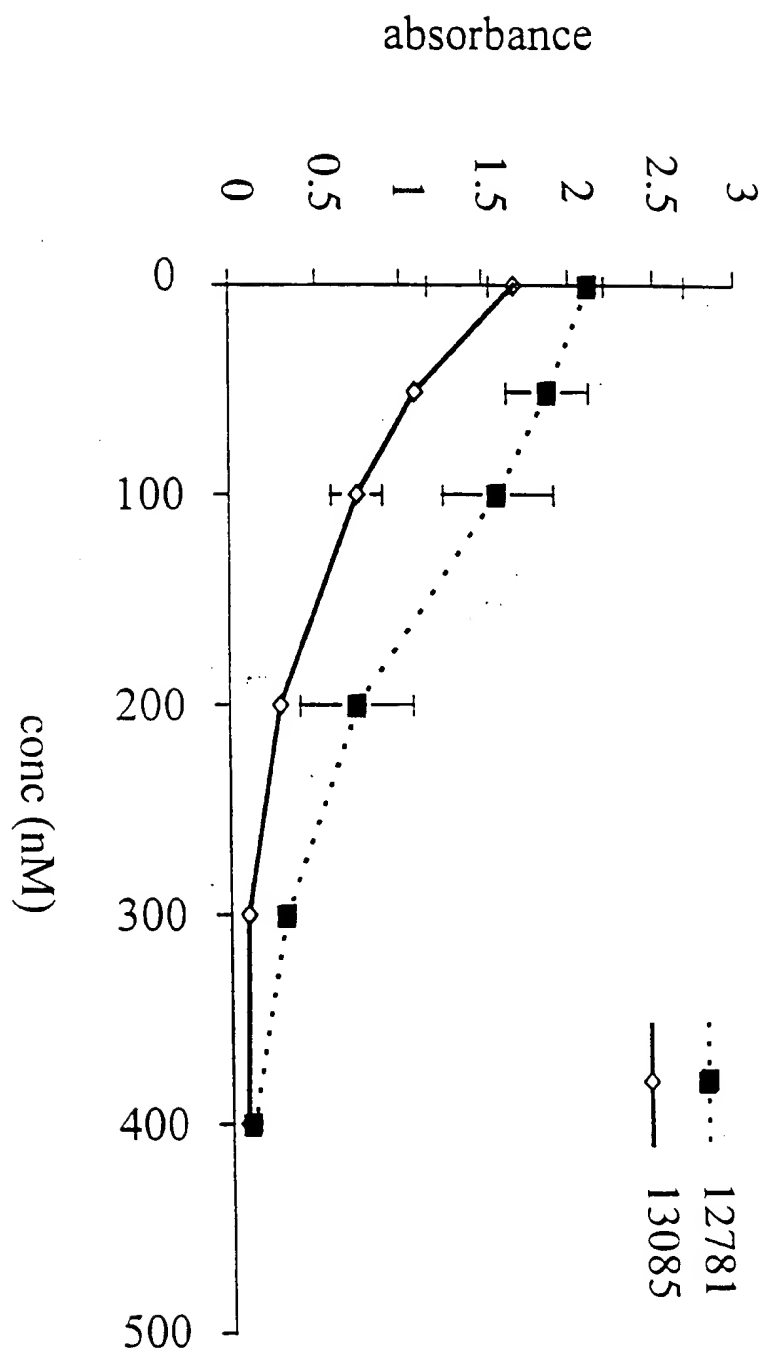


Fig. 15

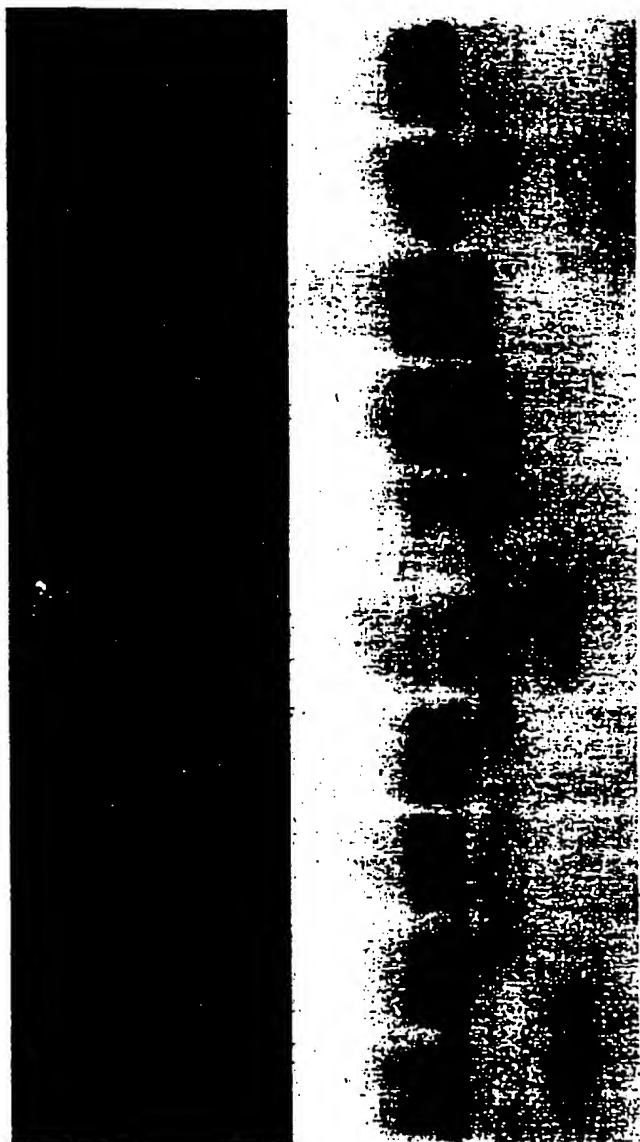


confidential

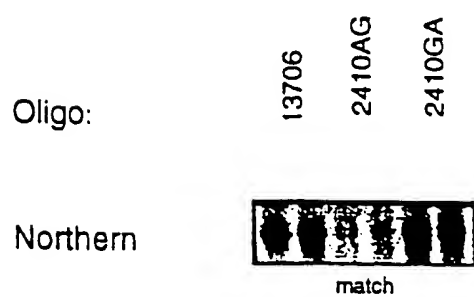
Suppression of Ribonucleotide Reductase mRNA

RR1030 RR1031 RR2410ga RR2410ag 13704

Fig. 16



MDA-MB 468 Cells



RNA

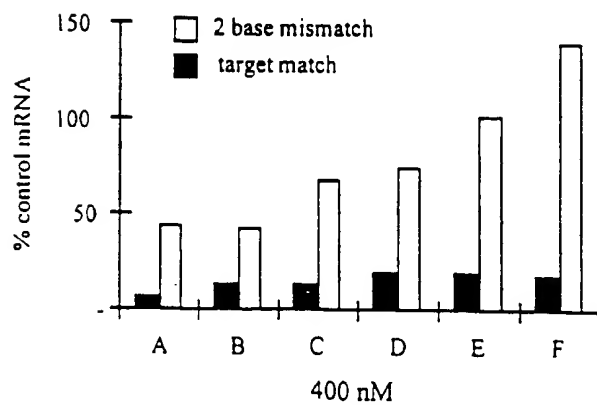


Fig. 17

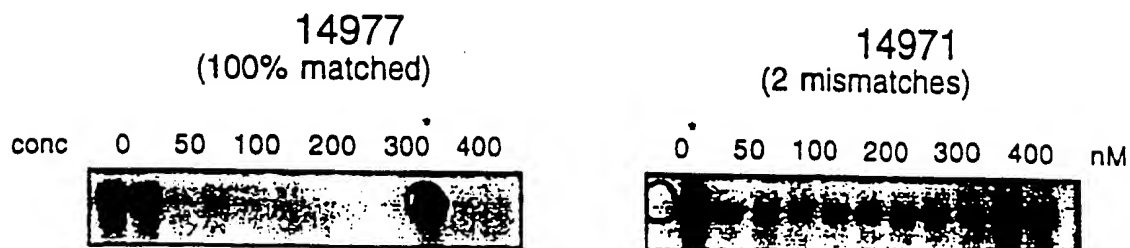
Fig. 18

Research Collaboration

| | |
|---|-----------------------------|
| | * * |
| A | ACAGCCACTTATGTCATGGT |
| B | ACAGCCACTTATGTCATGGT |
| C | <u>ACAGCCACTTATGTCATGGT</u> |
| D | CACTTATGTCATGGTATTCA |
| E | CACTTATGTCATGGTATTCA |
| F | <u>CACTTATGTCATGGTATTCA</u> |

Improved Allele-Specificity with
Advanced Chemistry

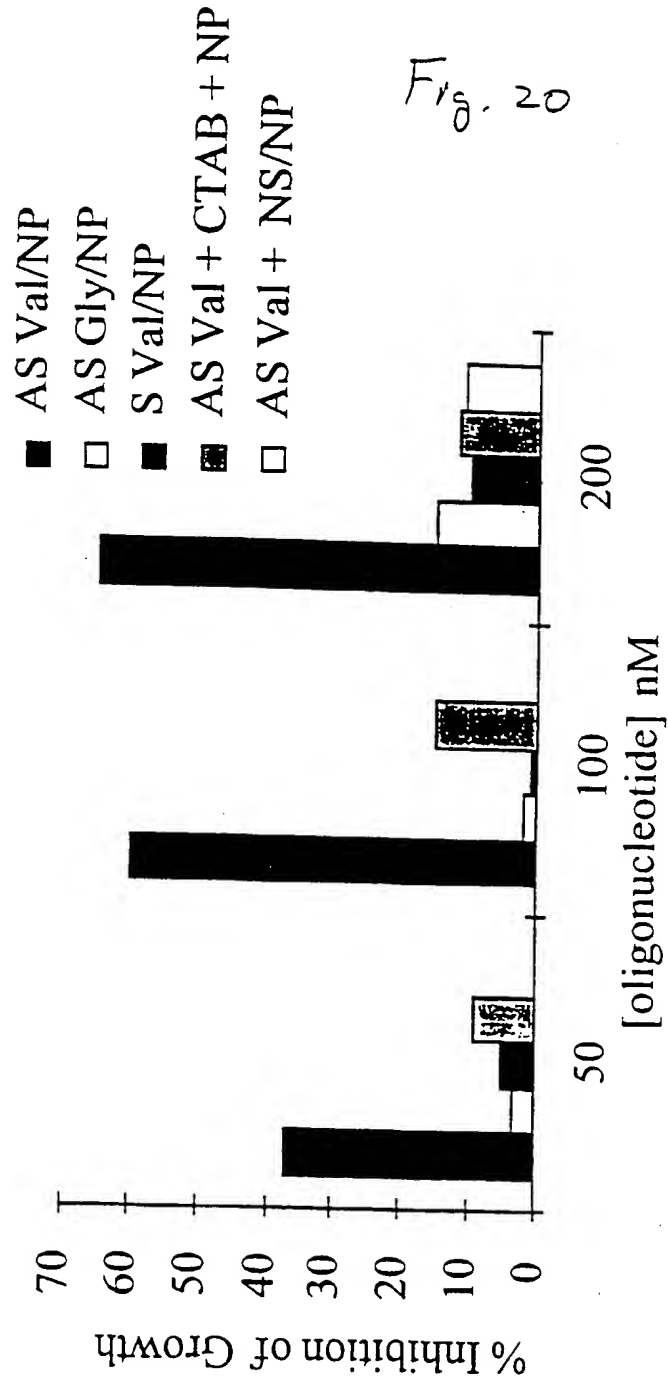
Effect of Antisense Oligomers on Glutamyl-
prolyl-tRNA Synthetase (EPRS) mRNA levels
(duplicates)



*circled samples were switched
when loaded on to the gel

Fig. 19

Example: Allele-Specific Inhibition of *Ras*



Schwab et al., 1994



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

| | | |
|--|-----------|--|
| (51) International Patent Classification ⁶ : C12Q 1/00, C07K 14/00, A61K 35/00, C12N 15/00 | A3 | (11) International Publication Number: WO 98/41648 (43) International Publication Date: 24 September 1998 (24.09.98) |
| (21) International Application Number: PCT/US98/05419 (22) International Filing Date: 19 March 1998 (19.03.98) (30) Priority Data: 60/041,057 20 March 1997 (20.03.97) US (71) Applicant (for all designated States except US): VARIAGEN-ICS, INC. [US/US]; One Kendall Square, Building 400, Cambridge, MA 02139-1562 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): HOUSMAN, David [US/US]; 64 Homer Street, Newton, MA 02159 (US). LEDLEY, Fred, D. [US/US]; 433 Grove Street, Needham, MA 02192 (US). STANTON, Vincent, P., Jr. [US/US]; 32 Royal Road, Belmont, MA 02178 (US). (74) Agents: WARBURG, Richard, J. et al.; Lyon & Lyon LLP, Suite 4700, 633 West Fifth Street, Los Angeles, CA 90071-2066 (US). | | (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 29 April 1999 (29.04.99) |
| (54) Title: TARGET GENES FOR ALLELE-SPECIFIC DRUGS (57) Abstract This disclosure concerns genetic targets which have been found to be useful for allele specific anti-tumor therapy. The strategy for such therapy involves the steps of: (1) identification of alternative alleles of genes coding for proteins essential for cell viability or cell growth and the loss of one of these alleles in cancer cells due to loss of heterozygosity (LOH) and (2) the development of inhibitors with high specificity for the single remaining alternative allele of the essential gene retained by the tumor cell after LOH. Particular categories of appropriate target genes are described, along with specific exemplary genes within those categories and methods of using such target genes. | | |

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| EE | Estonia | | | | | | |

INTERNATIONAL SEARCH REPORT

| | | |
|--|--|---|
| A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12Q1/00 C07K14/00 A61K35/00 C12N15/00 | | International Application No PCT/US 98/05419 |
| According to International Patent Classification (IPC) or to both national classification and IPC | | |
| B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12Q | | |
| Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched | | |
| Electronic data base consulted during the international search (name of data base and, where practical, search terms used) | | |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT | | |
| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| X | WO 95 03335 A (HOUSMAN DAVID E ;K O TECHNOLOGY INC (US)) 2 February 1995 cited in the application see the whole document --- | 1,13,21, 29,37, 38,53, 54,69, 77-79, 101,109 |
| A | WO 97 04087 A (KRUPP GUIDO ;MARGET MATTHIAS (DE); WESTPHAL ECKHARD (DE); MUELLER) 6 February 1997 --- | |
| A | WO 94 11494 A (UNIV JEFFERSON ;PROCKOP DARWIN (US); COLIGE ALAIN (BE); BASERGA RE) 26 May 1994 --- | |
| A | US 5 491 064 A (LICHY JACK H ET AL) 13 February 1996 --- | |
| -/- | | |
| <input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex. | | |
| * Special categories of cited documents : <div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <p>*A* document defining the general state of the art which is not considered to be of particular relevance</p> <p>*E* earlier document but published on or after the international filing date</p> <p>*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>*O* document referring to an oral disclosure, use, exhibition or other means</p> <p>*P* document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="width: 45%;"> <p>*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>*Z* document member of the same patent family</p> </div> </div> | | |
| Date of the actual completion of the international search <div style="text-align: center; font-size: 1.2em;">9 December 1998</div> | | Date of mailing of the international search report <div style="text-align: center; font-size: 1.2em;">16. 03. 1999</div> |
| Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016 | | Authorized officer <div style="text-align: center; font-size: 1.2em;">MOLINA GALAN E.</div> |

INTERNATIONAL SEARCH REPORT

Intern. Application No

PCT/US 98/05419

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|---|
| P,X | <p>WO 97 32024 A (TRINITY COLLEGE DUBLIN ;FARRAR GWENYTH JANE (IE); HUMPHRIES PETER) 4 September 1997</p> <p>see the whole document -----</p> | <p>1,13,21, 29,37, 38,53, 54,69, 77-79, 101,109</p> |

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/05419

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 37, 53, 69 and 109 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1, 13, 21, 29, 37, 38, 53, 54, 69, 77-79, 101 and 109

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1, 13, 21, 29, 37, 38, 53, 54, 69, 77-79,
101 and 109

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required for cell proliferation wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

2. Claims: 2, 14, 22, 30, 39, 40, 55, 56, 70, 80-82,
102 and 110

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain inorganic ions and vitamins at levels compatible with cell growth or survival wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

3. Claims: 3, 15, 23, 31, 41, 42, 57, 58, 71, 83-85,
103 and 111

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain organic compounds at levels compatible with cell growth or survival wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

4. Claims: 4, 16, 24, 32, 43, 44, 59, 60, 72, 86-88,
104 and 112

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain cellular proteins at levels compatible with cell growth or survival wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors

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and pharmaceutical compositions comprising them.

5. Claims: 5, 17, 25, 33, 45, 46, 61, 62, 73, 89-91,
105 and 113

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain cellular nucleotides at levels compatible with cell growth or survival wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

6. Claims: 6, 18, 26, 34, 47, 48, 63, 64, 74, 92-94,
106 and 114

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and encoding a product required to maintain the integrity and function of cellular and subcellular structures wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

7. Claims: 7-10, 19, 27, 35, 49, 50, 65, 66, 75, 95-97 and 107

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability and being located on a high frequency loss of heterozygosity chromosomal arm region, wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

8. Claims: 11, 12, 20, 28, 36, 51, 52, 67, 68, 76,
98-100 and 108

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene vital for cell growth or viability having at least two sequence variances which occur at frequencies such that at least 10% of a population is heterozygous for that gene and wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using

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such inhibitors and pharmaceutical compositions comprising them.

9. Claims: 115-129

Inhibitors (in particular nucleic acids) targeting at least one but less than all alleles of a gene conditionally vital for cell growth or viability wherein cells not targeted by the inhibitor have at least one alternative variant allele, methods for identifying, producing and using such inhibitors and pharmaceutical compositions comprising them.

10. Claims: 131-146

Methods using inhibitors targeting at least one but less than all alleles of a gene vital for cell growth or viability wherein cells not targeted by the inhibitor have at least one alternative variant allele related to transplantation and engraftment.

11. Claims: 147-150

Methods for separating a cell from a mixture using allele specific binding compounds targeting at least one but less than all alleles of a gene wherein cells not targeted by the compound have at least one alternative variant allele.

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